



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 06:41 AM UTC

PDB ID : 6WNT / pdb_00006wnt
EMDB ID : EMD-21856
Title : 50S ribosomal subunit without free 5S rRNA and perturbed PTC
Authors : Loveland, A.B.; Korostelev, A.A.; Mankin, A.S.; Huang, S.; Aleksashin, N.A.; Klepacki, D.; Reier, K.; Kefi, A.; Szal, A.; Remme, J.; Jaeger, L.; Vazquez-Laslop, N.
Deposited on : 2020-04-23
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

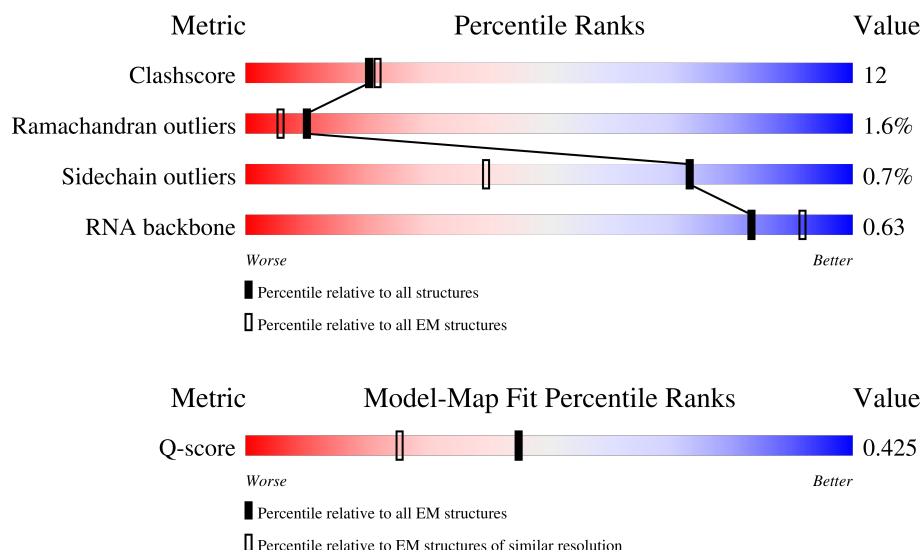
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



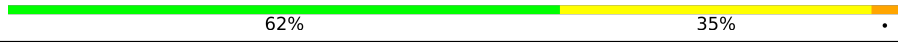
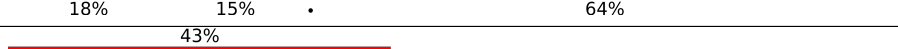
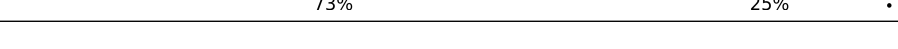
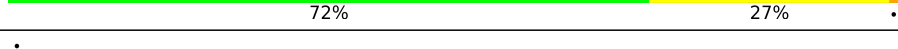
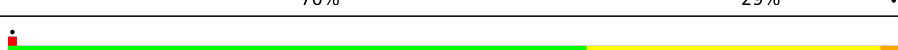
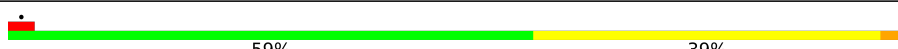
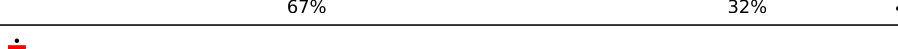
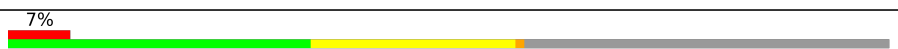
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	b	271	
2	c	209	
3	d	201	

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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	n	120	
13	o	116	
14	p	114	
15	q	117	
16	r	103	
17	s	110	
18	t	93	
19	u	102	
20	v	94	
21	w	75	
22	x	77	
23	y	63	
24	z	58	
25	A	70	
26	B	56	
27	D	46	
28	E	64	

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Mol	Chain	Length	Quality of chain
29	F	38	76%18%5%
30	a	223	42%39%19%40%
31	4	3031	51%42%6%

2 Entry composition

There are 31 unique types of molecules in this entry. The entry contains 91164 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	209	Total	C	N	O	S	0	0
			1564	979	288	293	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	201	Total	C	N	O	S	0	0
			1551	974	283	289	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	176	Total	C	N	O	S	0	0
			1322	832	243	245	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	53	Total	C	N	O	S	0	0
			409	261	74	73	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	141	Total	C	N	O	S	0	0
			1031	651	179	195	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	j	142	Total	C	N	O	S	0	0
			1128	714	212	198	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	143	Total	C	N	O	S	0	0
			1044	649	206	188	1		

- Molecule 12 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	n	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	o	116	Total	C	N	O	0	0
			891	552	178	161		

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	p	114	Total	C	N	O	S	0	0
			916	574	179	162	1		

- Molecule 15 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	q	117	Total	C	N	O	S	0	0
			946	604	192	150			

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	r	103	Total	C	N	O	S	0	0
			815	516	153	144	2		

- Molecule 17 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	s	110	Total	C	N	O	S	0	0
			856	532	166	155	3		

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	t	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	u	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 20 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	v	94	Total	C	N	O	S	0	0
			752	479	137	133	3		

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	w	75	Total	C	N	O	S	0	0
			574	356	116	101	1		

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	x	77	Total	C	N	O	S	0	0
			624	388	129	105	2		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	y	63	Total	C	N	O	S	0	0
			508	313	99	94	2		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 25 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A	41	Total	C	N	O	S	0	0
			315	192	57	60	6		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B	56	Total	C	N	O	S	0	0
			443	269	94	79	1		

- Molecule 27 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	D	46	Total	C	N	O	S	0	0
			376	228	90	56	2		

- Molecule 28 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	E	64	Total	C	N	O	S	0	0
			503	323	105	73	2		

- Molecule 29 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	F	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 30 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

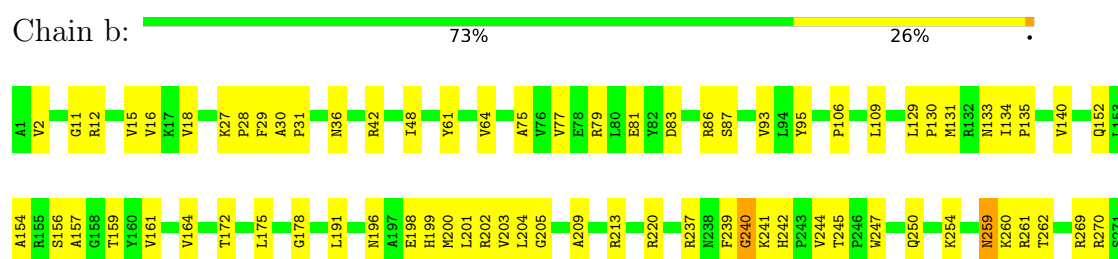
- Molecule 31 is a RNA chain called 23s-5s joint ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4	3025	Total	C	N	O	P	0	0
			64925	28962	11938	21001	3024		

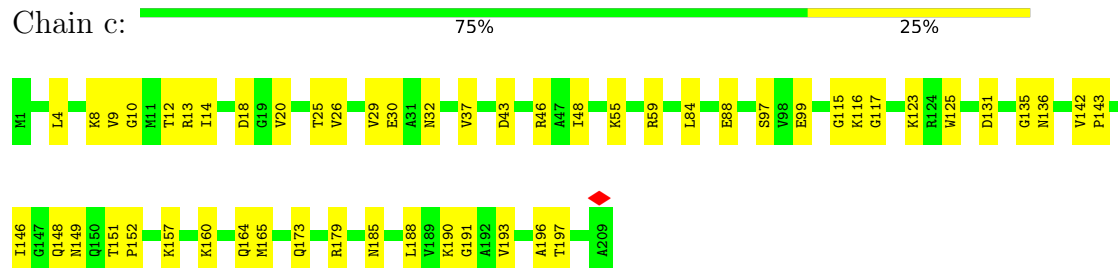
3 Residue-property plots [i](#)

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

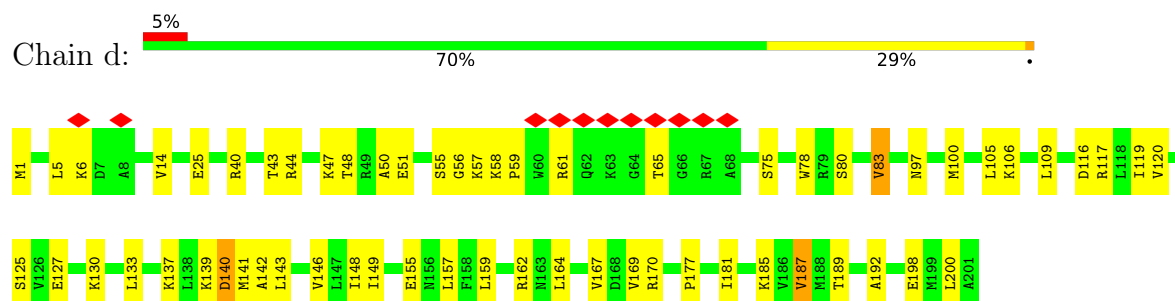
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

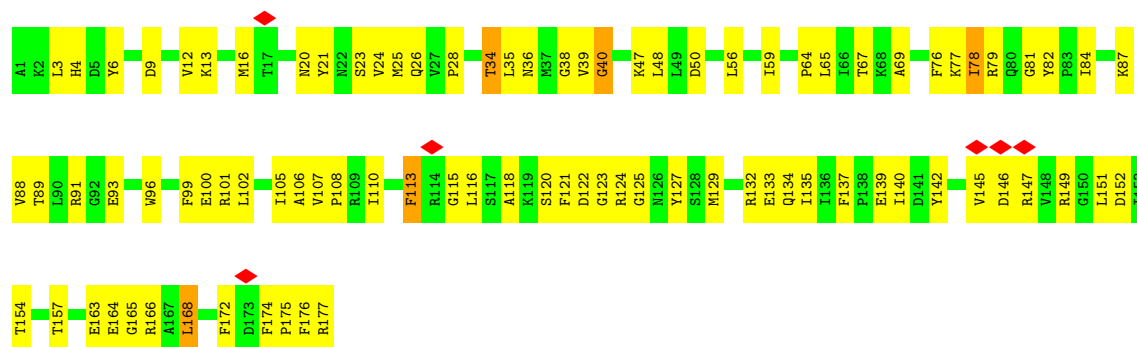


• Molecule 3: 50S ribosomal protein L4



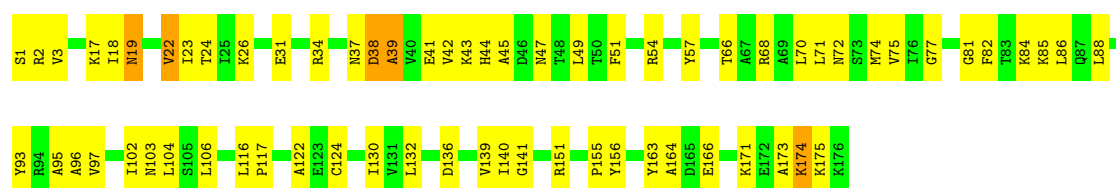
• Molecule 4: 50S ribosomal protein L5





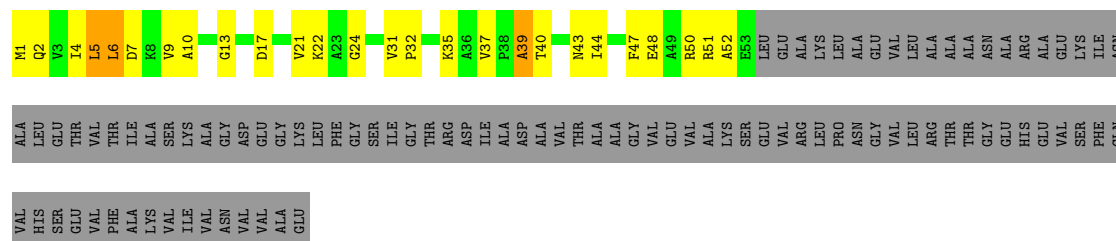
• Molecule 5: 50S ribosomal protein L6

Chain f: 62% 35% .



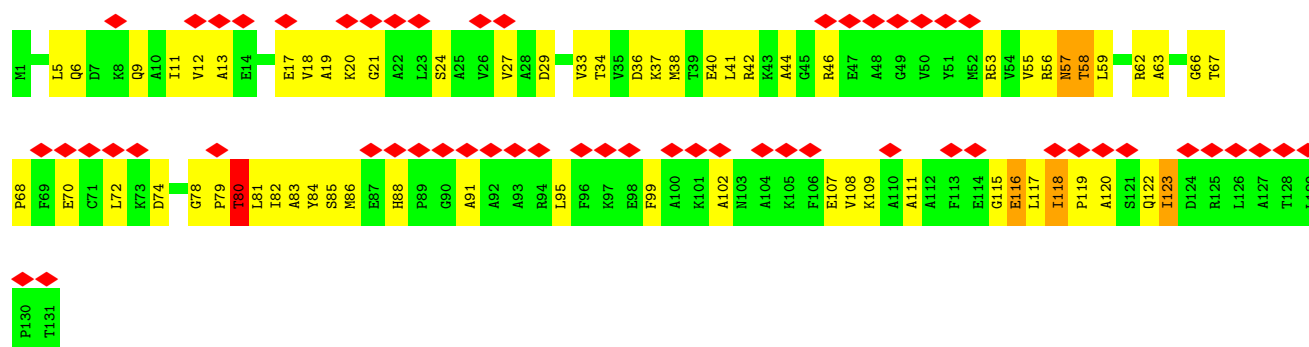
• Molecule 6: 50S ribosomal protein L9

Chain g: 18% 15% . 64%

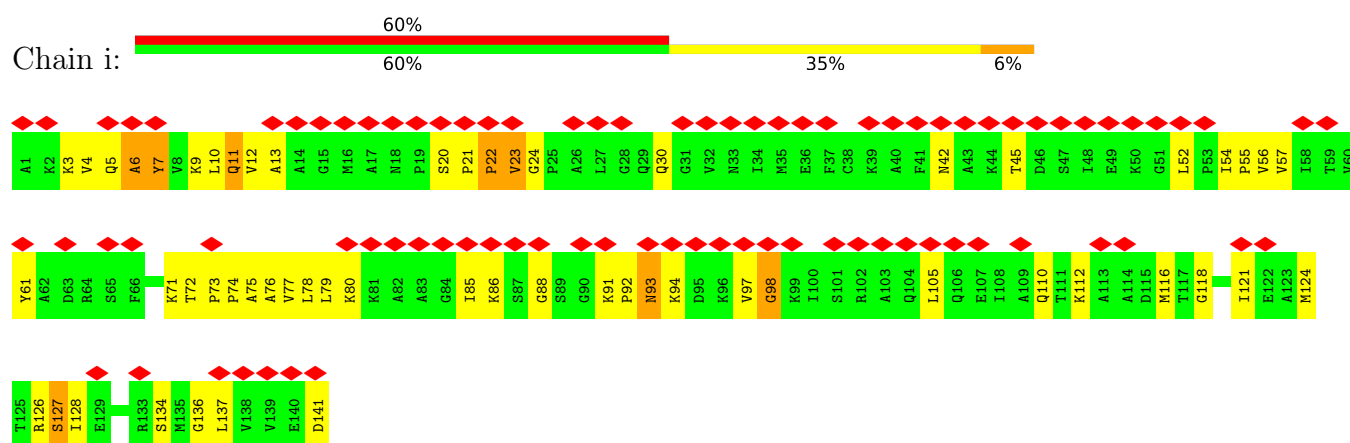


• Molecule 7: 50S ribosomal protein L10

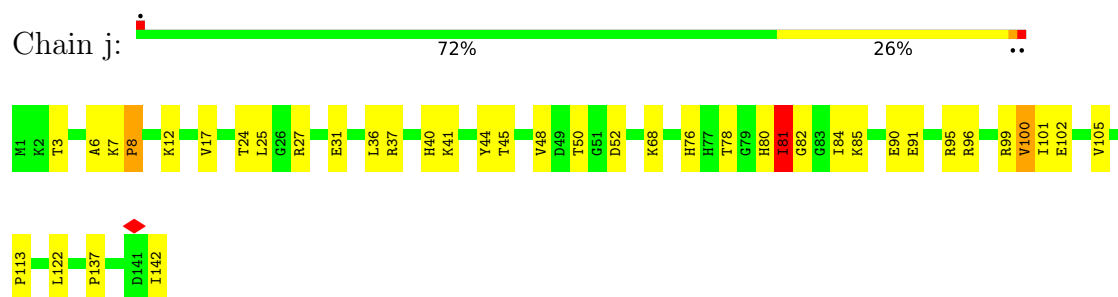
Chain h: 43% 51% 44% . .



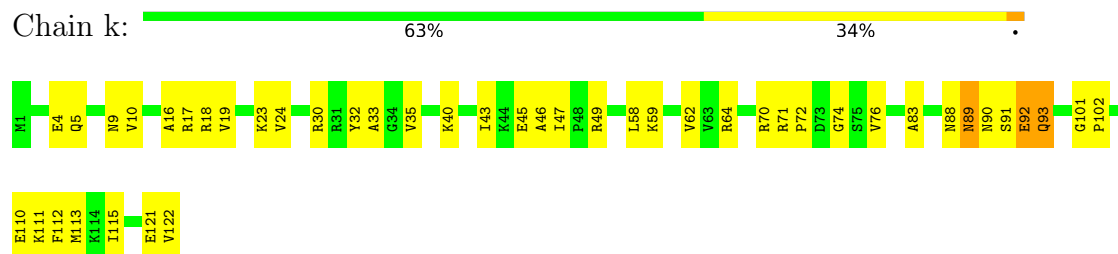
• Molecule 8: 50S ribosomal protein L11



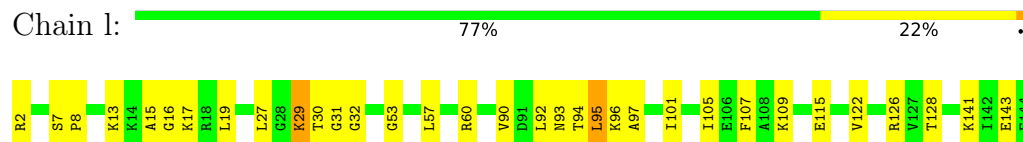
- Molecule 9: 50S ribosomal protein L13



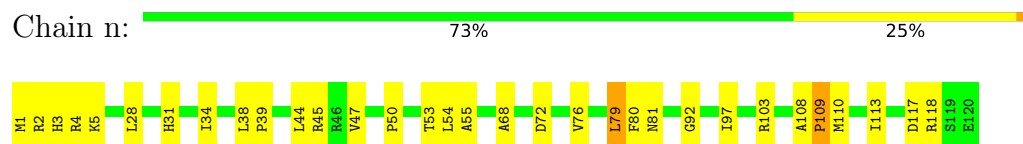
- Molecule 10: 50S ribosomal protein L14



- Molecule 11: 50S ribosomal protein L15

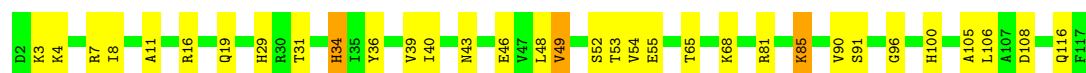


- Molecule 12: 50S ribosomal protein L17



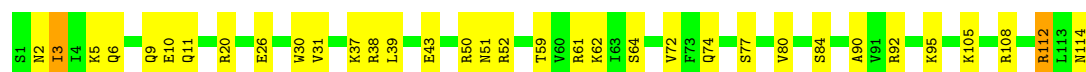
- Molecule 13: 50S ribosomal protein L18

Chain o:  72% 26%



- Molecule 14: 50S ribosomal protein L19

Chain p:  70% 28%



- Molecule 15: 50S ribosomal protein L20

Chain q:  83% 16%



- Molecule 16: 50S ribosomal protein L21

Chain r:  76% 21%



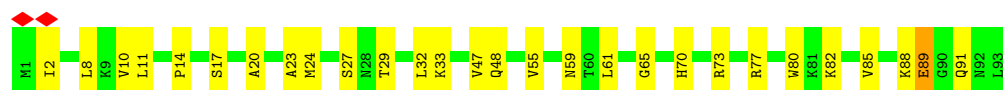
- Molecule 17: 50S ribosomal protein L22

Chain s:  72% 27%



- Molecule 18: 50S ribosomal protein L23

Chain t:  70% 29%

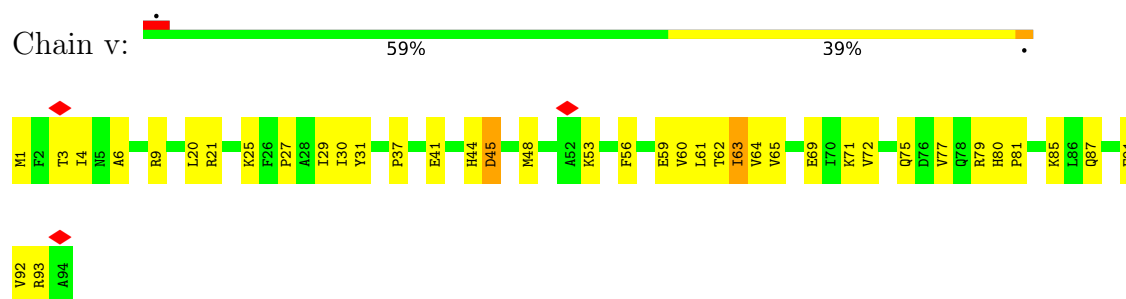


- Molecule 19: 50S ribosomal protein L24

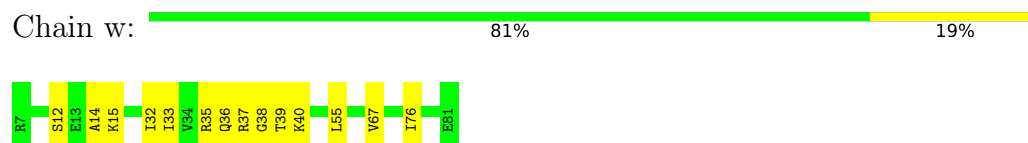
Chain u:  65% 33%



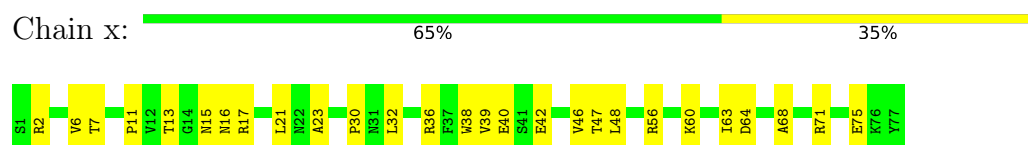
- Molecule 20: 50S ribosomal protein L25



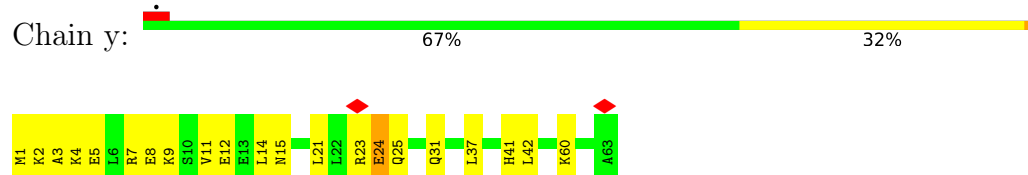
- Molecule 21: 50S ribosomal protein L27



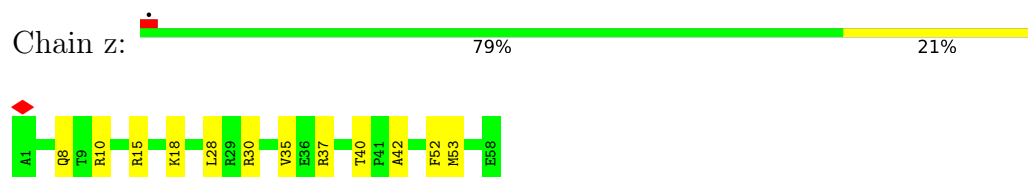
- Molecule 22: 50S ribosomal protein L28



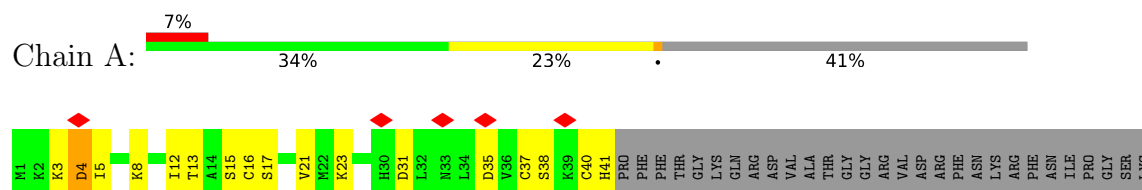
- Molecule 23: 50S ribosomal protein L29



- Molecule 24: 50S ribosomal protein L30

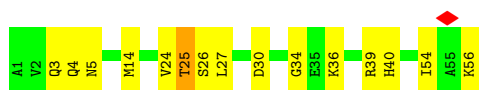


- Molecule 25: 50S ribosomal protein L31



- Molecule 26: 50S ribosomal protein L32

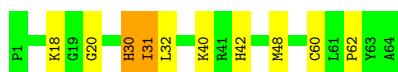
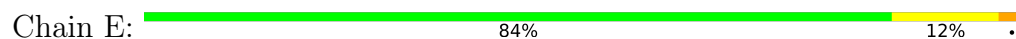




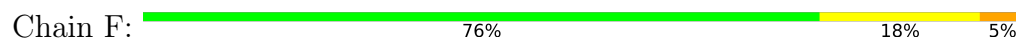
- Molecule 27: 50S ribosomal protein L34



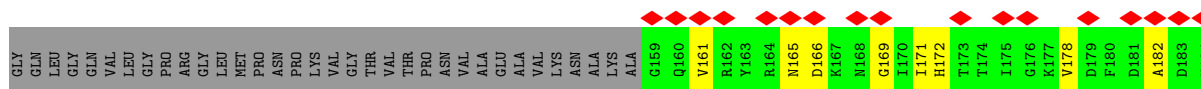
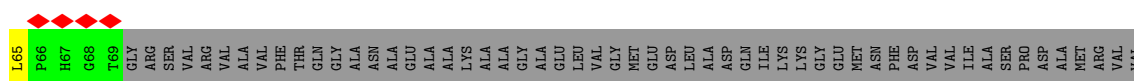
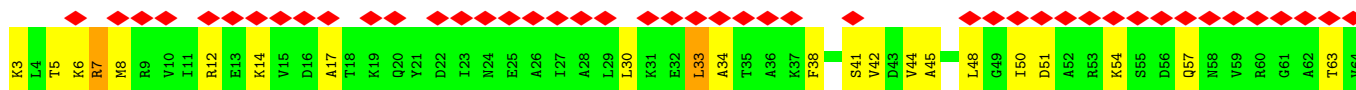
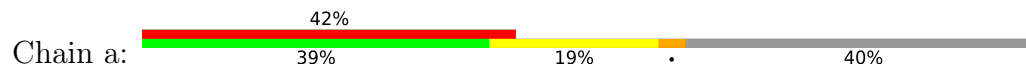
- Molecule 28: 50S ribosomal protein L35



- Molecule 29: 50S ribosomal protein L36



- Molecule 30: 50S ribosomal protein L1



- Molecule 31: 23s-5s joint ribosomal RNA



G1380	A1275	C1204	G1127	U1045	G954	C876	G797	U709	A609	G520	A415	A320	G215	U120
A1381	U1276	A1205	G1131	A1046	U955	A877	G798	U710	A613	U521	U416	U321	A216	G121
G1384	C1277	G1206	U1132	G1047	G956	A878		U714	A614	C522	U419	C322	A217	A127
G1394	C1278	C1207	G1133	G1048	U958	A879	A804	G715	U615	C523	C420	A324	A221	U133
U1395	A1279	A1208	G1136	A1050	U959	G882	C806	A716		C527	C421	G327	A222	G134
C1281	C1280	U1209	C1137	A1051	A960	G883	U810	C717	G622	A528	G424	U328	C225	
A1284	U1210	C961	G1138	C1052	G962	C885	U811	A718	C623	A529		G329	A226	U138
A1396	U1211	G963	G1139	U1053	U963	C886	C812	C719	A627	G530	C435	U330	A227	U139
C1398	A1212	U964	U1140	G1054	C963	U887	U813	A720	G628	A531	C436	C331	C228	C140
G1399	C1213	U965	U1141	G1055	C964	U888	C814	A721		A532		G332	C229	G141
A1400	G1215	C966	G1142	U1056		C889	C815	A722	A637	G533	G438	C335	G230	
G1407	A1216	G968	G1149	G1058	C968	C890	C816	G726	U638	U534	A439		G231	A149
C1417	C1217	G969	G1153	C1060	G970	G891	C817	A727	U639	G535	C440	A340	G232	U150
C1418	A1218	U970	U1153	A1061	G971	A892	G818	G728	C640	G536	U441	C341	U151	C151
C1419	G1219	C972	A1154	U1063	A972	C893	A819	G729		G537	G442		G242	A152
G1420	C1220	A973	A1155	C1064	A973	U894	U826	A730	A644	A538	A443	C353	G248	A155
C1425	G1221	G974	A1156	C1065	U975	U895	U827	G738	C645	G539	C444	U355	C249	A156
G1428	A1222	A976	G1157	U1066	A976	A896	U828	A739	U646	C544	C445	U356		
A1429	C1223	A979	G1158	G1067	A979	C897	U829		G649	G545	G446	C357	G254	A161
U1301	A1224	G980	G1159	C1068	A980	A898	G830	A743	C650	U546	U451	U358	A255	U162
U1302	U1225	A981	A1160	C1069	C982	A900	G831	U744	G651	A547		G359	C163	C164
A1303	A1226	C982	A1161	G1070	A983	C901	U832	G745	A654	G548	C456	U360	G266	
G1305	G1227	A983	G1162	C1071	C983	C902	A833	G746	U655	G549	A457	C361		
C1306	C1228	A984	U1163	A1081	C987	G903	G834	C747	A656	G458		A362	C275	A167
U1307	U1229	A988	G1164	G1082	A988	G904			G657		G467	G363	U276	G168
U1308	C1230	C995	G1168	C1085	C995	U905	U839	A752	U554	U554	U468	U369	G277	U170
C1309	A1231	A996	A1169	C1086	A996	U906	C840	A753	G555	G558	G469	U370	A278	U171
U1311	C1232	G997	G1170	G1087	G997	C907	U841	U754		U559		C371	A279	A172
U1312	U1233	C997	C1171	G1090	C997	C908	U842	G755	A668	C559	G473	G372	U280	
A1455	G1234	G997	C1172	U1091	A1001	A909	G843	A756	C669		G474	U373	C281	
A1456	C1235	A1001	C1173	G1092	A1001	A910	A844		A670	U562		U374	A282	A176
A1457	U1236	A1002	A1174	C1002	A1002	A911	A845	G757	C671	A563	G481	A374	G283	G177
C1458	C1237	A1009	G1175	U1093	A1009	C912	U846	G760	C672	U573	A482	G375	U284	
G1469	A1238	A1010	G1181	G1094	A1010	U913	U847	A761	A677	A574			U285	A181
U1472	U1241	C1101	A1182	A1100	U1012	A917	C848	U762		A575	C490	G381	U286	
C1473	C1242	C1102	G1184	C1102	C1013	A918	U849	G763	G682	A491	A492	A382	G287	C184
U1480	G1243	G1185	A1185	C1108	A1020	U929	U850	G765	U686	G578	G493	G386	A294	G189
A1481	C1248	U1186	U1186	G1109	G1021	U832	C851	U766		U580	G494	U387	G297	A190
A1482	U1249	G1187	G1187	G1110	G1022	A933	U852	U767	G680	C581	G495	C394	G298	A191
G1483	G1253	U1188	U1188	A1111	U1023	U934	G855	G768	C691	A582	G496	U395		C192
G1484	A1254	G1189	G1189	C1112	G1024	C935	G858	U769	C692	G585	G497	G396	G301	A196
C1485	U1255	G1190	G1190	C1113	G1025	A936	G859	G770	A693		A503	G400	C302	C197
G1486	G1256	C1191	G1191	U1114	G1026	C937	U860	G771		U588	A504	A401	G303	A198
A1487	C1257	C1192	C1192	C1115	U1028			G776	G696	U593	A505	A402	A197	C198
G1488	U1260	U1193	U1193	A1116	U1029	G940	G864	U779	G697	U594	A506	U403	U304	A199
G1489	A1261	U1194	U1194	C1117	G1030	A941	C865		C698	C595	A507	U404	A310	U200
A1493	C1263	A1195	A1195	A1118	U1031	G942	G869	A782	G699	G598	A508	G406	A311	C201
A1494	U1266	U1197	U1197	C1119	C1032	C946	U870	A783	U703	U598			G312	U202
A1495	G1267	A1198	A1198	U1121	G1038	A947	U871	G784	G704	A599	U511	G411	G313	A203
G1496	C1268	G1199	G1199	A1122	C1039	C948	U872	G785	A795	A603	G512	A412	G314	A207
A1501	U1269	C1200	C1200	A1123	G1043	C949	U873		A796	G518	G517	C413	G315	C208
G1506	A1270	A1201	A1201	A1125	A1043	G949	G874	A794	G795	G519	G518	A414	G316	C317
		C1202	C1202	C1126	G1044	G953	G875	C796	G708	A608			G317	A213
													G319	G214

C2640	U2551	G2458	A2394	G2314	G2248	C2171	G2073	A1994	A1912	A1818	C1692	U1604	U1507
C2641	C2555	G2459	A2395	U2315	G2249	C2172	U2074	G1995	A1913	C1819	C1693	U1605	A1511
C2642	C2556	G2460	A2396	U2316	U2250	C2173	C2075	G1996	A1914	C1820	C1694	G1610	C1514
C2643	C2557	U2462	A2397	U2317	G2251	G2174	G2076	C1997	C1918	A1829	A1697	U1613	C1515
C2644	A2558	G2463	A2400	U2322	G2252	C2175	U2083	C2002	G1919	C1831	A1698	U1614	G1516
C2645	A2563	G2464	U2401	U2323	A2254	G2176	G2089	C2003	G1920	C1832	A1700	U1615	
U2647	A2569	G2465	A2402	C2324	G2255	A2180	G2092	A2004	C1921	A1833	U1704	A1618	U1522
C2648	U2471	G2466	A2406	U2325	G2256	C2183	C2093	U2008	C1922	G1837	C1706	C1526	
C2649	U2472	A2467	A2407	A2326	U2258	C2184	C2094	C2009	C1923	G1838	U1705		
U2650	G2473	G2474	G2408	A2327	U2259	G2185	C2095	U2010	C1924	A1839	C1706		
G2651	A2474	G2475	G2409	U2328	U2260	A2186	A2098		G1925	A1719	U1719	U1533	
	A2576		A2409	G2329	U2261	G2187	U2099		G1926	C1720	C1627	U1534	
G2654	U2577		G2410	U2330	G2262	A2188	G2100	A2013	C1927				
C2655	A	C2478	G2411	U2331	G2263	G2189	G2101	A2018	C1928	U1853	C1723	C1542	
U2656	C	G2479	A2412	G2332	A2264	A2190	U2107	G2019	A1929	C1854	A1724	C1543	
G2657	A	A2480	C2413	A2333	G2265	C2191	C2108		G1934	C1855	A1632	G1544	
A2658	A	G2481	C2414	U2335	U2266	C2192	G2117	A2027	G1935	U1857	U1729	U1634	
A2659	G		A2415	C2336	G2267	C2193	G2118	A2028	A1936	C1858	U1730	C1635	A1547
G2660		C2487	A2416	G2337	U2267	C2194	U2119	A2029	A1937	U1859	U1731	A1636	A1548
A2661	C2584	G2488	U2419	U2338	G2268	G2197	U2120	C2033	A1938	C1860	A1736	A1637	C1556
A2662	U2585		G2420	A2339	G2269	A2198	U2121	G2034	G1939	U1864	A1737	G1638	G1557
	G2586	C2492	G2421	A2340	G2270	A2199	U2122	G2035	C1944	U1865	C1739	A1643	G1558
G2665	G2493	G2494	G2422		G2271	C2200	C2124	G2036	G1945	G1866			A1559
C2666	G2495		U2424	G2345	G2272	C2201	C2125	C2037	G1946	A1867	A1744	A1650	G1560
C2667		G2496	A2425	U2346	A2273	U2202	A2126	G2038	U1947	C1868	C1753	U1651	A1561
G2671	G2592	G2498	A2426	U2347	G2274	U2203	C2127	U2039	A1948	C1869	C1754	A1652	G1562
C2672	C2593	U2499	U2427	U2348	G2275	U2204	C2128	A2040	A1949			A1653	A1563
G2673	C2594	U2500	G2428	C2350	U2276	C2206	C2129	A2041	U1950	A1872	A1765	G1654	G1564
U2674	A2596	G2501	C2429	G2351	U2277	U2207		C2042	G1951	A1873	A1766	C1655	C1565
A2675	U2430		U2430	G2352	U2278	A2208	G2138	U2043	G1952	A1874	A1767	C1656	C1566
U2676	G2431	A2504	G2432	C2353	G2280	U2209	U2139	A2044	U1953	U1875	G1770	A1657	G1567
U2680	U2433	A2505	U2434	C2354	C2281	G2214	U2140	U2045	G1954	G1771	C1659	C1568	A1567
G2681	G2435		G2435	U2357	U2282	G2215	A2141	A2046	U1955	A1881	C1772	A1660	G1569
U2682	G2436	G2510	G2436	G2358	G2283	U2220	U2145	C2047	G1956	A1882	C1773	C1661	U1570
U2683	A2437	G2511	A2437	U2361	G2284	G2221	G2146	C2048	C1965	A1883	G1774	U1662	U1571
G2684	C2438	U2512	C2438	G2362	G2285	G2222	A2147	G2049	C1966	G1884	U1775	A1663	G1572
G2685	A2439	C2513	A2439	U2363	G2286	A2223	C2149	U2051	U1970	U1886	U1776	C1664	C1574
				G2366	G2287	G2224	U2150	C2052	C1971	A1887	U1785	G1665	C1575
U2618	U2619	G2517	U2440	U2367	C2288	A2225	C2149	C2053		C1889	C1786	G1666	G1576
U2620	U2621	U2518	C2441	G2368	C2289	U2226	U2151	C2054	G1974	A1890	G1668	G1667	G1577
G2622	G2623	G2519	A2442	U2371	A2291	U2227	G2152			G1891	C1789	G1669	G1578
C2624	A2443		G2443	U2372	C2292	C2231	U2156	G2057	A1975	C1892	U1790	U1670	C1579
A2625	G2444	C2523	A2445	U2373	C2293	C2232	G2157	C2058	A1976	G1893	U1791	G1671	C1582
U2630	G2446		G2446	A2375	U2294	U2233	A2158	U2059	G1977	G1894	G1794	A1672	
C2626	G2447		G2447	C2376		U2234	A2159	A2060	G1978	G1895	G1795	A1673	U1586
C2627	U2448	A2534	U2448	U2377	A2298	G2235	U2162	G2061	U1980	C1896			U1587
U2709	U2449	A2535	U2449	G2378	U2300	C2238	G2163	C2062	A1981		C1798	A1676	U1588
G2710	A2450		A2450	U2379	A2301	G2239	C2164	A2064	A1982	A1901	U1799	A1677	C1589
G2711	G2451	A2540	G2451	C2380	A2302	U2239	C2165	A2065	U1983	C1902	G1802	G1683	U1596
U2712	A2452	G2541	U2452	G2381	C2303	U2241	A2166	A2066	U1984	U1903			A1597
	G2453		G2453	U2385	C2304	U2242	U2167	U2067	G1985	G1904			A1598
A2718	U2632	C2547	C2454	C2386	A2304	A2242	U2168	U2068	A1986	U1808	U1602	G1688	
C2719	U2633	C2548	A2455	U2387	C2307	U2246	G2169		G1990	G1809	U1603	G1689	U1602
G2720	U2634	C2549	A2456	U2388	U2308	A2247	U2170	U2071	G1991	G1810	U1691	G1690	G1603
	U2635		U2457	U2390	U2309		A2247	U2072					
	G2636				U2313								

U2989	G2903	C2809	G2725
G2990	A2906	A2810	A2726
G2995	U2907	C2811	G2727
A2996	U2912	U2812	A2728
G2997	C2913	G2813	C2729
C2998	U2914	G2814	A2730
U2999	U2915	U2815	G2731
A3000	C2916	G2816	G2732
A3001	C2917	U2817	U2733
C3002	U2918	U2818	C2734
A3007	G2919	C2819	
C3008	C2923	G2820	U2737
A3011	U2924	G2821	C2738
U3012	U2925	G2822	C2739
G3013	U2926	U2823	C2740
C3024	U2927	U2826	A2742
U3025	A2928	C2827	U2743
U3026	G2929		
A3027	G2930	C2831	C2747
C3030	U2932	C2832	
U3031	G2933	C2838	G2751
	C2934	G2842	G2752
	U2935		G2753
	G2936	G2846	C2754
	A2937		G2755
	G2938	U2849	C2756
	G2939	G2850	U2757
	G2940	C2851	
	A2941	U2856	C2764
	U2946	G2857	U2765
	G2947	C2858	G2766
	A2948	G2859	A2767
	A2949	G2860	G2768
		A2861	G2769
	G2953		G2770
	A2954	U2871	G2771
	C2958	G2872	C2774
	G2962	C2873	U2775
	A2963	U2874	G2776
	U2964	G2875	C2777
	A2965	A2876	U2778
	G2966	G2877	
	G2967	G2878	A2782
	C2968	G2879	G2783
	C2969	C2883	U2784
	G2970		
	G2971	C2888	A2788
		A2889	
	G2974	G2892	G2789
	U2975	A2893	A2790
	G2976		G2791
	U2977	C2900	G2792
		C2901	A2793
			C2794
			G2802
			A2807
			U2808

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21705	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS TALOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	19.138	Depositor
Minimum map value	-6.456	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.774	Depositor
Recommended contour level	2.5	Depositor
Map size ($\text{\AA}$)	528.96, 528.96, 528.96	wwPDB
Map dimensions	608, 608, 608	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.87000006, 0.87000006, 0.87000006	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	b	0.35	0/2121	0.92	7/2852 (0.2%)
2	c	0.34	0/1585	0.86	0/2134
3	d	0.38	0/1570	0.86	3/2113 (0.1%)
4	e	0.44	0/1434	0.90	6/1926 (0.3%)
5	f	0.41	0/1342	0.87	5/1816 (0.3%)
6	g	0.43	0/414	1.01	3/556 (0.5%)
7	h	0.56	0/1001	1.09	8/1350 (0.6%)
8	i	0.58	0/1045	1.04	3/1410 (0.2%)
9	j	0.34	0/1151	0.86	3/1551 (0.2%)
10	k	0.36	0/947	0.92	2/1268 (0.2%)
11	l	0.35	0/1053	0.98	5/1403 (0.4%)
12	n	0.32	0/973	0.91	3/1301 (0.2%)
13	o	0.34	0/901	0.90	3/1209 (0.2%)
14	p	0.33	0/928	0.83	2/1242 (0.2%)
15	q	0.32	0/959	0.89	4/1278 (0.3%)
16	r	0.37	0/828	0.87	3/1107 (0.3%)
17	s	0.32	0/863	0.86	1/1156 (0.1%)
18	t	0.34	0/744	0.83	0/994
19	u	0.35	0/787	0.92	2/1051 (0.2%)
20	v	0.40	0/765	0.85	2/1025 (0.2%)
21	w	0.31	0/581	0.81	0/769
22	x	0.32	0/634	0.87	1/848 (0.1%)
23	y	0.34	0/509	0.83	0/677
24	z	0.31	0/452	0.79	0/605
25	A	0.41	0/319	0.82	2/426 (0.5%)
26	B	0.31	0/449	0.78	0/599
27	D	0.34	0/379	0.86	0/498
28	E	0.33	0/512	0.85	1/676 (0.1%)
29	F	0.30	0/303	0.81	0/397
30	a	0.53	0/1033	0.94	7/1387 (0.5%)
31	4	0.46	0/72710	0.50	5/113431 (0.0%)
All	All	0.44	0/99292	0.62	81/149055 (0.1%)

There are no bond length outliers.

All (81) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	g	10	ALA	N-CA-C	8.18	121.15	110.43
5	f	47	ASN	N-CA-C	-8.15	102.37	112.88
11	l	95	LEU	N-CA-C	-7.49	104.28	113.41
12	n	68	ALA	N-CA-C	-7.49	103.12	111.28
7	h	58	THR	N-CA-C	7.43	121.19	112.72
31	4	1025	G	C2'-C3'-O3'	7.39	120.58	109.50
4	e	4	HIS	N-CA-C	-7.35	102.65	111.69
7	h	123	ILE	N-CA-C	7.24	118.23	107.15
31	4	1020	A	C2'-C3'-O3'	6.88	119.82	109.50
11	l	96	LYS	N-CA-C	-6.77	103.70	112.23
17	s	24	ILE	N-CA-C	6.64	115.90	106.53
19	u	36	GLU	N-CA-C	6.59	118.81	110.24
8	i	93	ASN	N-CA-C	6.57	120.61	112.59
20	v	45	ASP	N-CA-C	6.54	119.00	111.02
11	l	92	LEU	N-CA-C	-6.35	104.46	111.82
7	h	57	ASN	N-CA-C	-6.31	102.97	111.87
9	j	96	ARG	CA-C-N	6.24	126.43	119.32
9	j	96	ARG	C-N-CA	6.24	126.43	119.32
7	h	102	ALA	N-CA-C	-6.17	104.66	111.82
3	d	198	GLU	N-CA-C	-6.14	104.86	112.90
28	E	30	HIS	N-CA-C	6.13	116.36	108.34
16	r	46	GLU	N-CA-C	6.09	119.40	109.59
3	d	141	MET	N-CA-C	-6.09	105.50	113.17
1	b	11	GLY	N-CA-C	-6.07	107.47	114.69
1	b	87	SER	N-CA-C	-5.97	105.83	113.23
7	h	117	LEU	N-CA-C	5.90	117.08	107.23
25	A	4	ASP	N-CA-C	5.87	119.64	111.90
11	l	115	GLU	N-CA-C	5.85	118.33	111.02
7	h	80	THR	N-CA-C	5.76	123.07	110.80
1	b	259	ASN	N-CA-C	-5.75	108.06	114.62
5	f	19	ASN	N-CA-C	-5.75	103.41	110.65
1	b	131	MET	N-CA-C	5.74	119.38	112.38
15	q	49	ARG	N-CA-C	-5.74	106.05	113.16
3	d	140	ASP	N-CA-C	-5.69	105.06	112.23
11	l	19	LEU	N-CA-C	5.66	118.89	110.52
8	i	7	TYR	N-CA-C	5.59	117.57	108.63
7	h	84	TYR	N-CA-C	5.56	118.47	109.40
15	q	70	GLN	N-CA-C	-5.56	105.37	111.82
12	n	79	LEU	N-CA-C	-5.56	102.29	110.52
30	a	209	ILE	N-CA-C	5.56	115.57	108.12
30	a	200	LYS	CA-C-N	5.55	125.86	119.92
30	a	200	LYS	C-N-CA	5.55	125.86	119.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	f	38	ASP	N-CA-C	-5.55	106.46	113.18
1	b	12	ARG	N-CA-C	-5.54	105.87	113.30
12	n	54	LEU	N-CA-C	-5.49	106.43	113.23
30	a	7	ARG	N-CA-C	5.47	116.93	110.97
14	p	3	ILE	N-CA-C	5.43	116.06	110.36
30	a	201	PRO	N-CA-C	5.42	119.74	111.34
4	e	134	GLN	N-CA-C	-5.40	105.32	112.94
16	r	45	GLU	N-CA-C	-5.36	100.96	109.76
5	f	39	ALA	N-CA-C	-5.35	105.61	111.82
20	v	63	ILE	N-CA-C	5.34	115.94	108.89
6	g	6	LEU	N-CA-C	-5.34	107.78	114.56
19	u	89	GLY	N-CA-C	-5.32	107.19	114.64
13	o	55	GLU	N-CA-C	-5.25	99.95	108.41
30	a	182	ALA	N-CA-C	5.25	117.42	111.02
25	A	8	LYS	N-CA-C	5.25	117.48	110.35
30	a	208	TYR	N-CA-C	5.23	121.95	110.80
15	q	50	ARG	N-CA-C	-5.21	107.58	114.04
5	f	18	ILE	N-CA-C	5.21	114.77	107.37
31	4	885	C	N1-C1'-C2'	5.17	119.76	112.00
31	4	1197	A	N9-C1'-C2'	5.16	119.75	112.00
1	b	213	ARG	N-CA-C	-5.16	107.03	113.38
4	e	48	LEU	N-CA-C	-5.15	105.75	111.36
9	j	100	VAL	N-CA-C	5.14	115.75	110.36
15	q	110	GLU	N-CA-C	-5.13	105.77	111.36
6	g	5	LEU	N-CA-C	5.12	117.14	110.43
16	r	15	SER	N-CA-C	-5.11	101.37	109.59
22	x	75	GLU	N-CA-C	-5.09	103.61	110.68
4	e	100	GLU	N-CA-C	-5.07	105.45	111.69
1	b	178	GLY	N-CA-C	-5.07	108.08	115.63
4	e	113	PHE	N-CA-C	5.07	116.78	108.52
8	i	127	SER	N-CA-C	-5.06	105.68	111.14
31	4	1191	G	N9-C1'-C2'	5.05	119.58	112.00
4	e	164	GLU	N-CA-C	-5.04	105.97	111.82
10	k	93	GLN	CA-C-N	5.03	125.03	119.90
10	k	93	GLN	C-N-CA	5.03	125.03	119.90
13	o	85	LYS	N-CA-C	-5.03	106.31	112.90
14	p	112	ARG	N-CA-C	5.03	116.77	111.28
7	h	44	ALA	N-CA-C	-5.03	105.90	112.23
13	o	116	GLN	N-CA-C	5.01	116.43	108.67

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	b	2082	0	2157	57	0
2	c	1564	0	1616	41	0
3	d	1551	0	1619	42	0
4	e	1410	0	1447	77	0
5	f	1322	0	1374	49	0
6	g	409	0	429	15	0
7	h	988	0	1025	57	0
8	i	1031	0	1088	60	0
9	j	1128	0	1162	30	0
10	k	938	0	1012	32	0
11	l	1044	0	1117	22	0
12	n	960	0	1000	19	0
13	o	891	0	923	25	0
14	p	916	0	965	29	0
15	q	946	0	1022	19	0
16	r	815	0	839	17	0
17	s	856	0	922	25	0
18	t	738	0	807	19	0
19	u	779	0	834	22	0
20	v	752	0	780	30	0
21	w	574	0	592	11	0
22	x	624	0	655	21	0
23	y	508	0	543	17	0
24	z	448	0	491	9	0
25	A	315	0	318	9	0
26	B	443	0	461	13	0
27	D	376	0	418	13	0
28	E	503	0	574	8	0
29	F	302	0	343	11	0
30	a	1026	0	1092	41	0
31	4	64925	0	32667	1219	0
All	All	91164	0	60292	1840	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 12.

All (1840) 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)
31:4:1024:G:H3'	31:4:1025:G:H2'	1.29	1.14
31:4:1307:G:H2'	31:4:1308:U:H4'	1.24	1.14
31:4:45:G:H5''	31:4:46:G:H5'	1.21	1.12
20:v:62:THR:HG22	20:v:69:GLU:HG2	1.32	1.10
8:i:4:VAL:HG21	31:4:1227:G:H5''	1.35	1.09
21:w:39:THR:H	31:4:2459:G:H4'	1.20	1.02
31:4:901:C:H3'	31:4:902:C:H5''	1.42	1.01
31:4:2043:U:H3'	31:4:2044:A:H5'	1.42	0.99
7:h:56:ARG:HD2	31:4:1212:A:H1'	1.39	0.99
31:4:2376:C:H2'	31:4:2377:U:H5'	1.41	0.97
31:4:279:A:H2'	31:4:280:U:H5'	1.47	0.97
31:4:906:U:H2'	31:4:907:G:H5''	1.43	0.96
31:4:1303:A:H3'	31:4:1304:U:H5'	1.46	0.96
7:h:34:THR:HG21	31:4:1185:A:H1'	1.46	0.95
23:y:9:LYS:HB3	23:y:12:GLU:HB2	1.45	0.94
5:f:136:ASP:HB3	5:f:139:VAL:HG22	1.50	0.93
31:4:959:A:H1'	31:4:2585:U:H4'	1.49	0.91
31:4:2040:A:H2'	31:4:2041:A:H2'	1.52	0.91
31:4:1660:A:H3'	31:4:1661:C:H5''	1.50	0.91
7:h:55:VAL:HA	31:4:1212:A:H4'	1.51	0.90
9:j:100:VAL:HG23	9:j:101:ILE:HD12	1.53	0.89
31:4:2064:A:H2	31:4:2071:U:H3	1.19	0.88
25:A:13:THR:HG22	25:A:23:LYS:HG2	1.55	0.88
31:4:655:A:H4'	31:4:656:G:H5'	1.56	0.88
31:4:1233:U:H2'	31:4:1234:G:H5''	1.53	0.87
31:4:2406:A:H3'	31:4:2407:G:H5''	1.56	0.86
18:t:11:LEU:HD11	18:t:32:LEU:HD13	1.58	0.85
31:4:956:G:H2'	31:4:957:C:H2'	1.59	0.85
1:b:16:VAL:HB	1:b:203:VAL:HG12	1.59	0.85
31:4:2190:A:O2'	31:4:2191:C:H5'	1.77	0.85
31:4:2258:U:H4'	31:4:2287:G:H1	1.39	0.84
8:i:92:PRO:HG2	31:4:1205:A:H1'	1.60	0.84
1:b:164:VAL:HG23	1:b:172:THR:HG23	1.60	0.83
30:a:5:THR:HG22	30:a:6:LYS:H	1.44	0.83
31:4:917:A:H5''	31:4:2396:A:H61	1.42	0.83
20:v:29:ILE:HD13	31:4:1141:G:H1'	1.61	0.82
31:4:2681:G:H3'	31:4:2682:U:H5''	1.62	0.81
31:4:138:U:H3'	31:4:139:U:H5''	1.63	0.80
31:4:704:G:H2'	31:4:726:G:H22	1.44	0.80
31:4:906:U:C2'	31:4:907:G:H5''	2.12	0.80
31:4:1069:C:H3'	31:4:1070:C:H5''	1.63	0.79
31:4:1205:A:H2'	31:4:1206:U:H5'	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:2284:G:H2'	31:4:2285:G:H5'	1.62	0.79
31:4:1660:A:C3'	31:4:1661:C:H5''	2.12	0.79
31:4:2414:G:H4'	31:4:2415:A:O4'	1.82	0.79
31:4:1173:C:H5'	31:4:1174:A:H5'	1.64	0.79
7:h:55:VAL:HA	31:4:1212:A:C4'	2.12	0.79
31:4:215:G:H4'	31:4:216:A:H4'	1.63	0.79
31:4:1660:A:H3'	31:4:1661:C:C5'	2.13	0.78
31:4:275:C:H2'	31:4:276:U:H4'	1.66	0.78
12:n:53:THR:HG21	31:4:2968:C:H5''	1.64	0.78
31:4:362:A:H3'	31:4:363:G:H8	1.49	0.78
12:n:2:ARG:HA	12:n:5:LYS:HD2	1.67	0.78
31:4:161:A:H3'	31:4:162:U:H5''	1.65	0.78
31:4:2043:U:H3'	31:4:2044:A:C5'	2.12	0.77
30:a:215:SER:HB2	31:4:2304:A:H1'	1.67	0.77
31:4:892:A:H2'	31:4:893:C:C5	2.20	0.77
31:4:704:G:H2'	31:4:726:G:N2	2.00	0.77
2:c:55:LYS:HE2	2:c:59:ARG:HG3	1.64	0.77
10:k:102:PRO:HB3	10:k:121:GLU:HB3	1.66	0.77
30:a:206:GLY:HA2	31:4:2004:A:O3'	1.85	0.76
31:4:1030:C:H2'	31:4:1154:A:H62	1.50	0.76
31:4:2262:A:C6	31:4:2285:G:H4'	2.20	0.76
31:4:2376:C:C2'	31:4:2377:U:H5'	2.16	0.76
8:i:74:PRO:HB2	8:i:77:VAL:HG22	1.65	0.76
2:c:151:THR:HB	2:c:152:PRO:HD3	1.67	0.76
2:c:148:GLN:HB2	2:c:152:PRO:HG2	1.66	0.75
31:4:2927:A:H2'	31:4:2928:A:H5'	1.69	0.75
31:4:2810:A:H61	31:4:2856:U:H1'	1.49	0.75
28:E:18:LYS:HG3	31:4:651:G:H5'	1.68	0.75
31:4:1050:A:H61	31:4:1131:U:H3'	1.49	0.75
31:4:1196:G:H21	31:4:1224:A:H5'	1.52	0.75
8:i:73:PRO:HB2	8:i:78:LEU:HD22	1.68	0.75
17:s:18:ARG:HE	31:4:518:G:H4'	1.50	0.74
30:a:7:ARG:HD3	31:4:2257:C:OP2	1.88	0.74
31:4:2257:C:H2'	31:4:2258:U:H5'	1.69	0.74
27:D:3:ARG:HH21	27:D:3:ARG:HA	1.52	0.74
1:b:106:PRO:HD2	1:b:109:LEU:HD22	1.68	0.74
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.69	0.74
31:4:1215:G:H2'	31:4:1217:A:O4'	1.88	0.74
3:d:143:LEU:HD13	3:d:146:VAL:HG11	1.69	0.73
18:t:47:VAL:HG13	18:t:55:VAL:HG21	1.69	0.73
30:a:200:LYS:HE2	30:a:204:ALA:HB1	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:1929:A:H5''	31:4:2331:U:H2'	1.69	0.73
31:4:1307:G:C2'	31:4:1308:U:H4'	2.13	0.73
31:4:2380:G:H2'	31:4:2381:G:H8	1.53	0.73
31:4:901:C:C3'	31:4:902:C:H5''	2.18	0.73
7:h:29:ASP:HB3	7:h:56:ARG:HH22	1.54	0.73
31:4:1303:A:H3'	31:4:1304:U:C5'	2.18	0.73
31:4:2186:A:H2'	31:4:2187:A:C5'	2.19	0.73
31:4:1269:U:H4'	31:4:1270:A:O4'	1.88	0.72
2:c:116:LYS:HG3	2:c:165:MET:HE2	1.71	0.72
31:4:2247:A:H5'	31:4:2248:G:OP2	1.89	0.72
8:i:10:LEU:O	8:i:11:GLN:HB2	1.89	0.72
31:4:1069:C:C3'	31:4:1070:C:H5''	2.19	0.72
31:4:2871:U:H2'	31:4:2872:G:H5''	1.69	0.72
31:4:2928:A:H3'	31:4:2929:G:H5'	1.72	0.72
31:4:1773:G:H5''	31:4:1774:C:H5'	1.70	0.72
31:4:2033:C:H4'	31:4:2057:G:H8	1.55	0.72
31:4:2257:C:C2'	31:4:2258:U:H5'	2.18	0.72
31:4:960:A:O2'	31:4:961:C:H6	1.72	0.72
5:f:174:LYS:HG3	5:f:175:LYS:H	1.56	0.71
27:D:24:THR:HG23	27:D:27:GLY:H	1.54	0.71
31:4:956:G:C6	31:4:958:U:H5'	2.25	0.71
20:v:30:ILE:HG12	20:v:91:PHE:HB2	1.72	0.71
30:a:166:ASP:OD1	31:4:2250:U:H4'	1.91	0.71
7:h:56:ARG:CD	31:4:1212:A:H1'	2.19	0.70
31:4:940:G:H2'	31:4:941:A:H5''	1.73	0.70
31:4:1907:U:H5	31:4:1912:A:N7	1.88	0.70
14:p:112:ARG:HD2	14:p:114:ASN:HD22	1.56	0.70
31:4:286:U:H2'	31:4:287:G:H8	1.56	0.70
31:4:644:A:H2'	31:4:645:C:H5''	1.74	0.70
31:4:1501:A:H5'	31:4:2340:A:H1'	1.74	0.70
19:u:35:VAL:HG13	19:u:38:ILE:HG13	1.73	0.70
31:4:729:G:H4'	31:4:763:G:H5'	1.72	0.70
31:4:2034:G:C3'	31:4:2035:G:H5''	2.21	0.70
8:i:77:VAL:HA	8:i:80:LYS:HD2	1.73	0.69
4:e:64:PRO:HA	4:e:88:VAL:HG12	1.73	0.69
9:j:80:HIS:HB3	9:j:81:ILE:HD12	1.72	0.69
31:4:2379:G:H1	31:4:2628:U:H3	1.40	0.69
15:q:36:GLN:HE21	31:4:1380:G:H1	1.41	0.69
30:a:214:ILE:HG23	30:a:222:VAL:HB	1.73	0.69
31:4:138:U:C3'	31:4:139:U:H5''	2.22	0.69
31:4:2034:G:H3'	31:4:2035:G:H5''	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:2620:U:H3'	31:4:2621:U:C5'	2.23	0.69
1:b:154:ALA:HB2	1:b:161:VAL:HG23	1.75	0.69
10:k:18:ARG:HB3	10:k:45:GLU:HB3	1.75	0.69
31:4:355:U:H2'	31:4:356:G:C8	2.27	0.69
31:4:2281:C:H2'	31:4:2282:A:H5'	1.75	0.69
5:f:2:ARG:NH1	31:4:1241:U:H5'	2.07	0.69
31:4:2250:U:H2'	31:4:2251:G:H5'	1.75	0.69
8:i:11:GLN:HB3	8:i:55:PRO:HA	1.74	0.68
31:4:580:U:H2'	31:4:581:C:C6	2.28	0.68
7:h:59:LEU:HB3	7:h:62:ARG:HB3	1.74	0.68
22:x:60:LYS:HD3	31:4:372:G:H5''	1.76	0.68
19:u:50:ALA:O	19:u:51:LEU:HG	1.93	0.68
31:4:1428:G:H4'	31:4:1429:A:C5'	2.22	0.68
4:e:149:ARG:H	4:e:149:ARG:HD2	1.59	0.68
31:4:310:A:C2'	31:4:311:A:H5''	2.23	0.68
31:4:2927:A:C2'	31:4:2928:A:H5'	2.24	0.68
31:4:355:U:H2'	31:4:356:G:H8	1.58	0.68
31:4:1303:A:C3'	31:4:1304:U:H5'	2.23	0.68
31:4:796:C:H2'	31:4:797:G:C8	2.29	0.67
31:4:2601:U:H2'	31:4:2602:U:H5'	1.75	0.67
5:f:17:LYS:HB2	5:f:24:THR:HB	1.75	0.67
31:4:1301:U:H2'	31:4:1302:U:H4'	1.75	0.67
31:4:2258:U:H4'	31:4:2287:G:N1	2.09	0.67
31:4:1175:G:H2'	31:4:1238:G:N1	2.09	0.67
3:d:162:ARG:NH1	31:4:321:U:H1'	2.10	0.67
31:4:78:U:H2'	31:4:79:C:C6	2.30	0.67
23:y:2:LYS:HE3	31:4:102:U:H1'	1.77	0.66
31:4:714:U:H1'	31:4:717:C:H5	1.60	0.66
31:4:2223:A:H61	31:4:2322:U:H3	1.43	0.66
20:v:53:LYS:HB2	20:v:56:PHE:HB2	1.76	0.66
31:4:876:C:H2'	31:4:877:A:H5'	1.77	0.66
4:e:147:ARG:HB3	4:e:149:ARG:HE	1.61	0.66
19:u:39:ASN:HD21	19:u:64:ILE:HB	1.61	0.66
31:4:2040:A:N6	31:4:2045:U:H1'	2.11	0.66
13:o:68:LYS:HE3	31:4:1115:C:H4'	1.78	0.66
31:4:2289:C:H2'	31:4:2290:G:C4'	2.25	0.66
4:e:133:GLU:HG3	4:e:135:ILE:HG22	1.78	0.66
7:h:53:ARG:HB3	31:4:1212:A:OP1	1.95	0.66
13:o:43:ASN:HD21	13:o:46:GLU:HG2	1.59	0.66
17:s:57:ASN:OD1	31:4:495:G:H1'	1.95	0.66
31:4:1197:A:C2	31:4:1224:A:H5''	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:u:65:GLN:HG3	31:4:328:U:O3'	1.96	0.65
31:4:639:U:H2'	31:4:640:C:C6	2.31	0.65
31:4:1935:G:H2'	31:4:1936:A:H5'	1.77	0.65
31:4:2640:C:H2'	31:4:2641:A:O4'	1.95	0.65
7:h:33:VAL:HG12	7:h:34:THR:H	1.61	0.65
31:4:1428:G:H4'	31:4:1429:A:H5''	1.77	0.65
31:4:2456:A:H2'	31:4:2457:U:C6	2.32	0.65
3:d:5:LEU:HA	3:d:120:VAL:HG13	1.77	0.65
30:a:50:ILE:HG21	30:a:57:GLN:HE21	1.61	0.65
31:4:357:C:H2'	31:4:358:U:C6	2.32	0.65
31:4:2284:G:C2'	31:4:2285:G:H5'	2.27	0.65
30:a:14:LYS:HD2	30:a:33:LEU:HD12	1.78	0.65
6:g:40:THR:HG22	6:g:43:ASN:ND2	2.11	0.65
31:4:871:U:H2'	31:4:872:U:C6	2.32	0.65
5:f:3:VAL:HG13	31:4:2879:G:H4'	1.79	0.64
5:f:72:ASN:O	5:f:75:VAL:HG12	1.97	0.64
19:u:94:PHE:HA	19:u:102:ILE:HG13	1.78	0.64
30:a:30:LEU:HA	30:a:33:LEU:HB2	1.79	0.64
10:k:64:ARG:HD3	10:k:102:PRO:O	1.97	0.64
11:l:107:PHE:HB3	11:l:126:ARG:HH12	1.63	0.64
31:4:2683:U:H2'	31:4:2684:C:H5'	1.79	0.64
31:4:1603:G:H1'	31:4:1860:C:H41	1.62	0.64
4:e:102:LEU:HA	4:e:106:ALA:HB3	1.78	0.64
4:e:116:LEU:HB3	4:e:175:PRO:O	1.96	0.64
8:i:13:ALA:HA	8:i:54:ILE:H	1.61	0.64
31:4:49:A:H5'	31:4:51:G:O4'	1.98	0.64
31:4:882:G:H2'	31:4:883:G:H8	1.63	0.64
22:x:17:ARG:HE	22:x:23:ALA:HB2	1.61	0.64
30:a:38:PHE:CE1	31:4:2255:G:H4'	2.33	0.64
4:e:12:VAL:HG22	4:e:16:MET:HE2	1.80	0.64
31:4:394:C:H2'	31:4:395:U:O4'	1.98	0.64
20:v:64:VAL:HA	20:v:69:GLU:HA	1.79	0.64
16:r:35:PHE:HB2	16:r:59:ILE:HB	1.80	0.64
31:4:511:U:H2'	31:4:512:G:H5'	1.80	0.64
31:4:873:C:H2'	31:4:874:G:C8	2.31	0.64
31:4:2380:G:H2'	31:4:2381:G:C8	2.32	0.64
10:k:76:VAL:H	14:p:72:VAL:HG22	1.61	0.63
31:4:2044:A:H2'	31:4:2045:U:O4'	1.97	0.63
31:4:1924:U:H2'	31:4:1925:G:C8	2.33	0.63
31:4:760:G:H2'	31:4:761:A:O4'	1.99	0.63
31:4:1306:C:H2'	31:4:1307:G:N7	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:j:31:GLU:HG3	9:j:142:ILE:HD12	1.79	0.63
13:o:100:HIS:HD2	31:4:1114:U:H4'	1.63	0.63
31:4:1341:A:N6	31:4:1364:G:H1'	2.12	0.63
31:4:195:A:H61	31:4:198:C:H3'	1.64	0.63
31:4:1216:A:H5'	31:4:1217:A:H5'	1.81	0.63
31:4:310:A:H2'	31:4:311:A:H5''	1.79	0.63
17:s:17:VAL:HG23	17:s:76:VAL:HG11	1.80	0.63
7:h:9:GLN:O	7:h:12:VAL:HG22	1.99	0.62
27:D:46:LYS:NZ	31:4:127:A:H62	1.97	0.62
31:4:2620:U:H3'	31:4:2621:U:H5''	1.81	0.62
6:g:50:ARG:HH21	6:g:51:ARG:HH22	1.47	0.62
31:4:176:A:O2'	31:4:177:G:H5'	1.99	0.62
4:e:116:LEU:H	4:e:175:PRO:HB2	1.64	0.62
19:u:85:ARG:HD3	19:u:87:GLU:OE2	1.99	0.62
31:4:714:U:H1'	31:4:717:C:C5	2.34	0.62
18:t:14:PRO:HA	18:t:32:LEU:HD23	1.81	0.62
31:4:2933:C:H2'	31:4:2934:C:H6	1.64	0.62
4:e:35:LEU:HD11	4:e:151:LEU:HD22	1.81	0.62
31:4:2040:A:H2'	31:4:2041:A:C2'	2.28	0.62
31:4:2632:U:H4'	31:4:2633:G:OP2	1.99	0.62
31:4:2681:G:C3'	31:4:2682:U:H5''	2.30	0.62
31:4:2473:G:N3	31:4:2509:A:H2'	2.15	0.62
1:b:130:PRO:HG2	1:b:133:ASN:HD22	1.64	0.62
4:e:99:PHE:HA	4:e:102:LEU:HD12	1.81	0.62
7:h:82:ILE:HD13	7:h:111:ALA:HB1	1.82	0.62
23:y:11:VAL:HA	23:y:14:LEU:HD12	1.81	0.62
31:4:871:U:H3	31:4:906:U:H3	1.47	0.62
31:4:1637:A:H2'	31:4:1638:G:C8	2.35	0.62
8:i:74:PRO:HB2	8:i:77:VAL:CG2	2.29	0.61
31:4:45:G:C5'	31:4:46:G:H5'	2.14	0.61
31:4:1575:C:H2'	31:4:1576:G:C8	2.35	0.61
5:f:86:LEU:HB2	5:f:130:ILE:HG23	1.82	0.61
8:i:127:SER:OG	31:4:1209:U:H1'	2.00	0.61
31:4:794:A:H2'	31:4:795:C:C6	2.36	0.61
31:4:2413:C:O2'	31:4:2415:A:H1'	1.99	0.61
31:4:414:C:H2'	31:4:415:A:H8	1.64	0.61
31:4:2199:A:H2'	31:4:2200:C:C6	2.34	0.61
7:h:56:ARG:HE	31:4:1234:G:H4'	1.65	0.61
24:z:40:THR:HG22	24:z:42:ALA:H	1.65	0.61
30:a:50:ILE:HG22	30:a:51:ASP:H	1.64	0.61
31:4:2361:U:H2'	31:4:2362:G:C8	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:2361:U:H2'	31:4:2362:G:H8	1.66	0.61
31:4:1175:G:H2'	31:4:1238:G:H1	1.64	0.61
31:4:1454:U:H2'	31:4:1455:A:H8	1.65	0.61
31:4:2424:U:H5''	31:4:2425:A:OP1	2.01	0.61
11:l:13:LYS:HE3	31:4:1373:G:OP1	2.01	0.61
31:4:1030:C:H2'	31:4:1154:A:N6	2.15	0.61
31:4:1069:C:H2'	31:4:1070:C:H5''	1.81	0.61
31:4:1676:A:H2'	31:4:1677:A:C8	2.34	0.61
14:p:90:ALA:HB2	14:p:112:ARG:HA	1.81	0.61
31:4:2871:U:C2'	31:4:2872:G:H5''	2.31	0.61
5:f:41:GLU:HA	5:f:54:ARG:HH21	1.64	0.61
8:i:97:VAL:HG12	8:i:136:GLY:O	2.00	0.61
10:k:4:GLU:O	10:k:5:GLN:HB2	2.01	0.61
21:w:39:THR:N	31:4:2459:G:H4'	2.04	0.61
31:4:879:G:N1	31:4:899:A:H1'	2.16	0.61
31:4:1994:A:H2'	31:4:1995:G:O4'	2.00	0.61
31:4:2214:U:H2'	31:4:2215:G:C8	2.36	0.61
31:4:404:A:H1'	31:4:406:G:C4	2.36	0.61
31:4:2685:G:H2'	31:4:2686:C:C6	2.36	0.61
31:4:2709:G:H2'	31:4:2709:G:N3	2.16	0.61
2:c:9:VAL:HG11	14:p:3:ILE:HD11	1.83	0.60
8:i:11:GLN:HA	8:i:23:VAL:HG21	1.83	0.60
31:4:891:G:C2'	31:4:892:A:H5'	2.31	0.60
31:4:414:C:H2'	31:4:415:A:C8	2.36	0.60
31:4:1955:U:O2'	31:4:1956:G:H5'	2.01	0.60
31:4:2371:U:H2'	31:4:2372:U:C6	2.35	0.60
6:g:6:LEU:HD12	6:g:37:VAL:HG22	1.83	0.60
12:n:38:LEU:HB3	12:n:39:PRO:HD3	1.83	0.60
20:v:37:PRO:HG2	31:4:1139:A:N1	2.15	0.60
31:4:118:A:OP2	31:4:119:A:H5''	2.01	0.60
31:4:171:U:H2'	31:4:172:A:H8	1.66	0.60
31:4:704:G:H1'	31:4:727:A:N6	2.17	0.60
28:E:32:LEU:HB3	28:E:40:LYS:HD3	1.82	0.60
31:4:1114:U:H2'	31:4:1115:C:C6	2.36	0.60
31:4:1182:A:H2'	31:4:1183:G:C8	2.36	0.60
31:4:2262:A:N6	31:4:2285:G:H4'	2.16	0.60
2:c:123:LYS:HE2	12:n:1:MET:HE1	1.84	0.60
31:4:360:U:H2'	31:4:361:G:C8	2.37	0.60
31:4:901:C:H2'	31:4:902:C:H4'	1.83	0.60
31:4:1212:A:H2'	31:4:1233:U:O2'	2.02	0.60
10:k:110:GLU:H	10:k:113:MET:HE3	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:s:73:LYS:HB2	17:s:106:VAL:HB	1.83	0.60
31:4:669:G:H2'	31:4:669:G:N3	2.17	0.60
31:4:917:A:H5''	31:4:2396:A:N6	2.15	0.60
31:4:1198:A:H3'	31:4:1200:C:OP1	2.01	0.60
31:4:1986:A:H1'	31:4:2013:A:C2	2.37	0.60
31:4:2289:C:H3'	31:4:2290:G:H5''	1.83	0.60
2:c:12:THR:HG22	2:c:13:ARG:H	1.67	0.60
31:4:121:G:H4'	31:4:149:A:H5'	1.83	0.60
31:4:1050:A:N6	31:4:1131:U:H3'	2.17	0.60
1:b:140:VAL:HG12	1:b:191:LEU:HD23	1.84	0.60
31:4:1069:C:C2'	31:4:1070:C:H5''	2.31	0.60
31:4:1207:C:H2'	31:4:1208:A:H8	1.66	0.60
31:4:2500:U:H2'	31:4:2501:G:C8	2.37	0.60
4:e:127:TYR:CZ	4:e:129:MET:HB3	2.37	0.60
5:f:3:VAL:HG21	31:4:2876:A:H4'	1.83	0.60
31:4:162:U:O2'	31:4:163:C:H5'	2.02	0.60
31:4:2033:C:H4'	31:4:2057:G:C8	2.37	0.60
31:4:2186:A:H2'	31:4:2187:A:H5''	1.83	0.60
31:4:2222:A:H2'	31:4:2223:A:C1'	2.32	0.60
4:e:115:GLY:HA3	4:e:177:ARG:HB3	1.84	0.59
10:k:121:GLU:OE2	10:k:122:VAL:HG23	2.02	0.59
29:F:36:ARG:CD	29:F:37:GLN:H	2.15	0.59
30:a:34:ALA:HB3	30:a:178:VAL:HG11	1.84	0.59
31:4:277:G:H4'	31:4:278:A:C5	2.36	0.59
31:4:1190:G:C2	31:4:1191:G:H1'	2.37	0.59
31:4:1219:G:H2'	31:4:1220:C:C6	2.37	0.59
31:4:1318:G:H2'	31:4:1319:G:H8	1.67	0.59
31:4:1428:G:C4'	31:4:1429:A:H5''	2.32	0.59
31:4:2002:C:H2'	31:4:2003:G:O4'	2.02	0.59
8:i:12:VAL:HG13	31:4:1189:U:N3	2.16	0.59
31:4:783:A:H2'	31:4:784:G:H5'	1.84	0.59
31:4:1029:G:N7	31:4:1154:A:H3'	2.17	0.59
31:4:2037:C:H2'	31:4:2038:G:H8	1.66	0.59
31:4:2048:C:H2'	31:4:2049:G:C8	2.37	0.59
27:D:14:ARG:HD2	31:4:771:G:OP1	2.02	0.59
31:4:2494:A:H2'	31:4:2495:G:O4'	2.02	0.59
31:4:1314:G:H2'	31:4:1315:G:O4'	2.03	0.59
4:e:3:LEU:HA	4:e:6:TYR:HB3	1.83	0.59
8:i:134:SER:OG	31:4:1207:C:H1'	2.03	0.59
9:j:81:ILE:HD12	9:j:81:ILE:H	1.67	0.59
8:i:6:ALA:HA	8:i:30:GLN:OE1	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:613:A:H2'	31:4:613:A:N3	2.16	0.59
31:4:528:A:C2	31:4:2170:A:H2'	2.37	0.59
4:e:28:PRO:HB2	4:e:168:LEU:HD12	1.83	0.59
31:4:1181:C:H2'	31:4:1182:A:H5''	1.83	0.59
31:4:1668:G:H2'	31:4:1669:C:C6	2.37	0.59
31:4:2278:C:C2'	31:4:2279:U:H5'	2.33	0.59
31:4:2395:A:H5''	31:4:2396:A:H5'	1.84	0.59
1:b:48:ILE:HG22	31:4:779:U:OP1	2.02	0.59
24:z:18:LYS:HE2	31:4:851:C:OP1	2.02	0.59
29:F:36:ARG:HD2	29:F:37:GLN:H	1.67	0.59
31:4:2231:C:H2'	31:4:2232:C:C6	2.38	0.59
1:b:242:HIS:HB3	1:b:250:GLN:HE22	1.67	0.58
5:f:155:PRO:HG3	31:4:2658:A:N6	2.18	0.58
31:4:2063:G:H1'	31:4:2092:G:N2	2.17	0.58
31:4:2193:C:H2'	31:4:2194:C:C6	2.38	0.58
31:4:2643:C:H2'	31:4:2644:A:H8	1.68	0.58
1:b:203:VAL:HG23	31:4:1920:G:C5'	2.33	0.58
18:t:88:LYS:HG3	18:t:89:GLU:H	1.67	0.58
31:4:226:A:H2'	31:4:227:A:O4'	2.02	0.58
31:4:1216:A:H5'	31:4:1217:A:C5'	2.33	0.58
31:4:1514:C:H2'	31:4:1515:A:C8	2.38	0.58
31:4:1985:G:H1'	31:4:2013:A:N6	2.17	0.58
31:4:2419:U:H2'	31:4:2420:U:C6	2.38	0.58
31:4:2774:C:H2'	31:4:2775:U:O4'	2.03	0.58
3:d:40:ARG:HG2	31:4:443:A:N7	2.17	0.58
9:j:84:ILE:HG23	9:j:84:ILE:O	2.03	0.58
31:4:2278:C:H2'	31:4:2279:U:H5'	1.85	0.58
17:s:4:ILE:H	17:s:4:ILE:HD12	1.67	0.58
31:4:1557:G:H2'	31:4:1558:G:H8	1.67	0.58
31:4:2728:A:O2'	31:4:2729:C:H5'	2.03	0.58
5:f:97:VAL:HG13	5:f:124:CYS:SG	2.43	0.58
8:i:3:LYS:O	8:i:4:VAL:HG13	2.03	0.58
31:4:1990:G:O2'	31:4:1991:G:H5'	2.02	0.58
31:4:2953:G:H2'	31:4:2954:A:H5'	1.85	0.58
31:4:441:U:H2'	31:4:442:G:C8	2.39	0.58
31:4:644:A:H2'	31:4:645:C:C5'	2.33	0.58
31:4:2313:U:H2'	31:4:2314:G:C8	2.38	0.58
31:4:2385:U:O2'	31:4:2386:C:H5'	2.04	0.58
7:h:67:THR:N	7:h:68:PRO:HD3	2.18	0.58
5:f:88:LEU:HD11	5:f:95:ALA:HB2	1.86	0.58
10:k:35:VAL:HA	10:k:62:VAL:HG23	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:71:ARG:HB3	10:k:72:PRO:HD2	1.85	0.58
13:o:39:VAL:HG12	13:o:48:LEU:HD12	1.85	0.58
19:u:48:VAL:HB	19:u:52:ASN:O	2.03	0.58
22:x:16:ASN:HD22	31:4:2209:U:H5''	1.67	0.58
31:4:901:C:H3'	31:4:902:C:C5'	2.28	0.58
31:4:956:G:H1'	31:4:960:A:N6	2.18	0.58
31:4:1636:A:H2'	31:4:1637:A:O4'	2.04	0.58
31:4:3026:U:H2'	31:4:3027:A:C8	2.38	0.58
3:d:137:LYS:HA	3:d:140:ASP:OD2	2.03	0.58
31:4:2628:U:O2'	31:4:2629:C:H5'	2.03	0.58
31:4:2860:G:O2'	31:4:2861:A:H5'	2.04	0.58
5:f:3:VAL:CG1	31:4:2879:G:H4'	2.34	0.58
9:j:6:ALA:H	9:j:45:THR:HG21	1.67	0.58
31:4:2871:U:C3'	31:4:2872:G:H5''	2.33	0.58
5:f:85:LYS:HB3	5:f:164:ALA:HB2	1.85	0.57
5:f:174:LYS:HB3	31:4:2657:G:H4'	1.86	0.57
12:n:45:ARG:HD3	12:n:97:ILE:HD11	1.86	0.57
14:p:77:SER:O	14:p:80:VAL:HG22	2.04	0.57
26:B:39:ARG:HG3	26:B:40:HIS:ND1	2.18	0.57
31:4:503:A:H4'	31:4:505:A:H5''	1.86	0.57
31:4:1205:A:C2'	31:4:1206:U:H5'	2.34	0.57
4:e:84:ILE:HD11	31:4:2439:A:N3	2.18	0.57
31:4:490:C:H4'	31:4:491:G:OP2	2.03	0.57
31:4:884:U:N3	31:4:892:A:C2	2.73	0.57
31:4:2289:C:H2'	31:4:2290:G:H4'	1.85	0.57
1:b:36:ASN:HB2	1:b:61:TYR:HB2	1.85	0.57
31:4:1048:G:H2'	31:4:1049:G:O4'	2.04	0.57
31:4:2348:U:H2'	31:4:2349:G:H8	1.69	0.57
3:d:1:MET:HB3	3:d:14:VAL:HG23	1.86	0.57
30:a:38:PHE:CD1	31:4:2255:G:H4'	2.40	0.57
31:4:419:U:H2'	31:4:420:C:C6	2.39	0.57
31:4:507:A:H5''	31:4:508:A:H2'	1.85	0.57
31:4:1637:A:H2'	31:4:1638:G:H8	1.69	0.57
31:4:2186:A:H2'	31:4:2187:A:H5'	1.86	0.57
31:4:2352:G:H4'	31:4:2354:C:C2	2.39	0.57
31:4:2450:A:H2'	31:4:2451:G:O4'	2.04	0.57
4:e:91:ARG:HD3	31:4:1111:A:H5'	1.85	0.57
31:4:864:G:O2'	31:4:865:C:H5'	2.04	0.57
31:4:1231:A:N3	31:4:1231:A:H2'	2.20	0.57
31:4:1924:U:H2'	31:4:1925:G:H8	1.68	0.57
31:4:2587:A:H61	31:4:2619:U:H3	1.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:91:LYS:HZ1	8:i:94:LYS:HD2	1.68	0.57
10:k:64:ARG:HB2	10:k:83:ALA:HB3	1.86	0.57
21:w:38:GLY:HA2	31:4:2458:G:H21	1.70	0.57
2:c:43:ASP:OD1	31:4:2912:U:H4'	2.05	0.57
10:k:102:PRO:CB	10:k:121:GLU:HB3	2.33	0.57
22:x:16:ASN:ND2	31:4:2209:U:H5''	2.20	0.57
6:g:4:ILE:HG23	6:g:37:VAL:HB	1.86	0.57
17:s:97:LEU:HD23	31:4:2141:A:OP1	2.04	0.57
31:4:897:C:H2'	31:4:898:C:C6	2.39	0.57
31:4:1307:G:H3'	31:4:1307:G:OP2	2.04	0.57
31:4:2642:U:H2'	31:4:2643:C:C6	2.40	0.57
1:b:269:ARG:NH1	1:b:269:ARG:HB3	2.20	0.57
31:4:362:A:H3'	31:4:363:G:C8	2.36	0.57
31:4:869:G:H2'	31:4:870:U:O4'	2.04	0.57
31:4:2348:U:H2'	31:4:2349:G:C8	2.39	0.57
9:j:90:GLU:OE2	9:j:91:GLU:HG3	2.04	0.56
31:4:878:A:H2'	31:4:900:A:H61	1.70	0.56
31:4:895:U:O2'	31:4:896:A:H5''	2.04	0.56
31:4:2059:U:O2'	31:4:2060:A:H5'	2.05	0.56
14:p:20:ARG:HD3	14:p:112:ARG:NH1	2.20	0.56
23:y:8:GLU:O	23:y:60:LYS:NZ	2.38	0.56
24:z:15:ARG:HG3	24:z:53:MET:HE1	1.87	0.56
31:4:1233:U:C2'	31:4:1234:G:H5''	2.29	0.56
31:4:1307:G:H2'	31:4:1308:U:C4'	2.17	0.56
31:4:2430:U:H2'	31:4:2431:G:C8	2.40	0.56
3:d:119:ILE:HB	3:d:187:VAL:HA	1.86	0.56
5:f:132:LEU:HD12	5:f:132:LEU:O	2.04	0.56
25:A:37:CYS:SG	25:A:38:SER:N	2.76	0.56
31:4:133:U:H2'	31:4:134:G:C8	2.40	0.56
31:4:1132:A:H4'	31:4:1133:G:C8	2.41	0.56
1:b:239:PHE:O	1:b:241:LYS:HG2	2.05	0.56
8:i:12:VAL:HG13	31:4:1189:U:C2	2.41	0.56
28:E:32:LEU:H	28:E:32:LEU:HD12	1.71	0.56
31:4:310:A:O2'	31:4:311:A:H5''	2.05	0.56
31:4:1634:U:H2'	31:4:1635:C:C6	2.39	0.56
31:4:2933:C:H2'	31:4:2934:C:C6	2.40	0.56
21:w:39:THR:H	31:4:2459:G:C4'	2.05	0.56
28:E:30:HIS:HD2	28:E:31:ILE:HG23	1.70	0.56
30:a:57:GLN:OE1	30:a:201:PRO:HB2	2.06	0.56
31:4:2037:C:H2'	31:4:2038:G:C8	2.41	0.56
31:4:2926:U:H4'	31:4:2927:A:C4	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:97:VAL:HG22	8:i:98:GLY:H	1.69	0.56
11:l:29:LYS:HD3	11:l:30:THR:HG23	1.87	0.56
31:4:12:U:H2'	31:4:13:A:H5'	1.87	0.56
31:4:890:C:H3'	31:4:891:G:H8	1.71	0.56
31:4:2234:U:H2'	31:4:2235:G:C8	2.40	0.56
1:b:240:GLY:HA3	31:4:2725:G:H5''	1.87	0.56
5:f:44:HIS:HA	5:f:49:LEU:HA	1.88	0.56
31:4:1974:G:H2'	31:4:1975:A:O4'	2.05	0.56
31:4:2270:A:H2'	31:4:2271:C:C2	2.41	0.56
31:4:2962:G:H2'	31:4:3007:A:H61	1.69	0.56
31:4:1122:G:H4'	31:4:1123:A:C8	2.40	0.56
31:4:1765:A:H5'	31:4:1888:C:O2'	2.05	0.56
4:e:118:ALA:HB2	4:e:176:PHE:HE1	1.70	0.56
9:j:68:LYS:HE3	31:4:1022:G:N7	2.21	0.56
10:k:23:LYS:HB3	10:k:40:LYS:HB3	1.87	0.56
14:p:30:TRP:HB3	14:p:37:LYS:HE2	1.87	0.56
31:4:492:A:H2'	31:4:493:G:O4'	2.06	0.56
31:4:528:A:N1	31:4:2170:A:H2'	2.20	0.56
31:4:1872:A:H3'	31:4:1873:A:H8	1.70	0.56
31:4:2665:U:H2'	31:4:2666:C:C6	2.40	0.56
31:4:2924:U:H4'	31:4:2925:U:H5	1.70	0.56
31:4:544:C:H2'	31:4:545:U:H1'	1.88	0.55
31:4:2349:G:O2'	31:4:2350:C:H5'	2.06	0.55
31:4:340:A:H2'	31:4:341:C:O4'	2.06	0.55
31:4:971:G:H2'	31:4:972:A:O4'	2.06	0.55
31:4:1218:A:H2'	31:4:1219:G:C8	2.41	0.55
31:4:2258:U:C4'	31:4:2287:G:H1	2.16	0.55
31:4:2630:G:O2'	31:4:2631:A:H5''	2.07	0.55
4:e:67:THR:HG21	31:4:2440:U:O3'	2.07	0.55
31:4:242:G:N2	31:4:254:G:H2'	2.22	0.55
31:4:1201:A:H2'	31:4:1202:G:O4'	2.05	0.55
31:4:2028:A:H1'	31:4:2098:A:H2'	1.89	0.55
31:4:2430:U:H2'	31:4:2431:G:H8	1.71	0.55
31:4:2603:C:H2'	31:4:2604:A:H5'	1.88	0.55
31:4:3026:U:H2'	31:4:3027:A:H8	1.72	0.55
10:k:112:PHE:HB3	10:k:115:ILE:HD12	1.87	0.55
14:p:6:GLN:O	14:p:10:GLU:HG2	2.06	0.55
31:4:1156:A:H2'	31:4:1157:A:C8	2.42	0.55
31:4:1206:U:H5''	31:4:1207:C:H5''	1.89	0.55
31:4:2273:C:H3'	31:4:2274:C:H5'	1.87	0.55
3:d:127:GLU:N	3:d:127:GLU:OE1	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:137:PHE:O	4:e:140:ILE:HG22	2.06	0.55
31:4:225:C:H2'	31:4:226:A:O4'	2.05	0.55
31:4:1214:A:H4'	31:4:1231:A:N1	2.22	0.55
31:4:1495:A:H2'	31:4:1496:G:H5'	1.88	0.55
31:4:2256:G:N2	31:4:2289:C:H1'	2.21	0.55
31:4:3012:U:H3'	31:4:3012:U:O2	2.07	0.55
4:e:78:ILE:HD11	31:4:2439:A:N3	2.22	0.55
19:u:73:ASN:HD22	19:u:76:THR:H	1.53	0.55
22:x:6:VAL:HG23	22:x:7:THR:HG23	1.88	0.55
25:A:37:CYS:H	25:A:40:CYS:HB2	1.70	0.55
29:F:36:ARG:HE	29:F:37:GLN:HB2	1.72	0.55
31:4:703:U:H2'	31:4:704:G:O4'	2.06	0.55
31:4:816:C:H2'	31:4:817:C:C6	2.42	0.55
5:f:136:ASP:HB3	5:f:139:VAL:CG2	2.31	0.55
8:i:85:ILE:HD11	8:i:137:LEU:HD21	1.89	0.55
31:4:37:C:H4'	31:4:451:U:OP1	2.06	0.55
31:4:358:U:H2'	31:4:359:G:H8	1.72	0.55
31:4:593:U:H2'	31:4:594:U:C6	2.42	0.55
31:4:906:U:H2'	31:4:907:G:C5'	2.27	0.55
4:e:23:SER:OG	31:4:1122:G:H5'	2.07	0.55
5:f:2:ARG:HH11	31:4:1241:U:H5'	1.69	0.55
17:s:88:ARG:HG3	17:s:94:ASP:OD2	2.06	0.55
30:a:6:LYS:HD3	31:4:2258:U:H5	1.71	0.55
31:4:668:A:H2'	31:4:670:A:H62	1.71	0.55
31:4:1126:C:H2'	31:4:1127:G:H8	1.72	0.55
31:4:1922:A:H2'	31:4:1923:C:C6	2.41	0.55
31:4:2977:U:H4'	31:4:2996:A:C2	2.42	0.55
2:c:146:ILE:HD11	31:4:2180:A:C8	2.42	0.55
5:f:122:ALA:HA	5:f:132:LEU:HA	1.89	0.55
31:4:1522:U:H4'	31:4:1731:A:H4'	1.89	0.55
4:e:147:ARG:O	4:e:149:ARG:HD2	2.07	0.54
7:h:55:VAL:HG22	31:4:1212:A:O5'	2.07	0.54
8:i:110:GLN:HG2	8:i:121:ILE:HD11	1.89	0.54
13:o:49:VAL:HG11	13:o:81:ARG:HB3	1.89	0.54
31:4:1207:C:H2'	31:4:1208:A:C8	2.41	0.54
31:4:1226:A:C2'	31:4:1227:G:H5'	2.37	0.54
31:4:2473:G:H5'	31:4:2475:C:H5'	1.90	0.54
4:e:149:ARG:HD2	4:e:149:ARG:N	2.21	0.54
8:i:74:PRO:HG3	31:4:1188:U:H5'	1.89	0.54
10:k:10:VAL:HG11	10:k:16:ALA:HB3	1.88	0.54
12:n:28:LEU:HD13	12:n:34:ILE:HG12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:p:38:ARG:HE	14:p:39:LEU:H	1.55	0.54
30:a:217:THR:HA	31:4:2252:G:H21	1.71	0.54
31:4:738:G:O2'	31:4:739:A:H5'	2.07	0.54
31:4:1025:G:H4'	31:4:1026:G:C5'	2.36	0.54
31:4:1239:A:O2'	31:4:1240:G:H4'	2.07	0.54
1:b:106:PRO:HG2	1:b:109:LEU:HB2	1.88	0.54
3:d:57:LYS:NZ	3:d:59:PRO:HG3	2.22	0.54
7:h:56:ARG:NE	31:4:1234:G:H4'	2.22	0.54
13:o:49:VAL:HG22	13:o:85:LYS:NZ	2.22	0.54
31:4:940:G:C2'	31:4:941:A:H5''	2.37	0.54
31:4:2788:A:H2'	31:4:2789:G:O4'	2.07	0.54
19:u:18:LYS:HE3	31:4:310:A:OP1	2.06	0.54
30:a:65:LEU:HD22	30:a:188:ASN:OD1	2.08	0.54
31:4:1542:C:H2'	31:4:1543:U:O4'	2.08	0.54
31:4:163:C:H2'	31:4:164:C:O4'	2.08	0.54
31:4:906:U:C3'	31:4:907:G:H5''	2.36	0.54
31:4:1239:A:H2'	31:4:1239:A:N3	2.22	0.54
31:4:2875:G:O6	31:4:2883:C:H5''	2.08	0.54
1:b:237:ARG:HE	31:4:2718:A:H5''	1.73	0.54
5:f:39:ALA:HA	5:f:57:TYR:CD2	2.43	0.54
9:j:24:THR:HB	9:j:27:ARG:HB2	1.89	0.54
16:r:17:GLY:H	16:r:98:ILE:HG23	1.73	0.54
26:B:54:ILE:HG23	26:B:56:LYS:H	1.72	0.54
31:4:215:G:C4'	31:4:216:A:H4'	2.35	0.54
31:4:796:C:H2'	31:4:797:G:H8	1.69	0.54
31:4:2074:U:H2'	31:4:2075:C:C6	2.42	0.54
3:d:106:LYS:HG3	3:d:200:LEU:HD23	1.89	0.54
27:D:26:ASN:CG	31:4:682:G:H5'	2.33	0.54
31:4:1624:A:H2'	31:4:1626:C:C4	2.43	0.54
17:s:97:LEU:HD23	17:s:97:LEU:H	1.73	0.54
21:w:33:ILE:HG21	21:w:76:ILE:HG21	1.90	0.54
31:4:895:U:C2'	31:4:896:A:H5''	2.38	0.54
31:4:959:A:H61	31:4:2622:G:N2	2.06	0.54
31:4:1268:C:H2'	31:4:1269:U:H5'	1.88	0.54
31:4:2035:G:H2'	31:4:2036:C:O4'	2.08	0.54
1:b:203:VAL:HG23	31:4:1920:G:H5'	1.90	0.54
7:h:55:VAL:HG23	31:4:1212:A:OP1	2.08	0.54
9:j:99:ARG:HD2	9:j:102:GLU:OE1	2.08	0.54
31:4:1192:C:H42	31:4:1197:A:H8	1.56	0.54
31:4:1789:G:H2'	31:4:1790:U:C6	2.42	0.54
31:4:2028:A:O4'	31:4:2098:A:H5''	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:2324:C:O2'	31:4:2325:U:H5'	2.08	0.54
31:4:963:U:O2'	31:4:964:C:H5'	2.08	0.54
8:i:76:ALA:O	8:i:80:LYS:HG3	2.08	0.53
9:j:76:HIS:CE1	9:j:85:LYS:HB2	2.43	0.53
31:4:435:C:H2'	31:4:436:C:H5'	1.89	0.53
31:4:1132:A:H5''	31:4:1133:G:OP1	2.08	0.53
31:4:1952:G:O2'	31:4:1953:U:H5'	2.08	0.53
31:4:2989:U:H2'	31:4:2990:G:H8	1.73	0.53
31:4:875:G:H1	31:4:902:C:H42	1.56	0.53
31:4:1046:A:H2'	31:4:1047:G:O4'	2.08	0.53
4:e:135:ILE:HA	4:e:140:ILE:HG21	1.88	0.53
15:q:14:LYS:HE3	31:4:1346:G:OP2	2.08	0.53
30:a:30:LEU:HB2	30:a:216:THR:HG21	1.89	0.53
31:4:371:A:H61	31:4:401:A:H3'	1.72	0.53
31:4:1081:A:H3'	31:4:1082:G:H8	1.73	0.53
31:4:554:U:H2'	31:4:555:G:O4'	2.08	0.53
31:4:1182:A:H2'	31:4:1183:G:H8	1.73	0.53
31:4:2595:C:H2'	31:4:2596:A:O4'	2.09	0.53
1:b:2:VAL:HG21	1:b:201:LEU:HD13	1.90	0.53
5:f:39:ALA:HA	5:f:57:TYR:CE2	2.43	0.53
24:z:8:GLN:HB2	24:z:28:LEU:HD13	1.89	0.53
31:4:644:A:H2'	31:4:645:C:C4'	2.38	0.53
31:4:1309:U:H2'	31:4:1310:G:C8	2.44	0.53
31:4:1938:A:H2'	31:4:1939:G:O4'	2.08	0.53
31:4:2630:G:C2'	31:4:2631:A:H5''	2.38	0.53
31:4:2700:A:OP1	31:4:2702:G:H4'	2.08	0.53
20:v:61:LEU:H	20:v:61:LEU:HD12	1.73	0.53
31:4:1117:G:H2'	31:4:1118:A:O4'	2.09	0.53
31:4:2050:G:H2'	31:4:2051:U:C6	2.44	0.53
31:4:1656:A:H2'	31:4:1657:G:O4'	2.09	0.53
31:4:1965:C:H2'	31:4:2027:A:H61	1.74	0.53
31:4:2406:A:C3'	31:4:2407:G:H5''	2.31	0.53
31:4:2410:G:H4'	31:4:2517:G:O2'	2.09	0.53
6:g:40:THR:O	6:g:44:ILE:HG13	2.09	0.53
31:4:45:G:H5''	31:4:46:G:C5'	2.15	0.53
31:4:544:C:H2'	31:4:545:U:C1'	2.39	0.53
31:4:594:U:H2'	31:4:595:C:C6	2.44	0.53
31:4:973:A:H5'	31:4:1316:U:H1'	1.90	0.53
31:4:2366:G:N3	31:4:2366:G:H2'	2.22	0.53
31:4:2765:U:H2'	31:4:2766:G:O4'	2.09	0.53
19:u:94:PHE:HB2	19:u:101:THR:HA	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:1569:G:H2'	31:4:1570:U:C6	2.44	0.53
31:4:2624:C:H42	31:4:2625:A:H62	1.56	0.53
1:b:86:ARG:NH2	31:4:1945:G:OP1	2.41	0.53
1:b:130:PRO:HG2	1:b:133:ASN:ND2	2.23	0.53
11:l:53:GLY:HA3	31:4:826:U:O2'	2.08	0.53
31:4:214:G:O2'	31:4:215:G:H5'	2.09	0.53
31:4:1196:G:N2	31:4:1224:A:H5'	2.24	0.53
31:4:2603:C:C2'	31:4:2604:A:H5'	2.38	0.53
11:l:30:THR:HG22	31:4:810:U:O4	2.10	0.52
15:q:58:GLN:HE21	31:4:1009:A:H5'	1.74	0.52
16:r:24:LYS:HA	16:r:94:THR:OG1	2.09	0.52
27:D:3:ARG:HA	27:D:3:ARG:NH2	2.20	0.52
31:4:138:U:H2'	31:4:139:U:C4'	2.39	0.52
31:4:360:U:H2'	31:4:361:G:N9	2.24	0.52
31:4:1049:G:H2'	31:4:1132:A:C2	2.44	0.52
31:4:2167:U:H2'	31:4:2168:G:C8	2.45	0.52
2:c:10:GLY:O	2:c:26:VAL:HG22	2.09	0.52
7:h:58:THR:HB	7:h:82:ILE:HB	1.91	0.52
9:j:45:THR:OG1	9:j:48:VAL:HB	2.09	0.52
31:4:1267:G:O2'	31:4:1268:C:H5'	2.08	0.52
20:v:72:VAL:HG12	20:v:93:ARG:HA	1.91	0.52
31:4:901:C:H2'	31:4:902:C:C4'	2.40	0.52
31:4:2165:A:H2'	31:4:2166:G:C8	2.44	0.52
8:i:9:LYS:HG3	31:4:1189:U:OP2	2.09	0.52
8:i:11:GLN:HG2	8:i:56:VAL:HG22	1.89	0.52
31:4:230:G:O2'	31:4:231:A:H5'	2.09	0.52
31:4:1425:C:OP1	31:4:2838:C:H4'	2.09	0.52
3:d:117:ARG:HH12	11:l:2:ARG:HG2	1.73	0.52
17:s:40:ASN:O	17:s:41:LYS:HG2	2.09	0.52
19:u:54:PRO:HG2	19:u:55:GLY:H	1.73	0.52
31:4:546:U:H2'	31:4:547:A:O4'	2.10	0.52
31:4:1568:U:H2'	31:4:1569:G:C8	2.44	0.52
31:4:2643:C:H2'	31:4:2644:A:C8	2.44	0.52
3:d:148:ILE:HA	3:d:187:VAL:HG13	1.91	0.52
10:k:16:ALA:HA	10:k:46:ALA:CB	2.39	0.52
20:v:75:GLN:HE22	31:4:1046:A:H5'	1.75	0.52
26:B:30:ASP:HB3	26:B:34:GLY:H	1.74	0.52
31:4:402:A:H2'	31:4:403:U:O4'	2.08	0.52
31:4:755:U:H2'	31:4:756:A:C8	2.45	0.52
2:c:173:GLN:NE2	31:4:2900:C:H5'	2.25	0.52
4:e:175:PRO:HG3	25:A:41:HIS:CE1	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:127:SER:HB2	31:4:1209:U:O2'	2.10	0.52
31:4:1168:A:H2	31:4:1243:G:H22	1.57	0.52
31:4:2191:C:H2'	31:4:2192:C:C6	2.45	0.52
31:4:2374:G:H2'	31:4:2375:A:C8	2.45	0.52
1:b:157:ALA:HB1	1:b:196:ASN:O	2.08	0.52
8:i:72:THR:HG21	8:i:112:LYS:HG3	1.92	0.52
20:v:77:VAL:HG22	20:v:79:ARG:HD2	1.92	0.52
25:A:12:ILE:HG23	25:A:31:ASP:OD1	2.10	0.52
31:4:1156:A:N6	31:4:1253:G:H2'	2.25	0.52
31:4:1668:G:H2'	31:4:1669:C:H6	1.75	0.52
31:4:2314:G:H2'	31:4:2315:U:O4'	2.10	0.52
7:h:37:LYS:O	7:h:41:LEU:HB2	2.10	0.52
31:4:445:C:O2'	31:4:446:G:H5'	2.10	0.52
31:4:482:A:H1'	31:4:498:G:N2	2.25	0.52
31:4:671:C:H2'	31:4:672:C:C6	2.45	0.52
31:4:709:U:H2'	31:4:710:U:C6	2.45	0.52
5:f:19:ASN:HB3	5:f:22:VAL:HG13	1.92	0.52
30:a:8:MET:HE2	31:4:2302:C:O2'	2.10	0.52
31:4:794:A:H2'	31:4:795:C:H6	1.73	0.52
31:4:1061:A:C2'	31:4:1062:U:H5'	2.40	0.52
31:4:1428:G:H4'	31:4:1429:A:H5'	1.89	0.52
31:4:2685:G:H2'	31:4:2686:C:H6	1.75	0.52
7:h:27:VAL:O	7:h:83:ALA:HB3	2.09	0.51
10:k:111:LYS:HD2	10:k:112:PHE:CZ	2.45	0.51
21:w:36:GLN:OE1	21:w:40:LYS:N	2.43	0.51
31:4:956:G:N1	31:4:958:U:H5'	2.23	0.51
31:4:1029:G:H4'	31:4:1030:C:O5'	2.10	0.51
31:4:1853:U:H2'	31:4:1854:C:C6	2.44	0.51
31:4:2307:C:H2'	31:4:2308:U:C6	2.45	0.51
7:h:37:LYS:HE3	31:4:1213:A:H62	1.75	0.51
31:4:898:C:H2'	31:4:899:A:O4'	2.09	0.51
31:4:2962:G:H2'	31:4:3007:A:N6	2.26	0.51
7:h:18:VAL:HG23	7:h:70:GLU:HG3	1.91	0.51
31:4:891:G:O2'	31:4:892:A:H5'	2.11	0.51
31:4:1488:G:H2'	31:4:1489:G:H5'	1.91	0.51
31:4:1691:U:H2'	31:4:1692:C:C6	2.45	0.51
31:4:2232:C:H42	31:4:2313:U:H3	1.57	0.51
31:4:2916:C:H2'	31:4:2917:C:C6	2.44	0.51
3:d:57:LYS:C	3:d:58:LYS:HD3	2.35	0.51
3:d:61:ARG:HD2	3:d:65:THR:HG23	1.93	0.51
13:o:36:TYR:HE1	13:o:54:VAL:HG13	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:467:G:O2'	31:4:468:G:H5'	2.11	0.51
31:4:1557:G:H2'	31:4:1558:G:C8	2.45	0.51
31:4:2064:A:H3'	31:4:2065:A:H5'	1.92	0.51
31:4:2371:U:H2'	31:4:2372:U:H6	1.76	0.51
31:4:2445:A:H2'	31:4:2446:G:O4'	2.10	0.51
5:f:71:LEU:HD23	5:f:74:MET:SD	2.50	0.51
9:j:105:VAL:HG11	9:j:122:LEU:HD22	1.93	0.51
13:o:68:LYS:HE3	31:4:1115:C:O3'	2.11	0.51
20:v:31:TYR:HB3	20:v:37:PRO:HG3	1.91	0.51
31:4:2099:U:H5'	31:4:2100:G:H5''	1.93	0.51
7:h:41:LEU:HD12	31:4:1211:U:OP1	2.11	0.51
31:4:1031:U:H2'	31:4:1032:C:O4'	2.11	0.51
31:4:1864:U:H2'	31:4:1865:G:O4'	2.09	0.51
1:b:245:THR:C	1:b:247:TRP:H	2.18	0.51
31:4:1965:C:H2'	31:4:2027:A:N6	2.25	0.51
31:4:2147:A:H2	31:4:2163:G:H22	1.59	0.51
1:b:86:ARG:HE	31:4:1945:G:H5''	1.76	0.51
3:d:43:THR:O	31:4:38:A:H1'	2.11	0.51
7:h:80:THR:HA	31:4:1236:U:H5'	1.92	0.51
31:4:885:C:H1'	31:4:891:G:H22	1.76	0.51
31:4:1570:U:H2'	31:4:1571:U:C6	2.46	0.51
31:4:1922:A:H2'	31:4:1923:C:H6	1.74	0.51
31:4:2231:C:H2'	31:4:2232:C:C5	2.44	0.51
1:b:16:VAL:HB	1:b:203:VAL:CG1	2.38	0.51
1:b:83:ASP:OD1	1:b:86:ARG:HG2	2.10	0.51
4:e:120:SER:HB2	4:e:127:TYR:CE1	2.45	0.51
17:s:5:ALA:HB3	17:s:54:ALA:HB2	1.93	0.51
28:E:20:GLY:HA3	28:E:48:MET:HE1	1.93	0.51
31:4:2192:C:H42	31:4:2574:G:H1	1.58	0.51
31:4:2240:G:H2'	31:4:2241:U:H5'	1.93	0.51
8:i:91:LYS:NZ	8:i:94:LYS:HD2	2.26	0.51
9:j:113:PRO:HD2	31:4:558:U:P	2.51	0.51
10:k:64:ARG:HH12	10:k:101:GLY:HA3	1.76	0.51
13:o:105:ALA:O	13:o:108:ASP:OD1	2.29	0.51
20:v:4:ILE:O	20:v:63:ILE:HG23	2.11	0.51
31:4:2492:C:H2'	31:4:2493:G:O4'	2.11	0.51
2:c:135:GLY:HA2	31:4:743:A:OP1	2.11	0.50
3:d:125:SER:HA	3:d:157:LEU:HD21	1.93	0.50
4:e:59:ILE:O	4:e:101:ARG:NH2	2.44	0.50
9:j:36:LEU:HD11	9:j:122:LEU:HD13	1.92	0.50
31:4:828:U:H4'	31:4:831:G:N1	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:847:U:O2	31:4:847:U:H2'	2.10	0.50
31:4:979:A:H2'	31:4:982:C:H42	1.76	0.50
31:4:1226:A:H2'	31:4:1227:G:H5'	1.92	0.50
31:4:1280:C:H2'	31:4:1281:C:H6	1.75	0.50
31:4:1480:U:O2'	31:4:1481:A:H5'	2.11	0.50
31:4:2226:U:H2'	31:4:2227:U:O4'	2.11	0.50
3:d:189:THR:HG23	3:d:192:ALA:H	1.76	0.50
12:n:103:ARG:HH21	12:n:110:MET:HE1	1.76	0.50
16:r:68:ARG:NH1	16:r:90:ARG:HB2	2.26	0.50
27:D:9:VAL:HG12	31:4:1437:G:OP1	2.10	0.50
31:4:1203:C:H2'	31:4:1204:C:C5'	2.41	0.50
31:4:2048:C:H2'	31:4:2049:G:H8	1.76	0.50
31:4:2193:C:H2'	31:4:2194:C:H6	1.76	0.50
2:c:25:THR:HG21	2:c:193:VAL:HG22	1.94	0.50
7:h:6:GLN:HA	7:h:9:GLN:HB2	1.93	0.50
19:u:39:ASN:ND2	19:u:64:ILE:HB	2.24	0.50
31:4:2257:C:H1'	31:4:2288:C:H42	1.76	0.50
2:c:46:ARG:HB2	2:c:84:LEU:HD12	1.94	0.50
2:c:59:ARG:HH11	31:4:2958:C:H3'	1.76	0.50
3:d:47:LYS:O	3:d:83:VAL:HG23	2.12	0.50
5:f:34:ARG:NE	5:f:70:LEU:HD13	2.26	0.50
7:h:27:VAL:HB	7:h:85:SER:HB2	1.94	0.50
30:a:63:THR:HG22	30:a:161:VAL:O	2.11	0.50
31:4:558:U:H2'	31:4:559:G:H8	1.76	0.50
31:4:1236:U:H2'	31:4:1237:C:C6	2.46	0.50
31:4:2831:C:H2'	31:4:2832:C:C6	2.46	0.50
26:B:5:ASN:ND2	31:4:2148:A:H62	2.10	0.50
28:E:60:CYS:C	28:E:62:PRO:HD3	2.37	0.50
31:4:69:C:O2'	31:4:70:G:H5'	2.11	0.50
31:4:327:G:O2'	31:4:328:U:H5'	2.12	0.50
31:4:766:U:H2'	31:4:767:U:C6	2.47	0.50
31:4:1030:C:H2'	31:4:1030:C:O2	2.11	0.50
31:4:2175:C:O2'	31:4:2176:G:H5'	2.12	0.50
31:4:2283:U:H2'	31:4:2284:G:H5'	1.92	0.50
31:4:2738:C:O5'	31:4:2738:C:H6	1.94	0.50
12:n:31:HIS:CD2	31:4:1407:G:H4'	2.47	0.50
16:r:78:ARG:HB3	16:r:83:TYR:HB3	1.93	0.50
31:4:27:G:N2	31:4:512:G:H1'	2.26	0.50
31:4:874:G:H2'	31:4:875:G:O4'	2.12	0.50
31:4:1562:A:H2'	31:4:1563:G:C8	2.46	0.50
31:4:2547:U:H2'	31:4:2548:C:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:149:ILE:HG23	3:d:149:ILE:O	2.10	0.50
4:e:120:SER:HB2	4:e:127:TYR:HE1	1.76	0.50
5:f:163:TYR:HB2	5:f:166:GLU:HB2	1.93	0.50
8:i:141:ASP:N	8:i:141:ASP:OD1	2.45	0.50
12:n:44:LEU:HD23	12:n:113:ILE:HD13	1.94	0.50
13:o:40:ILE:N	13:o:40:ILE:HD12	2.27	0.50
18:t:23:ALA:O	18:t:27:SER:HB3	2.11	0.50
22:x:56:ARG:NH2	31:4:400:G:N7	2.60	0.50
31:4:171:U:H2'	31:4:172:A:C8	2.46	0.50
31:4:1020:A:H1'	31:4:1021:A:OP2	2.12	0.50
31:4:1203:C:H2'	31:4:1204:C:H5'	1.93	0.50
31:4:2222:A:H2'	31:4:2223:A:H1'	1.92	0.50
13:o:52:SER:HB2	13:o:54:VAL:HG22	1.93	0.50
14:p:5:LYS:O	14:p:9:GLN:HG2	2.11	0.50
31:4:49:A:H2'	31:4:49:A:N3	2.26	0.50
31:4:2271:C:H2'	31:4:2272:G:H5'	1.93	0.50
6:g:7:ASP:OD1	6:g:35:LYS:HD3	2.11	0.50
6:g:24:GLY:HA3	31:4:2220:U:H5''	1.94	0.50
7:h:42:ARG:NH1	8:i:118:GLY:O	2.45	0.50
30:a:17:ALA:HB3	31:4:2233:U:H5''	1.94	0.50
31:4:163:C:O2'	31:4:164:C:H5'	2.11	0.50
31:4:420:C:O2'	31:4:421:C:H5'	2.11	0.50
31:4:1043:A:H2'	31:4:1044:G:O4'	2.12	0.50
31:4:1197:A:N6	31:4:1201:A:C8	2.80	0.50
31:4:1533:U:H2'	31:4:1534:U:C6	2.46	0.50
31:4:1603:G:H1'	31:4:1860:C:N4	2.26	0.50
31:4:2635:C:H2'	31:4:2636:G:C8	2.47	0.50
31:4:2719:C:H2'	31:4:2720:G:C8	2.47	0.50
3:d:130:LYS:HB3	3:d:133:LEU:HG	1.93	0.49
16:r:32:THR:HA	16:r:62:GLU:HA	1.94	0.49
23:y:3:ALA:O	23:y:7:ARG:NH1	2.45	0.49
31:4:1038:G:O2'	31:4:1039:C:H5'	2.12	0.49
31:4:2139:U:H2'	31:4:2140:G:O4'	2.12	0.49
31:4:2826:U:H2'	31:4:2827:C:C6	2.47	0.49
3:d:44:ARG:HD3	31:4:444:C:OP2	2.12	0.49
23:y:1:MET:O	23:y:5:GLU:HG3	2.11	0.49
31:4:12:U:O2	31:4:2754:C:H4'	2.13	0.49
31:4:896:A:H3'	31:4:897:C:O4'	2.12	0.49
31:4:1121:U:O2'	31:4:1122:G:H5'	2.11	0.49
31:4:1562:A:H2'	31:4:1563:G:H8	1.77	0.49
31:4:1676:A:H2'	31:4:1677:A:H8	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:163:GLU:HA	4:e:166:ARG:HB3	1.94	0.49
8:i:71:LYS:HD2	31:4:1187:G:H5'	1.94	0.49
19:u:46:LYS:N	19:u:46:LYS:HD2	2.26	0.49
31:4:191:A:H2'	31:4:192:C:C6	2.47	0.49
31:4:1053:U:H2'	31:4:1054:G:H8	1.77	0.49
31:4:1062:U:H2'	31:4:1065:G:H21	1.77	0.49
31:4:2008:U:H2'	31:4:2009:C:H6	1.78	0.49
31:4:2401:A:H2'	31:4:2402:A:C8	2.47	0.49
31:4:2426:A:H2'	31:4:2427:U:H5'	1.94	0.49
2:c:8:LYS:HD3	2:c:196:ALA:C	2.38	0.49
7:h:13:ALA:O	7:h:17:GLU:HG3	2.13	0.49
27:D:12:ARG:NH2	31:4:686:U:O4	2.43	0.49
31:4:1196:G:H2'	31:4:1197:A:O4'	2.12	0.49
31:4:1953:U:H2'	31:4:1954:G:C8	2.48	0.49
31:4:2034:G:H2'	31:4:2035:G:O4'	2.12	0.49
31:4:2167:U:H2'	31:4:2168:G:H8	1.76	0.49
31:4:2284:G:C3'	31:4:2285:G:H5'	2.42	0.49
31:4:2442:A:H2'	31:4:2443:G:C8	2.48	0.49
31:4:2586:G:H2'	31:4:2587:A:C8	2.47	0.49
1:b:129:LEU:N	1:b:129:LEU:HD23	2.26	0.49
15:q:50:ARG:HH11	15:q:50:ARG:HG3	1.77	0.49
31:4:57:C:H2'	31:4:58:G:O4'	2.12	0.49
31:4:207:A:H2'	31:4:208:C:O4'	2.12	0.49
31:4:353:C:H2'	31:4:354:A:H5'	1.93	0.49
31:4:877:A:H2	31:4:899:A:H61	1.59	0.49
31:4:1060:C:H2'	31:4:1061:A:C8	2.47	0.49
31:4:1829:A:H2'	31:4:1830:G:H5'	1.95	0.49
31:4:1955:U:C2'	31:4:1956:G:H5'	2.43	0.49
31:4:2257:C:H2'	31:4:2258:U:C5'	2.41	0.49
1:b:259:ASN:HD22	1:b:262:THR:HG23	1.78	0.49
8:i:74:PRO:HB3	31:4:1188:U:H5'	1.95	0.49
11:l:141:LYS:NZ	11:l:143:GLU:HB3	2.27	0.49
15:q:50:ARG:HD3	31:4:1284:A:C8	2.48	0.49
19:u:42:LYS:HG2	19:u:59:GLU:OE2	2.12	0.49
31:4:1396:A:H2'	31:4:1397:A:O4'	2.12	0.49
31:4:1837:U:H2'	31:4:1838:G:C8	2.47	0.49
31:4:2751:G:H2'	31:4:2752:G:H8	1.77	0.49
7:h:95:LEU:HD22	7:h:99:PHE:CE2	2.48	0.49
7:h:118:ILE:H	7:h:119:PRO:HD2	1.77	0.49
31:4:497:A:H2'	31:4:498:G:O4'	2.13	0.49
31:4:753:A:O2'	31:4:754:U:H5'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:813:U:H2'	31:4:814:C:C6	2.47	0.49
31:4:2107:U:O2'	31:4:2108:G:H5'	2.12	0.49
31:4:2858:C:O2'	31:4:2859:G:H5'	2.13	0.49
4:e:107:VAL:CG2	4:e:108:PRO:HD3	2.42	0.49
17:s:4:ILE:O	31:4:495:G:H4'	2.12	0.49
17:s:36:LEU:HD13	17:s:47:VAL:HG23	1.94	0.49
22:x:38:TRP:HE1	22:x:40:GLU:HG3	1.77	0.49
31:4:912:C:O2'	31:4:913:U:H5'	2.13	0.49
31:4:948:C:H2'	31:4:949:G:H8	1.77	0.49
31:4:1753:C:H2'	31:4:1754:A:O4'	2.13	0.49
8:i:9:LYS:HA	8:i:57:VAL:HG22	1.95	0.49
16:r:49:ILE:HD12	16:r:52:PRO:HA	1.94	0.49
21:w:14:ALA:HB1	31:4:2399:G:H5''	1.95	0.49
31:4:768:G:O2'	31:4:769:U:H5'	2.13	0.49
31:4:959:A:C1'	31:4:2585:U:H4'	2.34	0.49
31:4:1191:G:H2'	31:4:1191:G:N3	2.28	0.49
31:4:2040:A:H61	31:4:2045:U:H1'	1.76	0.49
31:4:2222:A:H2'	31:4:2223:A:O4'	2.12	0.49
31:4:2819:C:H2'	31:4:2820:G:H8	1.78	0.49
1:b:269:ARG:HB3	1:b:269:ARG:HH11	1.78	0.48
4:e:40:GLY:HA2	4:e:84:ILE:CG1	2.43	0.48
5:f:173:ALA:O	5:f:174:LYS:C	2.56	0.48
7:h:33:VAL:HG12	7:h:34:THR:N	2.27	0.48
8:i:10:LEU:HD21	31:4:1198:A:C2	2.47	0.48
11:l:109:LYS:HE2	11:l:128:THR:HG22	1.95	0.48
18:t:59:ASN:HB3	31:4:1469:G:H1'	1.94	0.48
27:D:9:VAL:HG22	27:D:13:ASN:ND2	2.28	0.48
31:4:892:A:H2'	31:4:893:C:C6	2.47	0.48
31:4:1561:A:H2'	31:4:1562:A:C8	2.48	0.48
31:4:2946:U:H2'	31:4:2947:G:H8	1.78	0.48
1:b:86:ARG:NE	31:4:1945:G:H5''	2.28	0.48
4:e:76:PHE:HB2	4:e:78:ILE:HD12	1.95	0.48
30:a:165:ASN:HD21	30:a:169:GLY:HA2	1.78	0.48
31:4:833:A:H2'	31:4:834:G:C8	2.48	0.48
31:4:874:G:H2'	31:4:875:G:C8	2.48	0.48
31:4:1485:C:H2'	31:4:1486:G:O4'	2.13	0.48
31:4:1770:G:O2'	31:4:1771:G:H5'	2.13	0.48
31:4:1984:U:H2'	31:4:1985:G:O4'	2.12	0.48
5:f:84:LYS:HB2	5:f:132:LEU:HD11	1.95	0.48
6:g:31:VAL:N	6:g:32:PRO:HD2	2.28	0.48
9:j:81:ILE:HD12	9:j:81:ILE:N	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:y:23:ARG:O	23:y:25:GLN:N	2.46	0.48
31:4:2044:A:H2'	31:4:2045:U:C4'	2.44	0.48
8:i:21:PRO:CB	8:i:22:PRO:HD3	2.38	0.48
13:o:49:VAL:HG22	13:o:85:LYS:HZ3	1.77	0.48
31:4:222:A:N6	31:4:232:G:H1'	2.29	0.48
31:4:598:U:H2'	31:4:599:A:C8	2.48	0.48
31:4:699:A:H2'	31:4:700:G:O4'	2.13	0.48
31:4:948:C:H2'	31:4:949:G:C8	2.49	0.48
31:4:974:G:H1'	31:4:975:A:C8	2.48	0.48
31:4:1182:A:H5'	31:4:1182:A:H8	1.78	0.48
31:4:2478:C:H2'	31:4:2479:G:O4'	2.13	0.48
4:e:34:THR:HG23	4:e:154:THR:HB	1.94	0.48
14:p:61:ARG:HH21	14:p:61:ARG:HG3	1.79	0.48
18:t:29:THR:HG23	18:t:85:VAL:C	2.38	0.48
20:v:44:HIS:CE1	20:v:85:LYS:HB2	2.48	0.48
31:4:581:C:H2'	31:4:582:A:C8	2.47	0.48
31:4:804:A:H2'	31:4:806:C:C4	2.49	0.48
31:4:940:G:C3'	31:4:941:A:H5''	2.43	0.48
31:4:1029:G:N7	31:4:1154:A:H5''	2.29	0.48
31:4:2413:C:H2'	31:4:2414:G:H5'	1.95	0.48
31:4:2681:G:H2'	31:4:2682:U:C4'	2.43	0.48
14:p:31:VAL:CG1	14:p:38:ARG:HB3	2.42	0.48
15:q:106:THR:O	15:q:109:VAL:HG22	2.13	0.48
31:4:1024:G:H3'	31:4:1025:G:C2'	2.22	0.48
31:4:1572:G:H2'	31:4:1573:G:H8	1.77	0.48
31:4:1659:C:H2'	31:4:1660:A:C8	2.48	0.48
31:4:1739:C:H5'	31:4:1739:C:H6	1.77	0.48
31:4:2053:C:H2'	31:4:2054:U:C6	2.48	0.48
31:4:2624:C:N4	31:4:2625:A:H62	2.12	0.48
15:q:48:ASP:HA	15:q:51:GLN:HB2	1.93	0.48
21:w:55:LEU:HD12	21:w:76:ILE:HD12	1.96	0.48
22:x:38:TRP:NE1	22:x:40:GLU:HG3	2.28	0.48
31:4:2052:C:H2'	31:4:2053:C:C6	2.49	0.48
5:f:103:ASN:C	5:f:104:LEU:HD22	2.39	0.48
6:g:6:LEU:HD23	6:g:6:LEU:O	2.14	0.48
7:h:118:ILE:HB	7:h:119:PRO:HD3	1.94	0.48
16:r:53:PHE:O	16:r:54:VAL:C	2.56	0.48
31:4:839:U:H2'	31:4:840:C:C6	2.49	0.48
31:4:1202:G:H2'	31:4:1203:C:O4'	2.14	0.48
31:4:1575:C:H2'	31:4:1576:G:H8	1.78	0.48
31:4:1901:A:H2'	31:4:1902:C:O4'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:190:LYS:HG2	2:c:191:GLY:N	2.28	0.48
31:4:443:A:H5''	31:4:444:C:H5''	1.95	0.48
31:4:891:G:H2'	31:4:892:A:H5'	1.96	0.48
31:4:1023:U:H2'	31:4:1024:G:H5'	1.96	0.48
31:4:1280:C:H2'	31:4:1281:C:C6	2.49	0.48
31:4:2281:C:C2'	31:4:2282:A:H5'	2.43	0.48
4:e:107:VAL:HG22	4:e:108:PRO:HD3	1.94	0.48
8:i:4:VAL:HG21	31:4:1227:G:C5'	2.25	0.48
17:s:13:SER:OG	17:s:16:LYS:HG3	2.14	0.48
22:x:2:ARG:NH1	31:4:1493:A:OP1	2.46	0.48
31:4:167:A:H2'	31:4:168:G:O4'	2.13	0.48
31:4:710:U:H3	31:4:721:A:H61	1.59	0.48
31:4:1874:A:H2'	31:4:1875:U:C6	2.49	0.48
31:4:2334:C:H2'	31:4:2335:C:C6	2.49	0.48
7:h:78:GLY:N	7:h:79:PRO:HD2	2.29	0.47
9:j:78:THR:HG21	9:j:85:LYS:HE2	1.96	0.47
20:v:61:LEU:H	20:v:61:LEU:CD1	2.26	0.47
31:4:894:U:O2'	31:4:895:U:H5'	2.14	0.47
31:4:1067:U:H2'	31:4:1068:G:C8	2.49	0.47
31:4:2278:C:H2'	31:4:2279:U:C5'	2.43	0.47
31:4:2409:A:O2'	31:4:2410:G:H5'	2.13	0.47
3:d:146:VAL:HA	3:d:185:LYS:O	2.13	0.47
11:l:8:PRO:HD3	31:4:1372:A:H5'	1.95	0.47
17:s:74:ILE:HG23	17:s:74:ILE:O	2.14	0.47
20:v:61:LEU:HD12	20:v:61:LEU:N	2.29	0.47
31:4:2322:U:H2'	31:4:2323:U:C6	2.48	0.47
2:c:46:ARG:NH2	2:c:88:GLU:O	2.47	0.47
14:p:105:LYS:HB3	14:p:108:ARG:HH22	1.79	0.47
20:v:45:ASP:HA	20:v:48:MET:HE2	1.96	0.47
31:4:833:A:H2'	31:4:834:G:H8	1.78	0.47
31:4:1065:G:H4'	31:4:1066:G:C8	2.49	0.47
31:4:1090:G:H4'	31:4:1091:U:C5	2.50	0.47
31:4:1729:G:O2'	31:4:1730:U:H5'	2.15	0.47
31:4:1883:A:H2'	31:4:1884:G:H5'	1.95	0.47
31:4:2394:A:H4'	31:4:2395:A:N3	2.28	0.47
31:4:2733:U:H2'	31:4:2734:C:C6	2.49	0.47
31:4:2989:U:H2'	31:4:2990:G:C8	2.49	0.47
1:b:203:VAL:HG23	31:4:1920:G:H5''	1.95	0.47
3:d:25:GLU:OE1	11:l:7:SER:N	2.46	0.47
3:d:57:LYS:C	3:d:57:LYS:HD3	2.40	0.47
31:4:1614:U:H2'	31:4:1615:U:C6	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:q:23:TYR:CD1	31:4:533:G:H5'	2.49	0.47
24:z:30:ARG:HD3	24:z:30:ARG:H	1.80	0.47
31:4:851:C:H2'	31:4:852:U:C6	2.50	0.47
31:4:859:G:H1'	31:4:860:U:H5	1.79	0.47
31:4:1514:C:H2'	31:4:1515:A:H8	1.79	0.47
31:4:2117:G:H2'	31:4:2118:C:O4'	2.14	0.47
31:4:2127:C:H5''	31:4:2851:C:O2'	2.15	0.47
14:p:95:LYS:HG3	31:4:2846:G:O3'	2.15	0.47
19:u:35:VAL:HG13	19:u:38:ILE:CG1	2.42	0.47
22:x:30:PRO:HG2	22:x:32:LEU:HG	1.97	0.47
30:a:215:SER:CB	31:4:2304:A:H1'	2.41	0.47
31:4:279:A:C2'	31:4:280:U:H5'	2.32	0.47
31:4:654:A:H3'	31:4:654:A:N3	2.30	0.47
31:4:1090:G:H4'	31:4:1091:U:H5	1.80	0.47
31:4:1125:A:H2'	31:4:1126:C:C6	2.49	0.47
31:4:1394:G:N2	31:4:2140:G:H2'	2.30	0.47
31:4:2308:U:H2'	31:4:2309:U:O4'	2.14	0.47
31:4:2651:G:H1'	31:4:2893:A:N7	2.30	0.47
1:b:75:ALA:HB2	1:b:95:TYR:CD1	2.50	0.47
1:b:152:GLN:HB3	31:4:1946:U:C4	2.50	0.47
4:e:36:ASN:OD1	4:e:87:LYS:HB3	2.13	0.47
4:e:89:THR:HG23	4:e:89:THR:O	2.13	0.47
4:e:172:PHE:HB2	4:e:174:PHE:CD1	2.50	0.47
5:f:140:ILE:HG13	5:f:141:GLY:N	2.29	0.47
8:i:10:LEU:HD11	31:4:1198:A:C2	2.50	0.47
8:i:52:LEU:HD23	8:i:73:PRO:HG2	1.97	0.47
9:j:17:VAL:HG23	9:j:137:PRO:HB2	1.97	0.47
19:u:44:HIS:HA	19:u:57:ILE:HG22	1.96	0.47
31:4:304:U:H3	31:4:313:G:H1	1.61	0.47
31:4:494:G:O2'	31:4:495:G:H5'	2.14	0.47
31:4:1560:G:O2'	31:4:1561:A:H5'	2.14	0.47
31:4:1613:U:H2'	31:4:1614:U:C6	2.50	0.47
31:4:2034:G:H2'	31:4:2035:G:H5''	1.97	0.47
31:4:2523:C:H42	31:4:2549:G:H1	1.63	0.47
31:4:2601:U:C2'	31:4:2602:U:H5'	2.43	0.47
31:4:2932:U:H2'	31:4:2933:C:C6	2.49	0.47
4:e:34:THR:HG21	31:4:2442:A:H5'	1.97	0.47
13:o:4:LYS:HD2	13:o:7:ARG:NH2	2.30	0.47
31:4:133:U:H2'	31:4:134:G:H8	1.80	0.47
31:4:1199:G:H1'	31:4:1217:A:C4	2.49	0.47
31:4:2128:C:O2'	31:4:2129:C:H5'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:2233:U:C2'	31:4:2234:U:H5'	2.44	0.47
31:4:2394:A:H4'	31:4:2395:A:C2	2.50	0.47
31:4:2719:C:H2'	31:4:2720:G:H8	1.80	0.47
2:c:14:ILE:HG23	14:p:11:GLN:HE22	1.79	0.47
4:e:87:LYS:HD2	31:4:2441:C:H4'	1.96	0.47
11:l:90:VAL:HB	11:l:122:VAL:HA	1.96	0.47
11:l:93:ASN:C	11:l:95:LEU:H	2.22	0.47
31:4:359:G:H2'	31:4:360:U:O4'	2.15	0.47
31:4:1597:A:H2'	31:4:1598:A:C8	2.50	0.47
31:4:2939:G:H2'	31:4:2940:G:H8	1.79	0.47
1:b:30:ALA:HB3	1:b:31:PRO:HD3	1.96	0.47
2:c:4:LEU:HB3	2:c:32:ASN:ND2	2.30	0.47
17:s:4:ILE:HD12	17:s:4:ILE:N	2.29	0.47
19:u:13:LEU:HD11	19:u:70:ALA:HB2	1.97	0.47
29:F:36:ARG:HD2	29:F:37:GLN:N	2.30	0.47
31:4:473:G:O2'	31:4:474:G:H5'	2.15	0.47
31:4:1061:A:H2'	31:4:1062:U:O4'	2.15	0.47
31:4:2336:C:H2'	31:4:2337:G:H8	1.80	0.47
31:4:2936:G:H5'	31:4:2937:A:OP1	2.15	0.47
2:c:8:LYS:HD3	2:c:196:ALA:O	2.14	0.46
3:d:105:LEU:O	3:d:109:LEU:HD23	2.15	0.46
31:4:522:A:H2'	31:4:523:C:C6	2.50	0.46
31:4:783:A:C2'	31:4:784:G:H5'	2.44	0.46
31:4:893:C:H2'	31:4:894:U:H5'	1.95	0.46
31:4:1153:U:C2	31:4:1154:A:C2	3.03	0.46
31:4:1572:G:H2'	31:4:1573:G:C8	2.50	0.46
31:4:1889:C:H2'	31:4:1890:A:O4'	2.15	0.46
31:4:2426:A:H2'	31:4:2427:U:C5'	2.46	0.46
31:4:2812:U:C4	31:4:2813:G:N7	2.83	0.46
2:c:125:TRP:CD1	2:c:160:LYS:HB3	2.50	0.46
2:c:135:GLY:O	31:4:2708:U:H5''	2.14	0.46
7:h:58:THR:HG21	7:h:82:ILE:C	2.41	0.46
9:j:37:ARG:NH1	9:j:44:TYR:OH	2.48	0.46
14:p:2:ASN:O	14:p:6:GLN:HG3	2.15	0.46
23:y:24:GLU:O	23:y:25:GLN:C	2.58	0.46
27:D:34:ARG:HD3	31:4:467:G:OP2	2.15	0.46
29:F:23:ILE:HD13	31:4:1160:A:H1'	1.98	0.46
31:4:297:G:H2'	31:4:298:G:O4'	2.15	0.46
31:4:1308:U:H5''	31:4:1309:U:H5	1.79	0.46
31:4:1855:C:H2'	31:4:1856:C:O4'	2.15	0.46
1:b:152:GLN:HB3	31:4:1946:U:N3	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:175:LEU:HD13	31:4:1927:G:C5	2.51	0.46
5:f:68:ARG:HD3	5:f:68:ARG:C	2.40	0.46
14:p:43:GLU:O	14:p:62:LYS:HG3	2.14	0.46
26:B:24:VAL:O	26:B:26:SER:N	2.48	0.46
31:4:721:A:H2'	31:4:722:A:C8	2.50	0.46
31:4:1114:U:H2'	31:4:1115:C:H6	1.80	0.46
31:4:1666:G:O2'	31:4:1667:U:H5'	2.15	0.46
1:b:198:GLU:HA	1:b:201:LEU:HD12	1.98	0.46
3:d:105:LEU:HD21	3:d:177:PRO:HG3	1.96	0.46
5:f:37:ASN:OD1	5:f:38:ASP:N	2.49	0.46
8:i:126:ARG:O	31:4:1208:A:O2'	2.33	0.46
10:k:59:LYS:HG3	10:k:89:ASN:OD1	2.15	0.46
27:D:46:LYS:HZ1	31:4:127:A:H62	1.63	0.46
30:a:7:ARG:CZ	31:4:2256:G:H5'	2.46	0.46
31:4:562:U:O4'	31:4:2164:C:H5'	2.16	0.46
31:4:858:G:H5'	31:4:859:G:OP2	2.15	0.46
31:4:1230:C:H2'	31:4:1231:A:H8	1.81	0.46
31:4:1719:A:H2'	31:4:1720:C:C6	2.49	0.46
31:4:2271:C:C2'	31:4:2272:G:H5'	2.46	0.46
1:b:15:VAL:HG22	1:b:205:GLY:HA3	1.97	0.46
13:o:11:ALA:HB2	13:o:96:GLY:N	2.30	0.46
31:4:96:C:O2'	31:4:97:C:H5'	2.15	0.46
31:4:639:U:H2'	31:4:640:C:H6	1.77	0.46
31:4:1669:C:H2'	31:4:1670:U:O4'	2.16	0.46
31:4:2202:U:H4'	31:4:2726:A:O4'	2.16	0.46
31:4:2427:U:H2'	31:4:2428:C:C6	2.50	0.46
31:4:2480:A:H2'	31:4:2481:G:O4'	2.16	0.46
16:r:32:THR:HG23	16:r:32:THR:O	2.16	0.46
20:v:1:MET:HG3	20:v:59:GLU:OE1	2.16	0.46
20:v:60:VAL:O	20:v:71:LYS:HG2	2.16	0.46
31:4:580:U:H2'	31:4:581:C:H6	1.78	0.46
31:4:797:G:H2'	31:4:798:G:H8	1.80	0.46
31:4:1309:U:H2'	31:4:1310:G:H8	1.80	0.46
31:4:1953:U:H2'	31:4:1954:G:H8	1.80	0.46
1:b:64:VAL:HG21	1:b:86:ARG:HH12	1.81	0.46
4:e:145:VAL:HG12	4:e:147:ARG:H	1.81	0.46
20:v:3:THR:HG23	20:v:64:VAL:HG23	1.98	0.46
20:v:21:ARG:HA	20:v:25:LYS:O	2.15	0.46
30:a:45:ALA:HB3	30:a:213:SER:HB2	1.98	0.46
31:4:1025:G:H4'	31:4:1026:G:H5'	1.98	0.46
31:4:2233:U:H2'	31:4:2234:U:H5'	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:2585:U:H2'	31:4:2586:G:H8	1.81	0.46
31:4:2764:C:H2'	31:4:2765:U:C6	2.50	0.46
17:s:109:ASP:OD1	17:s:110:ARG:NH2	2.49	0.46
23:y:41:HIS:CE1	31:4:96:C:H4'	2.50	0.46
31:4:283:G:H2'	31:4:284:U:O4'	2.16	0.46
31:4:959:A:O2'	31:4:960:A:H5'	2.15	0.46
31:4:2060:A:H2'	31:4:2061:G:O4'	2.16	0.46
31:4:2202:U:H2'	31:4:2203:U:C6	2.51	0.46
31:4:2962:G:O2'	31:4:2963:A:H5'	2.16	0.46
8:i:10:LEU:HD21	31:4:1198:A:C4	2.50	0.46
8:i:74:PRO:CB	31:4:1188:U:H5'	2.46	0.46
21:w:32:ILE:HG21	21:w:35:ARG:HG3	1.98	0.46
23:y:4:LYS:NZ	31:4:102:U:H3	2.14	0.46
25:A:16:CYS:SG	25:A:17:SER:N	2.88	0.46
31:4:275:C:H3'	31:4:276:U:H5''	1.98	0.46
31:4:718:A:H2'	31:4:719:C:O4'	2.15	0.46
31:4:2049:G:H2'	31:4:2050:G:O4'	2.16	0.46
31:4:2413:C:C2'	31:4:2414:G:H5'	2.46	0.46
31:4:2770:G:O2'	31:4:2771:G:H5'	2.16	0.46
1:b:199:HIS:O	1:b:202:ARG:HG2	2.15	0.46
1:b:220:ARG:HD2	31:4:1955:U:OP2	2.14	0.46
2:c:9:VAL:HB	2:c:26:VAL:HG23	1.98	0.46
3:d:181:ILE:HG23	11:l:2:ARG:HG3	1.98	0.46
4:e:101:ARG:O	4:e:105:ILE:HG22	2.16	0.46
7:h:119:PRO:O	7:h:120:ALA:HB3	2.16	0.46
11:l:101:ILE:HB	11:l:105:ILE:HG13	1.97	0.46
19:u:67:SER:OG	31:4:335:C:O2	2.34	0.46
31:4:327:G:H2'	31:4:328:U:O4'	2.16	0.46
31:4:671:C:H2'	31:4:672:C:H6	1.80	0.46
31:4:872:U:H2'	31:4:873:C:C6	2.52	0.46
31:4:1163:U:H2'	31:4:1164:G:C8	2.51	0.46
31:4:1327:U:H2'	31:4:1328:C:C6	2.51	0.46
31:4:1934:C:H2'	31:4:1935:G:O4'	2.15	0.46
31:4:1949:A:H2'	31:4:1950:C:C6	2.51	0.46
31:4:2008:U:H2'	31:4:2009:C:C6	2.51	0.46
31:4:2034:G:C2'	31:4:2035:G:H5''	2.46	0.46
31:4:2083:U:C4	31:4:2680:U:H1'	2.51	0.46
31:4:2929:G:H2'	31:4:2930:G:C8	2.50	0.46
31:4:2946:U:H2'	31:4:2947:G:C8	2.51	0.46
8:i:42:ASN:HA	8:i:45:THR:HG22	1.98	0.45
10:k:9:ASN:OD1	10:k:18:ARG:NH2	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:155:A:H2'	31:4:156:A:C8	2.51	0.45
31:4:1099:G:O2'	31:4:1100:A:H5'	2.16	0.45
31:4:1798:C:H2'	31:4:1799:U:O4'	2.16	0.45
31:4:2939:G:H2'	31:4:2940:G:C8	2.51	0.45
3:d:75:SER:HB3	3:d:78:TRP:CD1	2.50	0.45
31:4:374:A:H2'	31:4:375:G:O4'	2.16	0.45
31:4:538:A:H2'	31:4:539:G:O4'	2.15	0.45
2:c:115:GLY:N	31:4:2949:A:OP2	2.48	0.45
31:4:1670:U:H2'	31:4:1671:G:O4'	2.16	0.45
31:4:2600:G:H2'	31:4:2603:C:H42	1.81	0.45
4:e:47:LYS:HA	4:e:50:ASP:OD2	2.17	0.45
8:i:86:LYS:O	8:i:86:LYS:HD2	2.16	0.45
13:o:49:VAL:CG2	13:o:85:LYS:HG3	2.46	0.45
31:4:443:A:H5''	31:4:444:C:C5'	2.46	0.45
31:4:1230:C:H2'	31:4:1231:A:C8	2.52	0.45
31:4:1907:U:C5	31:4:1912:A:N7	2.77	0.45
1:b:204:LEU:HB3	1:b:209:ALA:HB3	1.98	0.45
21:w:15:LYS:HE3	31:4:2390:U:P	2.56	0.45
22:x:2:ARG:O	22:x:11:PRO:HD3	2.17	0.45
24:z:10:ARG:HH21	24:z:10:ARG:HG3	1.81	0.45
25:A:3:LYS:O	25:A:4:ASP:OD2	2.34	0.45
31:4:527:C:H4'	31:4:528:A:O4'	2.17	0.45
31:4:1818:A:H2'	31:4:1819:C:O4'	2.15	0.45
4:e:91:ARG:HD3	31:4:1111:A:C5'	2.47	0.45
5:f:102:ILE:HD13	5:f:130:ILE:HD11	1.98	0.45
9:j:80:HIS:O	9:j:81:ILE:C	2.59	0.45
11:l:94:THR:HA	11:l:97:ALA:HB3	1.99	0.45
12:n:3:HIS:O	12:n:4:ARG:HB2	2.15	0.45
12:n:92:GLY:O	31:4:3008:C:H1'	2.17	0.45
31:4:644:A:C2'	31:4:645:C:H5''	2.45	0.45
31:4:875:G:H2'	31:4:876:C:H6	1.81	0.45
31:4:904:G:H2'	31:4:905:A:C8	2.52	0.45
31:4:1657:G:H2'	31:4:1658:G:O4'	2.16	0.45
31:4:1981:A:H2'	31:4:1982:A:C8	2.51	0.45
7:h:37:LYS:HE2	31:4:1213:A:N7	2.31	0.45
17:s:42:LYS:HB2	31:4:2138:G:H5''	1.99	0.45
17:s:69:LEU:HD12	17:s:108:SER:O	2.17	0.45
18:t:91:GLN:O	18:t:91:GLN:HG2	2.16	0.45
30:a:198:LYS:NZ	31:4:1996:C:H4'	2.31	0.45
31:4:904:G:O2'	31:4:905:A:H5'	2.17	0.45
31:4:1069:C:H3'	31:4:1070:C:C5'	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:2425:A:H62	31:4:2447:G:H1'	1.81	0.45
5:f:38:ASP:OD2	5:f:54:ARG:NH1	2.49	0.45
20:v:60:VAL:HG12	20:v:71:LYS:HB3	1.97	0.45
31:4:783:A:H2'	31:4:784:G:C5'	2.46	0.45
31:4:917:A:C2	31:4:918:A:H1'	2.52	0.45
31:4:2376:C:OP2	31:4:2377:U:H5	2.00	0.45
1:b:64:VAL:HG21	1:b:86:ARG:NH1	2.31	0.45
3:d:6:LYS:HE3	3:d:119:ILE:HD12	1.97	0.45
8:i:93:ASN:ND2	31:4:1205:A:H4'	2.32	0.45
31:4:12:U:C2'	31:4:13:A:H5'	2.47	0.45
31:4:578:G:H21	31:4:1380:G:N2	2.14	0.45
31:4:690:G:O2'	31:4:691:C:H5'	2.17	0.45
31:4:1026:G:H2'	31:4:1027:C:O4'	2.17	0.45
31:4:1295:C:O2'	31:4:1296:G:H5'	2.17	0.45
31:4:1419:C:O2'	31:4:1420:G:H5'	2.16	0.45
31:4:1473:C:H5'	31:4:1473:C:H6	1.81	0.45
31:4:1515:A:H2'	31:4:1516:G:C8	2.51	0.45
31:4:1914:A:H1'	31:4:2066:A:N6	2.32	0.45
31:4:2575:G:H5''	31:4:2631:A:N6	2.32	0.45
6:g:22:LYS:HD2	31:4:2222:A:P	2.57	0.45
10:k:16:ALA:HA	10:k:46:ALA:HB1	1.97	0.45
14:p:74:GLN:HB2	14:p:77:SER:OG	2.17	0.45
17:s:14:ALA:O	17:s:18:ARG:HG3	2.17	0.45
31:4:12:U:H5'	31:4:12:U:H6	1.82	0.45
31:4:74:A:H4'	31:4:75:G:O5'	2.15	0.45
31:4:184:C:H4'	31:4:217:A:C2	2.52	0.45
31:4:1182:A:H2	31:4:1212:A:N1	2.15	0.45
31:4:1189:U:H4'	31:4:1198:A:C8	2.51	0.45
31:4:1199:G:H1'	31:4:1217:A:C5	2.52	0.45
31:4:1200:C:H5''	31:4:1225:U:OP1	2.16	0.45
4:e:93:GLU:HA	4:e:96:TRP:HD1	1.81	0.44
10:k:30:ARG:NH2	31:4:2802:G:H5'	2.32	0.44
30:a:217:THR:HG23	31:4:2252:G:C2	2.52	0.44
31:4:1578:G:O2'	31:4:1579:C:H5'	2.16	0.44
31:4:2632:U:H5''	31:4:2633:G:O5'	2.17	0.44
5:f:82:PHE:HB3	5:f:140:ILE:HD13	1.99	0.44
7:h:95:LEU:HD22	7:h:99:PHE:CD2	2.52	0.44
8:i:134:SER:OG	31:4:1207:C:C1'	2.66	0.44
16:r:46:GLU:OE1	16:r:48:LYS:HB2	2.17	0.44
17:s:17:VAL:CG2	17:s:76:VAL:HG11	2.44	0.44
17:s:57:ASN:CG	31:4:495:G:H1'	2.42	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:t:65:GLY:HA3	18:t:77:ARG:O	2.16	0.44
30:a:221:GLY:HA2	31:4:2304:A:O2'	2.16	0.44
31:4:934:U:H2'	31:4:935:C:C6	2.52	0.44
31:4:1097:C:H1'	31:4:1119:A:H61	1.81	0.44
31:4:2683:U:C2'	31:4:2684:C:H5'	2.46	0.44
31:4:2967:G:H2'	31:4:2968:C:C6	2.52	0.44
1:b:245:THR:C	1:b:247:TRP:N	2.76	0.44
5:f:93:TYR:HE2	5:f:151:ARG:HD2	1.83	0.44
7:h:57:ASN:O	7:h:63:ALA:HB2	2.17	0.44
10:k:47:ILE:HG22	10:k:49:ARG:H	1.82	0.44
15:q:88:GLU:OE2	16:r:52:PRO:HB3	2.17	0.44
29:F:1:MET:H2	31:4:2654:G:H1'	1.82	0.44
30:a:5:THR:HG22	30:a:6:LYS:N	2.22	0.44
31:4:96:C:H2'	31:4:97:C:C6	2.52	0.44
31:4:356:G:H2'	31:4:357:C:O4'	2.17	0.44
31:4:441:U:H2'	31:4:442:G:H8	1.83	0.44
31:4:1837:U:H2'	31:4:1838:G:H8	1.80	0.44
31:4:1918:C:H2'	31:4:1919:A:C5	2.53	0.44
31:4:1977:G:O2'	31:4:1978:G:H5'	2.17	0.44
31:4:2593:C:H2'	31:4:2594:C:H6	1.82	0.44
31:4:2661:U:H2'	31:4:2662:A:O4'	2.16	0.44
4:e:56:LEU:HD13	4:e:88:VAL:HG13	1.99	0.44
4:e:69:ALA:HB3	4:e:81:GLY:H	1.83	0.44
4:e:113:PHE:HZ	4:e:116:LEU:HB2	1.83	0.44
7:h:24:SER:HA	7:h:86:MET:HB3	1.98	0.44
11:l:57:LEU:HD13	11:l:60:ARG:NH1	2.33	0.44
12:n:79:LEU:O	12:n:80:PHE:HB2	2.18	0.44
26:B:4:GLN:O	31:4:2145:U:H4'	2.17	0.44
29:F:10:LEU:HD12	29:F:33:HIS:CG	2.52	0.44
31:4:202:U:H2'	31:4:203:A:O4'	2.18	0.44
31:4:1170:G:H2'	31:4:1171:C:C6	2.53	0.44
31:4:1215:G:H2'	31:4:1217:A:C4'	2.47	0.44
31:4:2556:G:H5''	31:4:2557:G:O5'	2.17	0.44
1:b:200:MET:HE3	31:4:1948:U:C6	2.51	0.44
14:p:51:ASN:HB2	31:4:2974:G:P	2.58	0.44
16:r:48:LYS:HG3	16:r:49:ILE:N	2.32	0.44
31:4:18:U:H2'	31:4:19:A:H8	1.83	0.44
31:4:368:A:H2'	31:4:369:U:O4'	2.16	0.44
31:4:395:U:H2'	31:4:396:G:C8	2.52	0.44
31:4:1832:C:H2'	31:4:1833:A:C8	2.53	0.44
31:4:2187:A:H2'	31:4:2189:G:OP1	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:2242:A:O2'	31:4:2294:U:H2'	2.17	0.44
3:d:57:LYS:HZ3	3:d:59:PRO:HG3	1.83	0.44
8:i:74:PRO:HG3	31:4:1188:U:C5'	2.47	0.44
10:k:110:GLU:HA	10:k:113:MET:HG2	2.00	0.44
31:4:870:U:O2'	31:4:871:U:H5'	2.18	0.44
31:4:875:G:H2'	31:4:876:C:C6	2.53	0.44
31:4:941:A:H2'	31:4:942:G:O4'	2.17	0.44
31:4:2307:C:H3'	31:4:2307:C:H6	1.82	0.44
4:e:65:LEU:HD22	31:4:1108:C:C4	2.52	0.44
7:h:42:ARG:CZ	7:h:46:ARG:HG3	2.48	0.44
19:u:10:VAL:HA	19:u:72:PHE:H	1.82	0.44
23:y:9:LYS:HG2	23:y:11:VAL:HG12	2.00	0.44
25:A:15:SER:HB2	25:A:21:VAL:HG22	1.99	0.44
31:4:44:A:H2'	31:4:45:G:O4'	2.17	0.44
31:4:108:G:O2'	31:4:109:C:H5'	2.17	0.44
31:4:1338:G:H5''	31:4:1340:G:O4'	2.17	0.44
31:4:2336:C:H2'	31:4:2337:G:C8	2.52	0.44
31:4:2498:G:H2'	31:4:2499:G:C8	2.53	0.44
31:4:2782:A:O3'	31:4:2783:G:H4'	2.18	0.44
1:b:270:ARG:NH2	31:4:1926:U:OP2	2.50	0.44
7:h:115:GLY:O	7:h:122:GLN:HG2	2.17	0.44
22:x:13:THR:HG21	31:4:189:G:OP2	2.18	0.44
26:B:24:VAL:C	26:B:26:SER:H	2.26	0.44
31:4:213:A:H2'	31:4:214:G:C8	2.52	0.44
31:4:319:G:H2'	31:4:320:A:O4'	2.18	0.44
31:4:608:A:H2'	31:4:609:A:C8	2.53	0.44
31:4:842:U:H2'	31:4:843:G:C8	2.53	0.44
31:4:896:A:H5'	31:4:897:C:C6	2.53	0.44
31:4:1311:U:H2'	31:4:1312:U:C6	2.52	0.44
31:4:2152:G:OP2	31:4:2162:U:H4'	2.17	0.44
3:d:55:SER:OG	3:d:56:GLY:N	2.51	0.44
4:e:168:LEU:HD23	4:e:168:LEU:C	2.43	0.44
5:f:51:PHE:CE2	5:f:68:ARG:HG2	2.53	0.44
11:l:30:THR:O	11:l:32:GLY:N	2.51	0.44
18:t:10:VAL:HG13	18:t:11:LEU:N	2.33	0.44
26:B:30:ASP:HB3	26:B:34:GLY:N	2.33	0.44
31:4:216:A:H2'	31:4:217:A:O4'	2.18	0.44
31:4:1085:C:H2'	31:4:1086:G:H8	1.83	0.44
31:4:2190:A:HO2'	31:4:2191:C:H5'	1.82	0.44
31:4:2999:U:H5'	31:4:3000:A:OP1	2.18	0.44
2:c:97:SER:HB2	2:c:99:GLU:HG2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:121:PHE:CZ	4:e:127:TYR:HB2	2.53	0.43
7:h:72:LEU:C	7:h:74:ASP:H	2.25	0.43
9:j:3:THR:HG22	31:4:995:C:N3	2.33	0.43
10:k:121:GLU:CD	10:k:122:VAL:HG23	2.43	0.43
11:l:29:LYS:O	11:l:30:THR:OG1	2.30	0.43
12:n:2:ARG:HG2	12:n:2:ARG:HH11	1.83	0.43
15:q:50:ARG:HG3	15:q:50:ARG:NH1	2.33	0.43
19:u:1:ALA:HB2	19:u:91:LYS:HD3	1.99	0.43
31:4:901:C:C3'	31:4:902:C:C5'	2.92	0.43
31:4:947:A:H2'	31:4:948:C:C6	2.53	0.43
31:4:1275:A:O2'	31:4:1276:U:H5'	2.18	0.43
31:4:1379:C:O2'	31:4:1380:G:H3'	2.17	0.43
31:4:1602:U:H2'	31:4:1603:G:O4'	2.18	0.43
31:4:1690:U:H2'	31:4:1691:U:C6	2.53	0.43
31:4:1794:G:O2'	31:4:1795:G:H5'	2.18	0.43
31:4:2291:A:H2'	31:4:2292:C:H5'	2.00	0.43
31:4:2673:G:H2'	31:4:2674:U:O4'	2.19	0.43
2:c:157:LYS:HE3	31:4:2747:C:OP1	2.18	0.43
5:f:1:SER:OG	5:f:2:ARG:N	2.50	0.43
14:p:26:GLU:HB3	14:p:84:SER:OG	2.18	0.43
31:4:170:U:H2'	31:4:171:U:C6	2.52	0.43
31:4:416:U:H3	31:4:2535:A:H61	1.64	0.43
31:4:519:U:H2'	31:4:520:G:C8	2.53	0.43
31:4:1001:A:H2'	31:4:1002:G:O4'	2.18	0.43
31:4:1979:U:H2'	31:4:1980:U:O4'	2.18	0.43
31:4:2009:C:H2'	31:4:2010:U:O4'	2.17	0.43
31:4:2198:A:H2'	31:4:2199:A:O4'	2.18	0.43
4:e:39:VAL:HG13	4:e:40:GLY:N	2.34	0.43
4:e:107:VAL:N	4:e:108:PRO:CD	2.81	0.43
5:f:116:LEU:HA	5:f:117:PRO:HD3	1.88	0.43
10:k:88:ASN:O	10:k:90:ASN:N	2.51	0.43
14:p:105:LYS:O	14:p:108:ARG:HG2	2.18	0.43
17:s:47:VAL:HA	17:s:50:VAL:HG12	2.00	0.43
17:s:57:ASN:O	17:s:61:ASN:ND2	2.51	0.43
20:v:92:VAL:HG13	20:v:92:VAL:O	2.18	0.43
21:w:37:ARG:HD3	21:w:37:ARG:HA	1.75	0.43
31:4:729:G:H4'	31:4:763:G:C5'	2.44	0.43
31:4:959:A:H2'	31:4:960:A:O4'	2.18	0.43
31:4:1050:A:H2'	31:4:1131:U:O4	2.18	0.43
31:4:1168:A:O2'	31:4:1169:G:H5'	2.18	0.43
31:4:1949:A:H2'	31:4:1950:C:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:2044:A:H2'	31:4:2045:U:C1'	2.48	0.43
31:4:2127:C:O2'	31:4:2128:C:H5'	2.18	0.43
31:4:2487:C:O2'	31:4:2488:G:H5'	2.18	0.43
31:4:2586:G:C6	31:4:2587:A:C6	3.07	0.43
31:4:2656:U:H2'	31:4:2658:A:O5'	2.18	0.43
3:d:149:ILE:HD12	3:d:170:ARG:O	2.19	0.43
18:t:17:SER:H	18:t:20:ALA:HB3	1.83	0.43
24:z:35:VAL:HG22	24:z:37:ARG:NH1	2.33	0.43
30:a:41:SER:OG	30:a:42:VAL:N	2.51	0.43
31:4:776:G:H1	31:4:2200:C:C5'	2.31	0.43
31:4:940:G:H2'	31:4:941:A:C5'	2.44	0.43
31:4:954:G:O2'	31:4:955:U:H5'	2.18	0.43
31:4:1025:G:C5	31:4:1263:C:H1'	2.53	0.43
31:4:1070:C:H4'	31:4:1070:C:OP1	2.19	0.43
31:4:1101:C:H2'	31:4:1102:C:O4'	2.17	0.43
31:4:1277:G:H2'	31:4:1278:C:C6	2.53	0.43
31:4:1603:G:O2'	31:4:1604:U:H6	2.02	0.43
31:4:2888:C:O2'	31:4:2889:A:H5'	2.17	0.43
4:e:122:ASP:OD2	4:e:123:GLY:N	2.51	0.43
4:e:124:ARG:NH1	31:4:2444:G:H4'	2.34	0.43
5:f:66:THR:HG23	31:4:2875:G:O2'	2.19	0.43
7:h:107:GLU:O	7:h:109:LYS:N	2.52	0.43
8:i:3:LYS:HD2	31:4:1228:C:OP1	2.18	0.43
8:i:88:GLY:HA2	8:i:97:VAL:HG21	1.99	0.43
9:j:12:LYS:O	9:j:41:LYS:NZ	2.51	0.43
12:n:3:HIS:CG	31:4:2948:A:H4'	2.53	0.43
15:q:88:GLU:OE2	15:q:88:GLU:N	2.51	0.43
20:v:6:ALA:HB3	20:v:65:VAL:HA	2.00	0.43
25:A:3:LYS:O	25:A:5:ILE:HG23	2.18	0.43
31:4:15:G:O2'	31:4:16:C:H5'	2.19	0.43
31:4:1318:G:H2'	31:4:1319:G:C8	2.51	0.43
31:4:1571:U:H2'	31:4:1572:G:C8	2.53	0.43
31:4:1692:C:O2'	31:4:1693:C:H5'	2.18	0.43
31:4:2093:C:H5''	31:4:2094:A:H2'	1.99	0.43
31:4:2471:U:H2'	31:4:2472:U:C6	2.53	0.43
1:b:240:GLY:HA3	31:4:2725:G:C5'	2.48	0.43
2:c:157:LYS:HG3	31:4:2747:C:H5''	2.00	0.43
4:e:146:ASP:OD2	4:e:146:ASP:N	2.50	0.43
5:f:42:VAL:C	5:f:43:LYS:HD3	2.43	0.43
16:r:7:SER:OG	16:r:8:GLY:N	2.51	0.43
31:4:284:U:H2'	31:4:285:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:974:G:H2'	31:4:974:G:N3	2.34	0.43
31:4:1029:G:H1'	31:4:1154:A:C6	2.54	0.43
31:4:1892:C:H2'	31:4:1893:U:C6	2.54	0.43
4:e:165:GLY:O	4:e:168:LEU:HB3	2.18	0.43
7:h:38:MET:HA	31:4:1210:U:O2'	2.18	0.43
8:i:92:PRO:CG	31:4:1205:A:H1'	2.40	0.43
10:k:70:ARG:NH1	10:k:74:GLY:O	2.51	0.43
31:4:622:G:H2'	31:4:623:C:C6	2.53	0.43
31:4:1190:G:OP1	31:4:1198:A:H5''	2.18	0.43
31:4:1197:A:H2	31:4:1224:A:H5''	1.78	0.43
31:4:1447:C:O2'	31:4:1448:C:H5'	2.18	0.43
31:4:1548:A:H2'	31:4:2339:A:H8	1.84	0.43
31:4:2425:A:N1	31:4:2449:U:H5	2.16	0.43
31:4:2711:G:H2'	31:4:2712:U:O4'	2.19	0.43
31:4:2777:C:H2'	31:4:2778:U:C6	2.54	0.43
8:i:79:LEU:H	8:i:79:LEU:HD12	1.83	0.43
9:j:25:LEU:HB3	31:4:1268:C:OP1	2.18	0.43
10:k:32:TYR:HH	31:4:2124:C:H5	1.66	0.43
19:u:90:LYS:HE2	19:u:90:LYS:HB3	1.84	0.43
20:v:3:THR:CG2	20:v:64:VAL:HG23	2.48	0.43
31:4:504:A:H2'	31:4:504:A:N3	2.33	0.43
31:4:581:C:H2'	31:4:582:A:H8	1.83	0.43
31:4:797:G:H2'	31:4:798:G:C8	2.54	0.43
31:4:1225:U:H2'	31:4:1226:A:C8	2.53	0.43
31:4:1394:G:H22	31:4:2140:G:H2'	1.84	0.43
31:4:1472:U:H3'	31:4:1473:C:H5'	2.00	0.43
31:4:2807:A:O2'	31:4:2808:U:H5'	2.18	0.43
31:4:2901:C:H2'	31:4:2902:C:H6	1.84	0.43
4:e:9:ASP:O	4:e:13:LYS:HE3	2.18	0.43
10:k:64:ARG:O	10:k:83:ALA:N	2.48	0.43
12:n:55:ALA:HA	12:n:80:PHE:CE1	2.54	0.43
13:o:90:VAL:HG22	13:o:91:SER:N	2.34	0.43
20:v:30:ILE:O	20:v:37:PRO:HA	2.19	0.43
31:4:138:U:C2'	31:4:139:U:H5''	2.49	0.43
31:4:445:C:C2'	31:4:446:G:H5'	2.48	0.43
31:4:535:G:O2'	31:4:536:G:H5'	2.18	0.43
31:4:558:U:H2'	31:4:559:G:C8	2.53	0.43
31:4:696:G:O2'	31:4:697:G:H5'	2.17	0.43
31:4:706:A:H2'	31:4:707:G:O4'	2.19	0.43
31:4:1069:C:H2'	31:4:1070:C:C5'	2.48	0.43
31:4:1085:C:H2'	31:4:1086:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:1255:A:H2'	31:4:1256:G:H5''	2.01	0.43
31:4:2067:U:O2'	31:4:2068:U:H5'	2.18	0.43
31:4:2618:G:O2'	31:4:2619:U:H6	2.01	0.43
31:4:2666:C:H2'	31:4:2667:C:C6	2.54	0.43
31:4:2871:U:H2'	31:4:2872:G:C5'	2.41	0.43
31:4:2974:G:H2'	31:4:2975:U:O4'	2.17	0.43
31:4:2997:G:H2'	31:4:2998:C:C6	2.54	0.43
3:d:162:ARG:HH12	31:4:321:U:H1'	1.82	0.43
4:e:116:LEU:N	4:e:175:PRO:HB2	2.31	0.43
5:f:26:LYS:HB3	5:f:31:GLU:HG3	2.01	0.43
6:g:2:GLN:O	6:g:39:ALA:HB3	2.18	0.43
9:j:81:ILE:HB	9:j:82:GLY:H	1.67	0.43
18:t:70:HIS:CE1	31:4:63:A:H2	2.36	0.43
22:x:46:VAL:HG12	22:x:48:LEU:HG	2.00	0.43
31:4:111:A:O2'	31:4:112:U:H5'	2.19	0.43
31:4:282:A:O2'	31:4:283:G:H5'	2.19	0.43
31:4:312:G:H5'	31:4:331:C:O2'	2.19	0.43
31:4:588:U:O4	31:4:670:A:H1'	2.19	0.43
31:4:1199:G:O2'	31:4:1217:A:H2'	2.19	0.43
31:4:1316:U:O2'	31:4:1317:A:H5'	2.18	0.43
31:4:2201:C:O2'	31:4:2202:U:H5'	2.19	0.43
31:4:2206:C:H2'	31:4:2207:U:C6	2.54	0.43
31:4:2345:G:O2'	31:4:2346:G:H5'	2.18	0.43
31:4:3024:C:H2'	31:4:3025:U:C6	2.54	0.43
4:e:59:ILE:HA	4:e:139:GLU:HG2	2.00	0.42
5:f:156:TYR:CZ	5:f:171:LYS:HD2	2.54	0.42
8:i:10:LEU:HD21	31:4:1198:A:C5	2.54	0.42
12:n:47:VAL:C	12:n:50:PRO:HD2	2.44	0.42
23:y:2:LYS:HD2	31:4:78:U:OP2	2.18	0.42
24:z:37:ARG:HH21	31:4:929:U:H4'	1.83	0.42
31:4:1704:U:O2'	31:4:1705:C:H5'	2.19	0.42
31:4:2214:U:H2'	31:4:2215:G:H8	1.82	0.42
31:4:2709:G:H4'	31:4:2710:G:O5'	2.19	0.42
1:b:18:VAL:O	1:b:18:VAL:HG13	2.18	0.42
2:c:146:ILE:HD11	31:4:2180:A:N7	2.33	0.42
4:e:38:GLY:HA3	31:4:2440:U:O2	2.20	0.42
4:e:125:GLY:O	4:e:157:THR:OG1	2.35	0.42
5:f:106:LEU:O	5:f:151:ARG:NH2	2.51	0.42
7:h:11:ILE:HD12	7:h:66:GLY:HA3	2.01	0.42
7:h:19:ALA:HB3	7:h:20:LYS:NZ	2.34	0.42
7:h:21:GLY:HA2	7:h:88:HIS:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:o:16:ARG:HA	13:o:19:GLN:HG2	2.01	0.42
17:s:2:GLU:HB3	17:s:106:VAL:CG1	2.48	0.42
26:B:14:MET:SD	31:4:2173:C:H5'	2.59	0.42
29:F:1:MET:HB2	29:F:34:LYS:O	2.19	0.42
31:4:310:A:O2'	31:4:311:A:H2'	2.18	0.42
31:4:1303:A:C5'	31:4:1304:U:H5'	2.48	0.42
31:4:1672:A:H2'	31:4:1673:A:C8	2.54	0.42
31:4:2455:A:H2'	31:4:2456:A:C8	2.54	0.42
31:4:2457:U:H2'	31:4:2458:G:C8	2.54	0.42
31:4:2946:U:H4'	31:4:2965:A:C4'	2.49	0.42
4:e:40:GLY:HA2	4:e:84:ILE:HG13	2.02	0.42
5:f:96:ALA:HB3	5:f:103:ASN:HB3	2.00	0.42
7:h:55:VAL:HG22	31:4:1212:A:P	2.60	0.42
8:i:75:ALA:HB1	8:i:128:ILE:HG23	2.00	0.42
9:j:95:ARG:HG2	9:j:95:ARG:HH11	1.84	0.42
15:q:101:ASP:HB3	15:q:104:ALA:HB3	2.01	0.42
20:v:4:ILE:N	20:v:4:ILE:HD12	2.34	0.42
20:v:20:LEU:HD21	20:v:41:GLU:HG3	2.01	0.42
30:a:12:ARG:HG2	30:a:220:ALA:HB1	2.01	0.42
30:a:48:LEU:HD11	30:a:165:ASN:OD1	2.19	0.42
31:4:150:U:H2'	31:4:151:C:C6	2.54	0.42
31:4:677:A:O2'	31:4:2199:A:H5'	2.19	0.42
31:4:936:A:H2'	31:4:937:C:C6	2.54	0.42
31:4:1049:G:H2'	31:4:1132:A:N1	2.35	0.42
31:4:1232:C:H2'	31:4:1233:U:O4'	2.20	0.42
31:4:2540:A:H2'	31:4:2541:G:O4'	2.19	0.42
31:4:3012:U:H2'	31:4:3013:G:C8	2.54	0.42
5:f:71:LEU:HA	5:f:74:MET:HB2	2.01	0.42
11:l:93:ASN:OD1	11:l:94:THR:N	2.51	0.42
31:4:106:C:H2'	31:4:107:G:H8	1.85	0.42
31:4:162:U:C2'	31:4:163:C:H5'	2.50	0.42
31:4:438:G:H2'	31:4:439:A:C8	2.54	0.42
31:4:755:U:H2'	31:4:756:A:H8	1.83	0.42
31:4:832:U:H2'	31:4:833:A:C8	2.54	0.42
31:4:1136:C:H2'	31:4:1137:C:C6	2.54	0.42
31:4:2263:A:H2'	31:4:2264:G:O4'	2.19	0.42
31:4:2374:G:H2'	31:4:2375:A:H8	1.84	0.42
31:4:2671:G:H2'	31:4:2672:G:C8	2.54	0.42
31:4:2970:G:O2'	31:4:2971:G:H5'	2.19	0.42
1:b:79:ARG:NH1	1:b:81:GLU:OE2	2.52	0.42
2:c:29:VAL:O	2:c:185:ASN:HB3	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:110:ILE:HG22	4:e:113:PHE:HB2	2.02	0.42
8:i:20:SER:O	8:i:24:GLY:HA3	2.19	0.42
9:j:7:LYS:HA	9:j:8:PRO:HD3	1.85	0.42
15:q:91:ARG:HD3	31:4:997:G:OP1	2.20	0.42
17:s:50:VAL:HG22	17:s:105:VAL:HG22	2.02	0.42
18:t:8:LEU:HD13	23:y:21:LEU:HB3	2.00	0.42
22:x:36:ARG:HA	22:x:47:THR:HA	2.01	0.42
23:y:41:HIS:CE1	23:y:42:LEU:HG	2.55	0.42
31:4:35:G:H2'	31:4:36:G:O4'	2.19	0.42
31:4:138:U:H2'	31:4:139:U:H4'	2.01	0.42
31:4:493:G:O2'	31:4:494:G:H5'	2.20	0.42
31:4:1287:U:O2'	31:4:1288:G:H5'	2.20	0.42
31:4:1808:U:H2'	31:4:1809:G:O4'	2.19	0.42
31:4:1868:G:O2'	31:4:1869:C:H5'	2.19	0.42
31:4:2468:A:H2'	31:4:2469:G:H8	1.84	0.42
31:4:2648:C:O2'	31:4:2649:C:H5'	2.19	0.42
31:4:2767:A:H2'	31:4:2768:G:O4'	2.18	0.42
31:4:2873:C:C4	31:4:2874:U:C4	3.08	0.42
8:i:4:VAL:HG12	8:i:7:TYR:HB3	2.02	0.42
11:l:16:GLY:HA2	31:4:662:G:O3'	2.18	0.42
15:q:111:LYS:HD2	15:q:111:LYS:HA	1.85	0.42
30:a:57:GLN:CD	30:a:201:PRO:HB2	2.44	0.42
30:a:206:GLY:H	31:4:2004:A:H5''	1.85	0.42
31:4:78:U:H2'	31:4:79:C:H6	1.79	0.42
31:4:622:G:O2'	31:4:623:C:H5'	2.19	0.42
31:4:957:C:C4	31:4:2586:G:H1'	2.55	0.42
31:4:1171:C:H2'	31:4:1172:C:O4'	2.20	0.42
31:4:1239:A:C2'	31:4:1240:G:H4'	2.50	0.42
31:4:2156:U:H2'	31:4:2157:G:O4'	2.20	0.42
2:c:9:VAL:HA	2:c:197:THR:HG23	2.01	0.42
3:d:48:THR:H	3:d:51:GLU:CD	2.28	0.42
4:e:107:VAL:HA	4:e:110:ILE:HG13	2.02	0.42
4:e:124:ARG:HD3	4:e:124:ARG:HA	1.91	0.42
18:t:2:ILE:O	18:t:2:ILE:HG12	2.20	0.42
31:4:176:A:C2'	31:4:177:G:H5'	2.49	0.42
31:4:301:G:H1'	31:4:302:C:C6	2.55	0.42
31:4:745:G:H2'	31:4:746:U:H5'	2.02	0.42
31:4:1081:A:H3'	31:4:1082:G:C8	2.53	0.42
31:4:1187:G:H1	31:4:1207:C:H42	1.66	0.42
31:4:1495:A:C2'	31:4:1496:G:H5'	2.50	0.42
31:4:1785:U:H2'	31:4:1786:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:2425:A:N6	31:4:2447:G:H1'	2.35	0.42
31:4:2426:A:C2'	31:4:2427:U:H5'	2.50	0.42
31:4:2468:A:H2'	31:4:2469:G:C8	2.55	0.42
1:b:27:LYS:HA	1:b:28:PRO:HD3	1.90	0.42
2:c:59:ARG:NH1	31:4:2958:C:H3'	2.34	0.42
3:d:51:GLU:OE1	3:d:51:GLU:N	2.53	0.42
4:e:152:ASP:OD1	4:e:152:ASP:N	2.52	0.42
6:g:1:MET:N	6:g:21:VAL:O	2.52	0.42
7:h:36:ASP:O	7:h:40:GLU:HG2	2.20	0.42
13:o:31:THR:OG1	13:o:34:HIS:O	2.38	0.42
18:t:33:LYS:HG2	18:t:80:TRP:CE3	2.55	0.42
31:4:439:A:O2'	31:4:440:C:H5'	2.19	0.42
31:4:655:A:H4'	31:4:656:G:C5'	2.37	0.42
31:4:882:G:H2'	31:4:883:G:C8	2.49	0.42
31:4:953:G:O2'	31:4:954:G:H5'	2.19	0.42
31:4:1226:A:H2'	31:4:1227:G:O4'	2.19	0.42
31:4:1775:U:P	31:4:1775:U:H3'	2.59	0.42
31:4:2378:G:N7	31:4:2623:G:OP2	2.53	0.42
31:4:2415:A:O2'	31:4:2416:A:H2'	2.19	0.42
31:4:2555:C:H5'	31:4:2557:G:H5'	2.02	0.42
31:4:2822:G:H2'	31:4:2823:U:O4'	2.18	0.42
7:h:29:ASP:HB3	7:h:56:ARG:NH2	2.29	0.42
8:i:116:MET:HB3	8:i:124:MET:HE2	2.02	0.42
9:j:91:GLU:O	9:j:95:ARG:HG2	2.19	0.42
12:n:79:LEU:C	12:n:81:ASN:H	2.28	0.42
13:o:34:HIS:HA	13:o:53:THR:OG1	2.20	0.42
14:p:20:ARG:HD3	14:p:112:ARG:HH12	1.85	0.42
18:t:61:LEU:HD21	18:t:82:LYS:HD2	2.00	0.42
31:4:816:C:H2'	31:4:817:C:H6	1.84	0.42
31:4:1061:A:H2'	31:4:1062:U:H5'	2.01	0.42
31:4:2940:G:H2'	31:4:2941:A:O4'	2.20	0.42
4:e:76:PHE:CE2	31:4:2438:C:H2'	2.55	0.42
8:i:74:PRO:CG	31:4:1188:U:H5'	2.48	0.42
23:y:31:GLN:HG2	23:y:37:LEU:HB2	2.01	0.42
31:4:704:G:H1'	31:4:727:A:H61	1.84	0.42
31:4:1001:A:H2'	31:4:1002:G:H5'	2.02	0.42
31:4:1061:A:H2'	31:4:1062:U:C5'	2.50	0.42
31:4:1063:U:H2'	31:4:1066:G:H22	1.85	0.42
31:4:1654:C:H2'	31:4:1655:G:O4'	2.19	0.42
31:4:2442:A:H2'	31:4:2443:G:H8	1.83	0.42
31:4:2625:A:O2'	31:4:2626:C:H5'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:37:VAL:HG12	2:c:48:ILE:HG22	2.02	0.41
9:j:41:LYS:HD2	9:j:50:THR:HG22	2.01	0.41
11:l:17:LYS:HB3	11:l:27:LEU:HD13	2.02	0.41
11:l:141:LYS:HZ3	11:l:143:GLU:HB3	1.85	0.41
14:p:61:ARG:HG3	14:p:61:ARG:NH2	2.35	0.41
15:q:10:ARG:HH11	15:q:10:ARG:HG3	1.85	0.41
19:u:50:ALA:C	19:u:52:ASN:H	2.28	0.41
22:x:63:ILE:HG23	22:x:64:ASP:N	2.35	0.41
31:4:845:A:N7	31:4:847:U:H1'	2.35	0.41
31:4:961:C:H2'	31:4:962:G:H5'	2.02	0.41
31:4:1266:G:H2'	31:4:1267:G:O4'	2.20	0.41
31:4:1308:U:H5'	31:4:1309:U:OP2	2.20	0.41
31:4:1970:G:H2'	31:4:1971:C:C6	2.55	0.41
31:4:2075:C:H2'	31:4:2076:G:H8	1.84	0.41
31:4:2814:G:H2'	31:4:2815:U:O4'	2.20	0.41
31:4:2849:A:H2'	31:4:2850:G:O4'	2.20	0.41
4:e:132:ARG:HH22	31:4:2434:C:H5'	1.85	0.41
4:e:135:ILE:HD12	4:e:140:ILE:HG21	2.02	0.41
6:g:5:LEU:HG	6:g:13:GLY:HA2	2.02	0.41
8:i:118:GLY:HA3	8:i:124:MET:HB2	2.03	0.41
13:o:3:LYS:NZ	31:4:1113:C:OP2	2.50	0.41
14:p:59:THR:HA	14:p:72:VAL:HA	2.02	0.41
22:x:68:ALA:HA	22:x:71:ARG:NH1	2.34	0.41
24:z:52:PHE:CD2	31:4:1149:G:H4'	2.55	0.41
31:4:151:C:H2'	31:4:152:A:H8	1.84	0.41
31:4:381:G:O2'	31:4:382:A:H5'	2.19	0.41
31:4:404:A:H1'	31:4:406:G:N3	2.34	0.41
31:4:548:G:H2'	31:4:549:G:O4'	2.20	0.41
31:4:859:G:C2'	31:4:860:U:OP2	2.68	0.41
31:4:1156:A:H2'	31:4:1157:A:H8	1.85	0.41
31:4:1660:A:C2'	31:4:1661:C:H5''	2.49	0.41
31:4:1705:C:H2'	31:4:1706:U:O4'	2.20	0.41
31:4:1810:G:N3	31:4:1885:A:H1'	2.35	0.41
31:4:2270:A:H2'	31:4:2271:C:N1	2.35	0.41
31:4:2947:G:H2'	31:4:2949:A:N7	2.35	0.41
1:b:261:ARG:NH2	31:4:1929:A:C8	2.89	0.41
15:q:91:ARG:NH2	31:4:1281:C:OP1	2.51	0.41
18:t:24:MET:O	18:t:24:MET:HE3	2.20	0.41
22:x:21:LEU:HB2	31:4:200:U:H4'	2.03	0.41
28:E:30:HIS:CD2	28:E:31:ILE:HG23	2.52	0.41
31:4:458:G:N2	31:4:469:G:H2'	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:1052:C:H2'	31:4:1053:U:O4'	2.20	0.41
31:4:1237:C:H2'	31:4:1238:G:O4'	2.20	0.41
31:4:1303:A:H5''	31:4:1304:U:H5'	2.01	0.41
31:4:1624:A:H2'	31:4:1626:C:N4	2.36	0.41
31:4:1985:G:H1'	31:4:2013:A:H61	1.81	0.41
31:4:2555:C:C5'	31:4:2557:G:H5'	2.50	0.41
1:b:77:VAL:HA	1:b:93:VAL:HA	2.03	0.41
1:b:156:SER:O	1:b:159:THR:OG1	2.36	0.41
5:f:174:LYS:NZ	31:4:2659:A:OP1	2.54	0.41
12:n:72:ASP:O	12:n:76:VAL:HG23	2.21	0.41
16:r:68:ARG:HA	16:r:92:TRP:HA	2.02	0.41
18:t:10:VAL:HG13	18:t:11:LEU:H	1.85	0.41
22:x:40:GLU:OE1	22:x:40:GLU:N	2.46	0.41
29:F:32:LYS:HE3	31:4:2606:A:H5'	2.02	0.41
29:F:37:GLN:HG2	29:F:38:GLY:N	2.35	0.41
31:4:691:C:O2'	31:4:692:C:H5'	2.20	0.41
31:4:904:G:H2'	31:4:905:A:H8	1.85	0.41
31:4:1634:U:H2'	31:4:1635:C:C5	2.55	0.41
7:h:5:LEU:HD12	7:h:6:GLN:N	2.35	0.41
7:h:19:ALA:HB3	7:h:20:LYS:HZ2	1.85	0.41
13:o:4:LYS:HE2	13:o:8:ILE:HD11	2.02	0.41
15:q:5:ARG:NH1	31:4:585:G:N7	2.67	0.41
23:y:12:GLU:O	23:y:15:ASN:ND2	2.54	0.41
30:a:12:ARG:NH1	31:4:2304:A:H5'	2.36	0.41
31:4:69:C:H2'	31:4:70:G:C8	2.55	0.41
31:4:996:A:H2'	31:4:997:G:H8	1.84	0.41
31:4:1189:U:H3'	31:4:1190:G:C5'	2.50	0.41
31:4:1627:C:H2'	31:4:1628:G:H8	1.86	0.41
31:4:2425:A:N1	31:4:2449:U:C5	2.89	0.41
31:4:2783:G:O2'	31:4:2784:U:C5	2.73	0.41
2:c:131:ASP:O	2:c:136:ASN:ND2	2.40	0.41
2:c:142:VAL:HB	2:c:143:PRO:HD2	2.02	0.41
2:c:149:ASN:HB2	31:4:2702:G:O2'	2.20	0.41
3:d:97:ASN:HB2	3:d:100:MET:HB2	2.03	0.41
3:d:155:GLU:OE2	3:d:159:LEU:HG	2.21	0.41
7:h:24:SER:HB2	7:h:116:GLU:HB2	2.02	0.41
10:k:24:VAL:HG13	10:k:33:ALA:HB2	2.03	0.41
13:o:29:HIS:HB3	13:o:36:TYR:HB2	2.02	0.41
13:o:106:LEU:O	13:o:106:LEU:HD23	2.21	0.41
14:p:50:ARG:NH1	14:p:52:ARG:HG3	2.34	0.41
31:4:987:C:H2'	31:4:988:A:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:1868:G:H2'	31:4:1869:C:O4'	2.21	0.41
31:4:2223:A:H2'	31:4:2223:A:N3	2.36	0.41
31:4:2592:G:H2'	31:4:2593:C:C6	2.55	0.41
31:4:2793:A:O2'	31:4:2794:C:H5'	2.21	0.41
31:4:2871:U:H3'	31:4:2872:G:H5''	2.02	0.41
31:4:2926:U:H4'	31:4:2927:A:C5	2.55	0.41
3:d:48:THR:C	3:d:50:ALA:H	2.28	0.41
4:e:64:PRO:CA	4:e:88:VAL:HG12	2.45	0.41
6:g:47:PHE:CD2	6:g:52:ALA:HB2	2.56	0.41
7:h:37:LYS:NZ	31:4:1210:U:H2'	2.36	0.41
7:h:56:ARG:HD2	31:4:1212:A:C1'	2.28	0.41
10:k:91:SER:O	10:k:92:GLU:C	2.64	0.41
13:o:68:LYS:HE3	31:4:1115:C:C4'	2.49	0.41
27:D:30:VAL:O	27:D:34:ARG:HG2	2.21	0.41
29:F:1:MET:N	31:4:2654:G:H1'	2.36	0.41
31:4:756:A:H2'	31:4:757:G:O4'	2.20	0.41
31:4:1289:C:H2'	31:4:1290:G:H8	1.86	0.41
31:4:1341:A:H62	31:4:1364:G:H1'	1.82	0.41
31:4:2018:A:H2'	31:4:2019:G:O4'	2.20	0.41
31:4:2461:A:H5''	31:4:2462:U:OP1	2.20	0.41
4:e:76:PHE:HB2	4:e:78:ILE:CD1	2.51	0.41
5:f:77:GLY:O	5:f:81:GLY:HA2	2.20	0.41
6:g:5:LEU:HD23	6:g:17:ASP:O	2.21	0.41
14:p:92:ARG:HD3	31:4:1881:G:OP1	2.20	0.41
23:y:11:VAL:O	23:y:14:LEU:HB2	2.21	0.41
26:B:27:LEU:HB3	26:B:36:LYS:HB3	2.02	0.41
26:B:39:ARG:O	26:B:40:HIS:HB2	2.20	0.41
30:a:3:LYS:HB2	31:4:2302:C:OP1	2.19	0.41
30:a:54:LYS:HE2	30:a:57:GLN:HB2	2.03	0.41
31:4:1157:A:H2'	31:4:1158:C:O4'	2.21	0.41
31:4:1305:G:H2'	31:4:1306:C:O4'	2.20	0.41
31:4:1769:A:H2'	31:4:1770:G:O4'	2.20	0.41
31:4:2593:C:H2'	31:4:2594:C:C6	2.55	0.41
1:b:42:ARG:HD2	1:b:42:ARG:N	2.36	0.41
2:c:179:ARG:HB3	2:c:188:LEU:HD12	2.02	0.41
4:e:21:TYR:HD1	4:e:26:GLN:HE21	1.69	0.41
4:e:113:PHE:CE2	4:e:175:PRO:HG2	2.56	0.41
5:f:23:ILE:HD12	5:f:71:LEU:HD11	2.03	0.41
7:h:123:ILE:HG23	7:h:123:ILE:O	2.21	0.41
9:j:40:HIS:NE2	9:j:52:ASP:OD2	2.50	0.41
10:k:17:ARG:HD3	10:k:17:ARG:HA	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:p:59:THR:HG22	14:p:72:VAL:HG12	2.01	0.41
16:r:38:VAL:HG13	16:r:54:VAL:HG23	2.01	0.41
16:r:42:ALA:HB2	16:r:46:GLU:HG2	2.02	0.41
20:v:9:ARG:NH1	20:v:27:PRO:HB3	2.35	0.41
26:B:3:GLN:HA	31:4:2743:U:N3	2.35	0.41
28:E:42:HIS:HE1	31:4:2479:G:N7	2.19	0.41
30:a:7:ARG:NH2	31:4:2256:G:H5'	2.36	0.41
31:4:18:U:H2'	31:4:19:A:C8	2.56	0.41
31:4:322:A:H5'	31:4:340:A:H1'	2.03	0.41
31:4:598:U:H2'	31:4:599:A:H8	1.85	0.41
31:4:849:A:H2'	31:4:850:U:C6	2.56	0.41
31:4:893:C:C2'	31:4:894:U:H5'	2.51	0.41
31:4:907:G:H2'	31:4:908:C:O4'	2.21	0.41
31:4:968:C:H2'	31:4:969:G:C8	2.56	0.41
31:4:1053:U:H2'	31:4:1054:G:C8	2.55	0.41
31:4:1656:A:C2'	31:4:1657:G:H5'	2.50	0.41
31:4:2328:C:H2'	31:4:2329:G:H8	1.86	0.41
31:4:2357:U:H2'	31:4:2358:G:H8	1.84	0.41
31:4:2675:A:H2'	31:4:2676:U:C6	2.56	0.41
1:b:42:ARG:HG2	1:b:42:ARG:HH11	1.85	0.41
2:c:18:ASP:OD2	2:c:20:VAL:HG23	2.21	0.41
2:c:117:GLY:HA2	2:c:164:GLN:HE22	1.85	0.41
7:h:118:ILE:H	7:h:119:PRO:CD	2.33	0.41
12:n:108:ALA:HA	12:n:109:PRO:HD3	1.94	0.41
13:o:65:THR:HG23	13:o:65:THR:O	2.21	0.41
22:x:39:VAL:HG12	22:x:42:GLU:H	1.86	0.41
26:B:24:VAL:O	26:B:25:THR:HG22	2.21	0.41
30:a:171:ILE:HG13	30:a:171:ILE:O	2.21	0.41
31:4:195:A:N6	31:4:198:C:H3'	2.33	0.41
31:4:358:U:H2'	31:4:359:G:C8	2.55	0.41
31:4:854:C:O2'	31:4:855:G:H5'	2.20	0.41
31:4:1483:G:H2'	31:4:1484:G:H8	1.86	0.41
31:4:1586:U:H4'	31:4:1587:G:O4'	2.20	0.41
31:4:1976:A:H2'	31:4:1977:G:O4'	2.21	0.41
31:4:2338:U:C2	31:4:2340:A:N7	2.89	0.41
31:4:2420:U:H2'	31:4:2421:G:H8	1.86	0.41
31:4:2618:G:HO2'	31:4:2619:U:H6	1.66	0.41
31:4:2657:G:OP2	31:4:2658:A:H5''	2.21	0.41
31:4:2753:G:H2'	31:4:2754:C:C6	2.56	0.41
1:b:134:ILE:HA	1:b:135:PRO:HD3	1.96	0.40
1:b:242:HIS:O	1:b:244:VAL:HG13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:9:VAL:HB	2:c:26:VAL:CG2	2.52	0.40
3:d:58:LYS:HA	3:d:59:PRO:HD3	1.91	0.40
4:e:24:VAL:HG12	4:e:25:MET:HE2	2.03	0.40
8:i:79:LEU:HD22	8:i:105:LEU:HD12	2.03	0.40
10:k:19:VAL:HG12	10:k:43:ILE:HG12	2.03	0.40
14:p:51:ASN:HB2	31:4:2974:G:OP2	2.20	0.40
15:q:23:TYR:CE1	31:4:533:G:H5'	2.56	0.40
20:v:80:HIS:CG	20:v:87:GLN:HE21	2.39	0.40
31:4:119:A:H4'	31:4:120:U:H5'	2.04	0.40
31:4:386:G:H3'	31:4:387:U:C5'	2.51	0.40
31:4:622:G:H2'	31:4:623:C:H6	1.86	0.40
31:4:1099:G:H2'	31:4:1100:A:O4'	2.21	0.40
31:4:1596:U:H2'	31:4:1650:A:N6	2.36	0.40
31:4:1981:A:N1	31:4:2215:G:H1'	2.36	0.40
31:4:2636:G:H4'	31:4:2683:U:C4'	2.51	0.40
31:4:2902:C:H2'	31:4:2903:G:O4'	2.22	0.40
31:4:2929:G:H2'	31:4:2930:G:H8	1.85	0.40
31:4:2946:U:H4'	31:4:2965:A:H4'	2.03	0.40
1:b:29:PHE:CE2	1:b:31:PRO:HB2	2.56	0.40
14:p:31:VAL:HG12	14:p:38:ARG:HB3	2.03	0.40
18:t:73:ARG:HD3	18:t:73:ARG:HA	1.84	0.40
20:v:80:HIS:ND1	20:v:81:PRO:HD2	2.36	0.40
22:x:60:LYS:HD3	31:4:372:G:C5'	2.48	0.40
31:4:546:U:H2'	31:4:547:A:C1'	2.51	0.40
31:4:649:G:H2'	31:4:650:C:C6	2.57	0.40
31:4:754:U:H2'	31:4:755:U:C6	2.56	0.40
31:4:1242:C:O2'	31:4:1243:G:H5'	2.20	0.40
31:4:1248:G:H2'	31:4:1249:C:O4'	2.21	0.40
31:4:1798:C:H6	31:4:1798:C:O5'	2.05	0.40
31:4:1954:G:H2'	31:4:1955:U:C6	2.57	0.40
31:4:2009:C:C2'	31:4:2010:U:H5'	2.51	0.40
31:4:2504:A:H2'	31:4:2505:A:O4'	2.21	0.40
31:4:2650:U:H2'	31:4:2651:G:H5'	2.03	0.40
4:e:77:LYS:HE2	4:e:77:LYS:HB2	1.96	0.40
7:h:58:THR:HG21	7:h:82:ILE:O	2.21	0.40
8:i:10:LEU:HD21	31:4:1198:A:C6	2.56	0.40
9:j:113:PRO:HD2	31:4:558:U:OP1	2.21	0.40
15:q:30:VAL:HG13	31:4:580:U:O3'	2.21	0.40
16:r:68:ARG:CZ	16:r:90:ARG:HB2	2.51	0.40
22:x:15:ASN:HD22	31:4:381:G:H5'	1.86	0.40
30:a:44:VAL:O	30:a:172:HIS:HA	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:76:C:H2'	31:4:77:G:H8	1.86	0.40
31:4:281:C:N4	31:4:282:A:N6	2.70	0.40
31:4:301:G:C6	31:4:317:G:C6	3.09	0.40
31:4:885:C:C1'	31:4:891:G:H22	2.35	0.40
31:4:1895:G:O2'	31:4:1896:C:H5'	2.22	0.40
31:4:1903:U:H2'	31:4:1904:G:O4'	2.21	0.40
31:4:2588:U:H3	31:4:2618:G:H1	1.70	0.40
1:b:48:ILE:HG23	1:b:48:ILE:O	2.21	0.40
2:c:151:THR:CB	2:c:152:PRO:HD3	2.46	0.40
3:d:139:LYS:C	3:d:142:ALA:H	2.29	0.40
3:d:148:ILE:HB	3:d:169:VAL:HG22	2.03	0.40
3:d:164:LEU:HB3	3:d:167:VAL:HG22	2.04	0.40
4:e:79:ARG:HB2	4:e:82:TYR:CE2	2.57	0.40
31:4:96:C:H2'	31:4:97:C:H6	1.86	0.40
31:4:315:G:H2'	31:4:316:C:O4'	2.21	0.40
31:4:692:C:O2'	31:4:693:A:H5'	2.21	0.40
31:4:1699:A:H2'	31:4:1700:A:C8	2.57	0.40
31:4:2289:C:C3'	31:4:2290:G:H5''	2.48	0.40
31:4:2754:C:H2'	31:4:2755:G:O4'	2.21	0.40
31:4:2790:A:H2'	31:4:2791:G:O4'	2.21	0.40
4:e:16:MET:O	4:e:20:ASN:HA	2.21	0.40
27:D:41:ARG:HH21	27:D:41:ARG:HG3	1.87	0.40
31:4:275:C:H3'	31:4:276:U:C5'	2.51	0.40
31:4:441:U:O2'	31:4:442:G:H5'	2.21	0.40
31:4:817:C:H2'	31:4:818:G:O4'	2.22	0.40
31:4:1515:A:H5'	31:4:1597:A:H1'	2.03	0.40
31:4:1565:C:H2'	31:4:1566:U:C6	2.55	0.40
31:4:1723:C:H2'	31:4:1724:A:C8	2.57	0.40
31:4:1789:G:H2'	31:4:1790:U:H6	1.83	0.40
31:4:2052:C:H2'	31:4:2053:C:O4'	2.22	0.40
31:4:2242:A:N3	31:4:2242:A:H2'	2.36	0.40
31:4:2435:G:H5'	31:4:2436:G:N3	2.36	0.40
31:4:2519:G:N3	31:4:2519:G:H2'	2.37	0.40
31:4:2913:C:H2'	31:4:2914:U:C6	2.56	0.40
31:4:2923:C:C2'	31:4:2924:U:H5'	2.51	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	b	269/271 (99%)	237 (88%)	29 (11%)	3 (1%)	11	39
2	c	207/209 (99%)	187 (90%)	19 (9%)	1 (0%)	24	57
3	d	199/201 (99%)	177 (89%)	20 (10%)	2 (1%)	12	41
4	e	175/177 (99%)	150 (86%)	23 (13%)	2 (1%)	11	39
5	f	174/176 (99%)	157 (90%)	15 (9%)	2 (1%)	11	39
6	g	51/149 (34%)	37 (72%)	11 (22%)	3 (6%)	1	8
7	h	129/131 (98%)	97 (75%)	26 (20%)	6 (5%)	2	11
8	i	139/141 (99%)	114 (82%)	20 (14%)	5 (4%)	2	16
9	j	140/142 (99%)	131 (94%)	7 (5%)	2 (1%)	9	34
10	k	120/122 (98%)	99 (82%)	18 (15%)	3 (2%)	4	21
11	l	141/143 (99%)	122 (86%)	16 (11%)	3 (2%)	5	25
12	n	118/120 (98%)	104 (88%)	11 (9%)	3 (2%)	4	21
13	o	114/116 (98%)	105 (92%)	8 (7%)	1 (1%)	14	44
14	p	112/114 (98%)	96 (86%)	15 (13%)	1 (1%)	14	44
15	q	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
16	r	101/103 (98%)	88 (87%)	11 (11%)	2 (2%)	6	25
17	s	108/110 (98%)	98 (91%)	8 (7%)	2 (2%)	6	27
18	t	91/93 (98%)	82 (90%)	8 (9%)	1 (1%)	11	39
19	u	100/102 (98%)	85 (85%)	11 (11%)	4 (4%)	2	13
20	v	92/94 (98%)	81 (88%)	11 (12%)	0	100	100
21	w	73/75 (97%)	65 (89%)	7 (10%)	1 (1%)	9	34
22	x	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
23	y	61/63 (97%)	57 (93%)	3 (5%)	1 (2%)	7	30
24	z	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
25	A	39/70 (56%)	35 (90%)	4 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	B	54/56 (96%)	47 (87%)	6 (11%)	1 (2%)	6	27
27	D	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
28	E	62/64 (97%)	56 (90%)	5 (8%)	1 (2%)	7	30
29	F	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	4	20
30	a	130/223 (58%)	114 (88%)	14 (11%)	2 (2%)	8	32
All	All	3325/3601 (92%)	2925 (88%)	347 (10%)	53 (2%)	10	30

All (53) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	c	30	GLU
3	d	83	VAL
5	f	174	LYS
6	g	9	VAL
7	h	80	THR
7	h	108	VAL
9	j	81	ILE
10	k	89	ASN
11	l	31	GLY
16	r	54	VAL
19	u	6	ARG
21	w	12	SER
23	y	24	GLU
26	B	25	THR
29	F	37	GLN
30	a	217	THR
7	h	81	LEU
8	i	5	GLN
8	i	6	ALA
8	i	11	GLN
8	i	98	GLY
12	n	118	ARG
19	u	56	GLY
30	a	202	THR
11	l	15	ALA
11	l	29	LYS
19	u	54	PRO
4	e	142	TYR
7	h	91	ALA
7	h	118	ILE

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Mol	Chain	Res	Type
10	k	92	GLU
16	r	52	PRO
17	s	3	THR
19	u	51	LEU
1	b	254	LYS
1	b	260	LYS
3	d	80	SER
6	g	48	GLU
7	h	116	GLU
8	i	22	PRO
10	k	93	GLN
12	n	117	ASP
13	o	34	HIS
17	s	74	ILE
18	t	89	GLU
5	f	45	ALA
6	g	39	ALA
14	p	64	SER
28	E	31	ILE
9	j	8	PRO
12	n	109	PRO
1	b	240	GLY
4	e	40	GLY

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	b	216/216 (100%)	216 (100%)	0	100	100
2	c	164/164 (100%)	164 (100%)	0	100	100
3	d	165/165 (100%)	163 (99%)	2 (1%)	63	78
4	e	148/148 (100%)	145 (98%)	3 (2%)	48	72
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	82
6	g	42/114 (37%)	42 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	h	100/100 (100%)	100 (100%)	0	100	100
8	i	109/109 (100%)	107 (98%)	2 (2%)	51	73
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	80
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	79
11	l	102/102 (100%)	102 (100%)	0	100	100
12	n	100/100 (100%)	100 (100%)	0	100	100
13	o	86/86 (100%)	85 (99%)	1 (1%)	63	78
14	p	99/99 (100%)	99 (100%)	0	100	100
15	q	89/89 (100%)	89 (100%)	0	100	100
16	r	84/84 (100%)	83 (99%)	1 (1%)	63	78
17	s	93/93 (100%)	93 (100%)	0	100	100
18	t	80/80 (100%)	79 (99%)	1 (1%)	61	77
19	u	83/83 (100%)	83 (100%)	0	100	100
20	v	78/78 (100%)	78 (100%)	0	100	100
21	w	57/57 (100%)	56 (98%)	1 (2%)	51	73
22	x	67/67 (100%)	67 (100%)	0	100	100
23	y	55/55 (100%)	55 (100%)	0	100	100
24	z	48/48 (100%)	48 (100%)	0	100	100
25	A	38/62 (61%)	37 (97%)	1 (3%)	40	68
26	B	47/47 (100%)	47 (100%)	0	100	100
27	D	38/38 (100%)	37 (97%)	1 (3%)	40	68
28	E	51/51 (100%)	51 (100%)	0	100	100
29	F	34/34 (100%)	33 (97%)	1 (3%)	37	66
30	a	110/174 (63%)	108 (98%)	2 (2%)	51	73
All	All	2739/2899 (94%)	2720 (99%)	19 (1%)	73	82

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

Mol	Chain	Res	Type
3	d	116	ASP
3	d	187	VAL
4	e	34	THR
4	e	78	ILE
4	e	168	LEU

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Mol	Chain	Res	Type
5	f	22	VAL
8	i	23	VAL
8	i	61	TYR
9	j	81	ILE
10	k	58	LEU
13	o	49	VAL
16	r	54	VAL
18	t	48	GLN
21	w	67	VAL
25	A	35	ASP
27	D	44	VAL
29	F	36	ARG
30	a	33	LEU
30	a	214	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (72) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	52	HIS
1	b	85	ASN
1	b	127	ASN
1	b	250	GLN
1	b	259	ASN
2	c	49	GLN
2	c	164	GLN
2	c	173	GLN
3	d	29	HIS
3	d	41	GLN
3	d	97	ASN
3	d	165	HIS
4	e	26	GLN
4	e	80	GLN
5	f	103	ASN
5	f	115	GLN
5	f	138	GLN
7	h	6	GLN
7	h	122	GLN
8	i	33	ASN
9	j	47	HIS
9	j	58	ASN
9	j	80	HIS
9	j	86	GLN

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Mol	Chain	Res	Type
10	k	3	GLN
10	k	89	ASN
12	n	3	HIS
12	n	18	GLN
12	n	31	HIS
13	o	29	HIS
13	o	100	HIS
14	p	55	HIS
14	p	65	ASN
14	p	114	ASN
15	q	36	GLN
15	q	43	GLN
15	q	58	GLN
16	r	11	GLN
16	r	12	HIS
17	s	7	HIS
17	s	40	ASN
18	t	15	HIS
18	t	48	GLN
18	t	59	ASN
18	t	70	HIS
19	u	39	ASN
19	u	53	GLN
19	u	73	ASN
20	v	12	GLN
20	v	24	ASN
20	v	87	GLN
21	w	53	HIS
22	x	15	ASN
22	x	16	ASN
23	y	20	ASN
23	y	41	HIS
23	y	45	GLN
23	y	58	ASN
24	z	19	HIS
25	A	41	HIS
26	B	3	GLN
26	B	5	ASN
27	D	13	ASN
27	D	26	ASN
27	D	29	GLN
28	E	30	HIS

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Mol	Chain	Res	Type
28	E	42	HIS
29	F	37	GLN
30	a	20	GLN
30	a	24	ASN
30	a	47	ASN
30	a	57	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	4	3023/3031 (99%)	371 (12%)	9 (0%)

All (371) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
31	4	10	A
31	4	12	U
31	4	34	U
31	4	35	G
31	4	46	G
31	4	51	G
31	4	63	A
31	4	71	A
31	4	74	A
31	4	75	G
31	4	119	A
31	4	120	U
31	4	138	U
31	4	139	U
31	4	140	C
31	4	141	G
31	4	162	U
31	4	163	C
31	4	181	A
31	4	196	A
31	4	199	A
31	4	216	A
31	4	221	A
31	4	222	A
31	4	228	C
31	4	229	C

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Mol	Chain	Res	Type
31	4	248	G
31	4	249	C
31	4	255	A
31	4	266	G
31	4	276	U
31	4	278	A
31	4	280	U
31	4	281	C
31	4	285	G
31	4	294	A
31	4	301	G
31	4	311	A
31	4	323	C
31	4	324	A
31	4	329	G
31	4	330	A
31	4	361	G
31	4	362	A
31	4	371	A
31	4	372	G
31	4	386	G
31	4	387	U
31	4	396	G
31	4	404	A
31	4	406	G
31	4	411	G
31	4	412	A
31	4	424	G
31	4	456	C
31	4	473	G
31	4	481	G
31	4	491	G
31	4	504	A
31	4	505	A
31	4	508	A
31	4	529	A
31	4	531	C
31	4	532	A
31	4	543	G
31	4	545	U
31	4	548	G
31	4	563	A

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Mol	Chain	Res	Type
31	4	573	U
31	4	574	A
31	4	575	A
31	4	603	A
31	4	614	A
31	4	615	U
31	4	627	A
31	4	628	G
31	4	637	A
31	4	646	U
31	4	654	A
31	4	656	G
31	4	669	G
31	4	686	U
31	4	730	A
31	4	747	C
31	4	752	A
31	4	757	G
31	4	764	A
31	4	776	G
31	4	782	A
31	4	784	G
31	4	785	G
31	4	805	G
31	4	812	C
31	4	819	A
31	4	827	U
31	4	828	U
31	4	830	G
31	4	845	A
31	4	846	U
31	4	847	U
31	4	860	U
31	4	877	A
31	4	878	A
31	4	886	A
31	4	887	U
31	4	888	C
31	4	896	A
31	4	897	C
31	4	898	C
31	4	902	C

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Mol	Chain	Res	Type
31	4	907	G
31	4	910	A
31	4	932	U
31	4	941	A
31	4	946	C
31	4	959	A
31	4	974	G
31	4	983	A
31	4	995	C
31	4	996	A
31	4	1012	U
31	4	1013	C
31	4	1021	A
31	4	1022	G
31	4	1025	G
31	4	1026	G
31	4	1030	C
31	4	1050	A
31	4	1051	A
31	4	1058	G
31	4	1063	U
31	4	1064	C
31	4	1066	G
31	4	1067	U
31	4	1070	C
31	4	1090	G
31	4	1101	C
31	4	1110	G
31	4	1133	G
31	4	1155	A
31	4	1161	U
31	4	1173	C
31	4	1174	A
31	4	1175	G
31	4	1182	A
31	4	1190	G
31	4	1191	G
31	4	1193	U
31	4	1194	U
31	4	1198	A
31	4	1199	G
31	4	1200	C

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Mol	Chain	Res	Type
31	4	1204	C
31	4	1207	C
31	4	1212	A
31	4	1216	A
31	4	1217	A
31	4	1231	A
31	4	1232	C
31	4	1234	G
31	4	1239	A
31	4	1260	U
31	4	1261	A
31	4	1263	C
31	4	1297	A
31	4	1301	U
31	4	1302	U
31	4	1303	A
31	4	1304	U
31	4	1307	G
31	4	1334	G
31	4	1340	G
31	4	1366	G
31	4	1378	G
31	4	1379	C
31	4	1381	A
31	4	1384	G
31	4	1399	G
31	4	1400	A
31	4	1417	C
31	4	1429	A
31	4	1457	U
31	4	1458	C
31	4	1473	C
31	4	1493	A
31	4	1506	A
31	4	1507	U
31	4	1511	A
31	4	1526	C
31	4	1544	G
31	4	1547	A
31	4	1548	A
31	4	1556	C
31	4	1582	C

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Mol	Chain	Res	Type
31	4	1589	C
31	4	1610	G
31	4	1618	A
31	4	1626	C
31	4	1632	A
31	4	1643	A
31	4	1652	G
31	4	1658	G
31	4	1660	A
31	4	1661	C
31	4	1663	A
31	4	1664	C
31	4	1665	G
31	4	1683	G
31	4	1688	G
31	4	1697	A
31	4	1706	U
31	4	1736	A
31	4	1739	C
31	4	1744	A
31	4	1775	U
31	4	1776	U
31	4	1802	G
31	4	1843	G
31	4	1857	U
31	4	1858	C
31	4	1860	C
31	4	1866	G
31	4	1886	U
31	4	1892	C
31	4	1901	A
31	4	1908	A
31	4	1912	A
31	4	1928	C
31	4	1929	A
31	4	1936	A
31	4	1944	C
31	4	1957	A
31	4	1975	A
31	4	2029	A
31	4	2034	G
31	4	2035	G

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Mol	Chain	Res	Type
31	4	2041	A
31	4	2044	A
31	4	2047	A
31	4	2057	G
31	4	2058	G
31	4	2065	A
31	4	2066	A
31	4	2072	U
31	4	2083	U
31	4	2095	C
31	4	2098	A
31	4	2100	G
31	4	2119	U
31	4	2121	U
31	4	2125	C
31	4	2150	U
31	4	2151	C
31	4	2158	A
31	4	2159	A
31	4	2171	C
31	4	2183	C
31	4	2184	G
31	4	2187	A
31	4	2188	A
31	4	2189	G
31	4	2190	A
31	4	2197	G
31	4	2200	C
31	4	2221	G
31	4	2223	A
31	4	2238	G
31	4	2239	U
31	4	2240	G
31	4	2246	U
31	4	2247	A
31	4	2254	A
31	4	2255	G
31	4	2259	U
31	4	2260	U
31	4	2261	G
31	4	2274	C
31	4	2276	G

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Mol	Chain	Res	Type
31	4	2277	U
31	4	2290	G
31	4	2298	A
31	4	2300	U
31	4	2301	A
31	4	2317	U
31	4	2326	A
31	4	2331	U
31	4	2332	G
31	4	2339	A
31	4	2353	A
31	4	2366	G
31	4	2378	G
31	4	2379	G
31	4	2407	G
31	4	2411	C
31	4	2415	A
31	4	2425	A
31	4	2428	C
31	4	2431	G
31	4	2433	U
31	4	2435	G
31	4	2437	A
31	4	2453	G
31	4	2455	A
31	4	2462	U
31	4	2478	C
31	4	2511	G
31	4	2513	C
31	4	2530	U
31	4	2534	A
31	4	2535	A
31	4	2551	U
31	4	2557	G
31	4	2558	A
31	4	2563	A
31	4	2569	U
31	4	2575	G
31	4	2576	A
31	4	2585	U
31	4	2604	A
31	4	2619	U

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Mol	Chain	Res	Type
31	4	2620	U
31	4	2621	U
31	4	2623	G
31	4	2627	C
31	4	2630	G
31	4	2631	A
31	4	2632	U
31	4	2633	G
31	4	2646	A
31	4	2648	C
31	4	2657	G
31	4	2675	A
31	4	2682	U
31	4	2694	A
31	4	2695	G
31	4	2700	A
31	4	2701	C
31	4	2730	A
31	4	2731	G
31	4	2737	U
31	4	2739	C
31	4	2741	U
31	4	2757	U
31	4	2783	G
31	4	2810	A
31	4	2817	U
31	4	2818	U
31	4	2842	G
31	4	2872	G
31	4	2876	A
31	4	2878	A
31	4	2892	A
31	4	2893	A
31	4	2906	A
31	4	2907	U
31	4	2919	G
31	4	2925	U
31	4	2927	A
31	4	2928	A
31	4	2937	A
31	4	2948	A
31	4	2949	A

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Mol	Chain	Res	Type
31	4	2995	G
31	4	2996	A
31	4	3000	A
31	4	3001	A
31	4	3002	C
31	4	3008	C
31	4	3011	A
31	4	3012	U
31	4	3030	C

All (9) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
31	4	490	C
31	4	859	G
31	4	1020	A
31	4	1025	G
31	4	2424	U
31	4	2430	U
31	4	2454	C
31	4	2632	U
31	4	3001	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

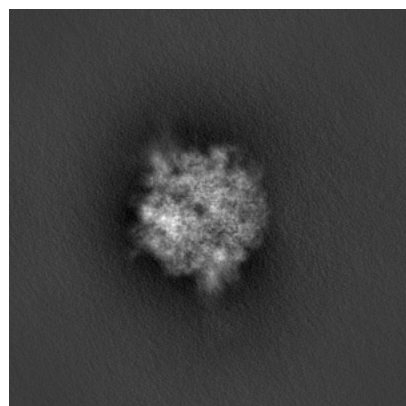
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21856. These allow visual inspection of the internal detail of the map and identification of artifacts.

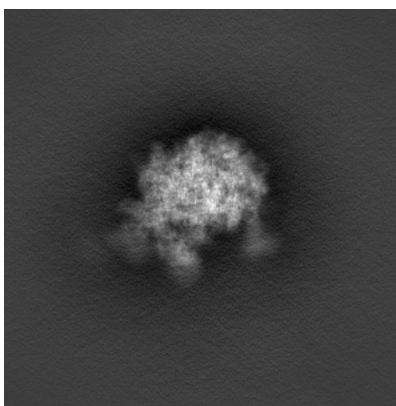
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

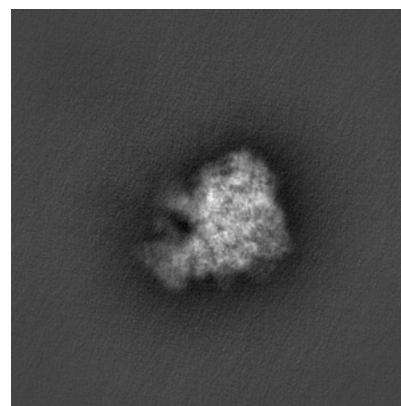
6.1.1 Primary map



X

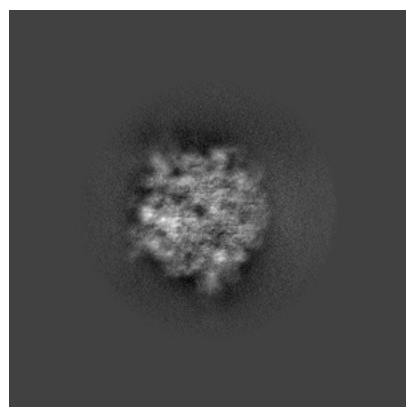


Y

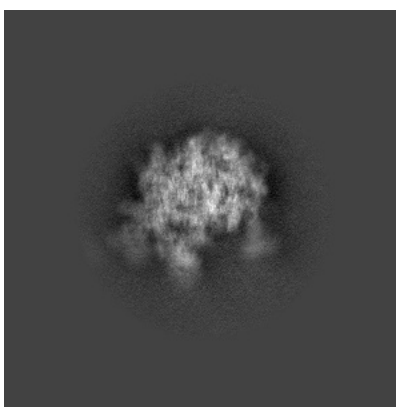


Z

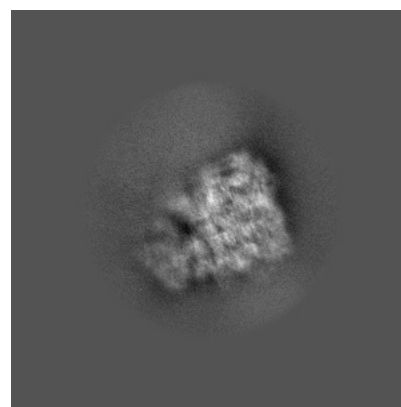
6.1.2 Raw map



X



Y

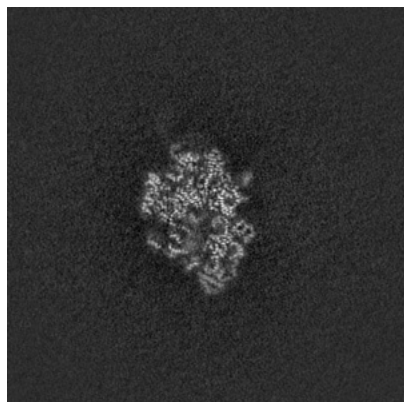


Z

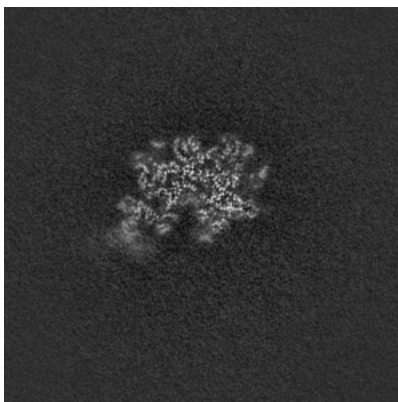
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

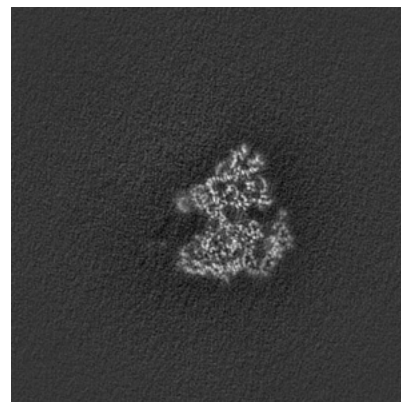
6.2.1 Primary map



X Index: 304

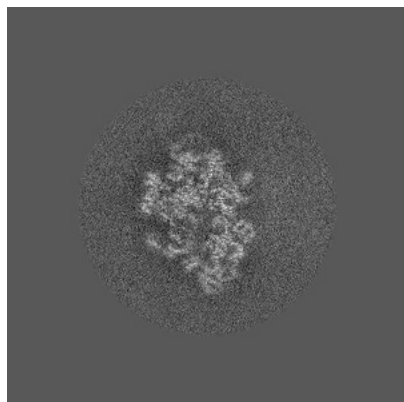


Y Index: 304

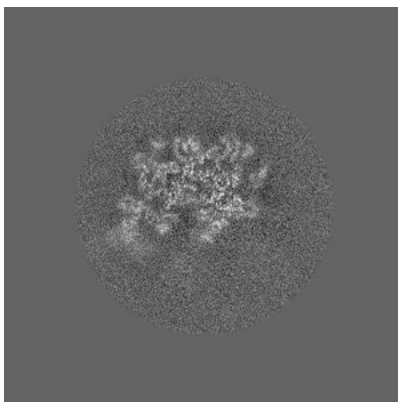


Z Index: 304

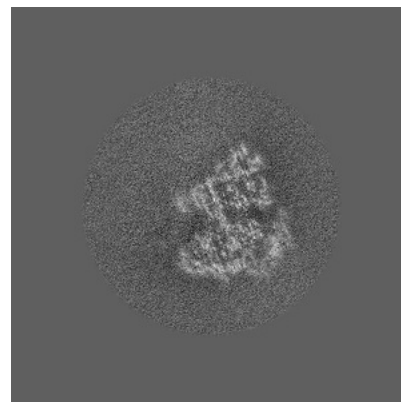
6.2.2 Raw map



X Index: 304



Y Index: 304

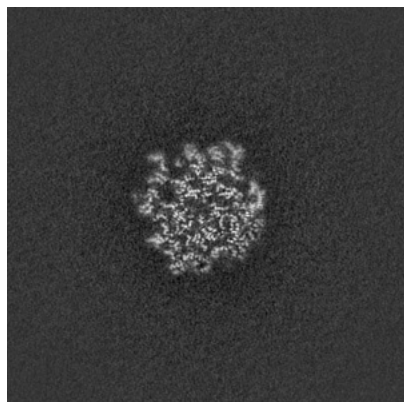


Z Index: 304

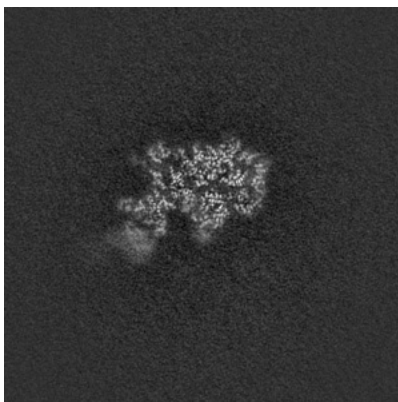
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

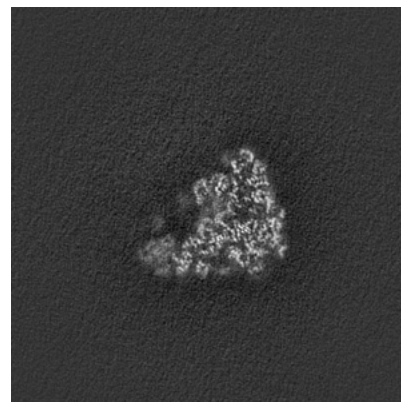
6.3.1 Primary map



X Index: 339

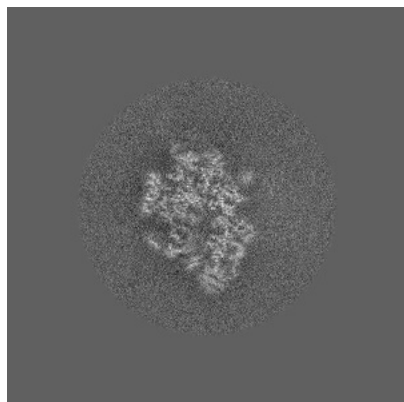


Y Index: 316

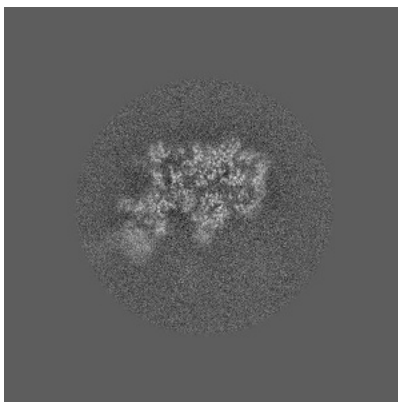


Z Index: 290

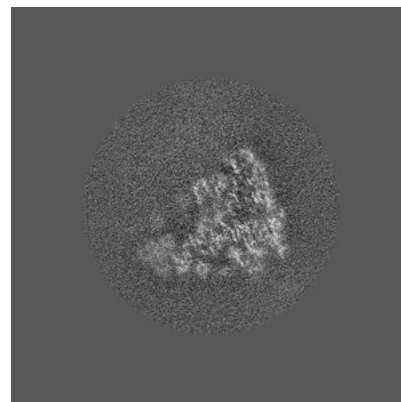
6.3.2 Raw map



X Index: 303



Y Index: 316

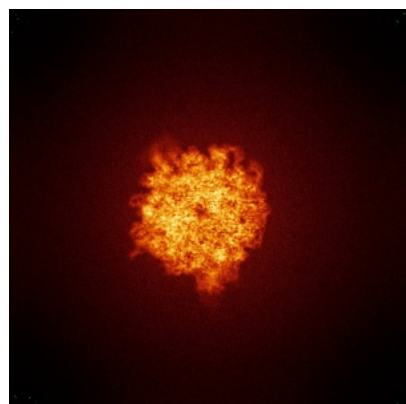


Z Index: 290

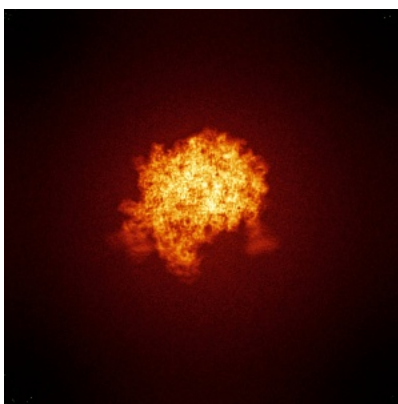
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

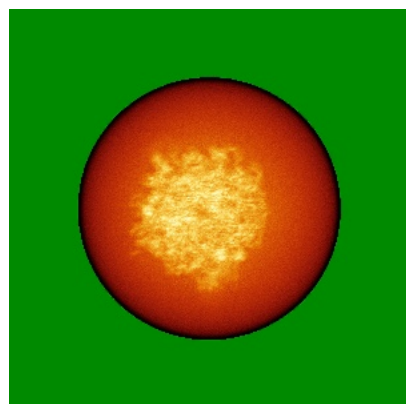


Y

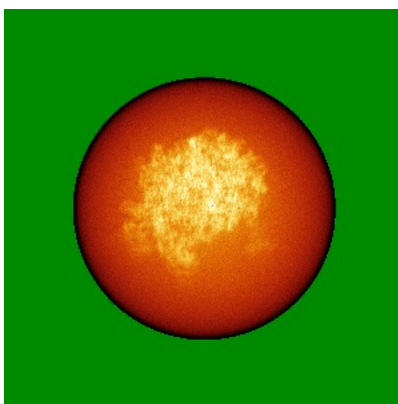


Z

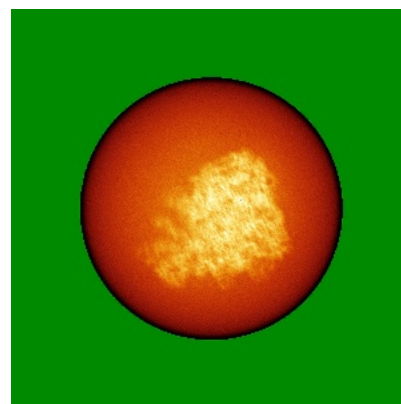
6.4.2 Raw map



X



Y

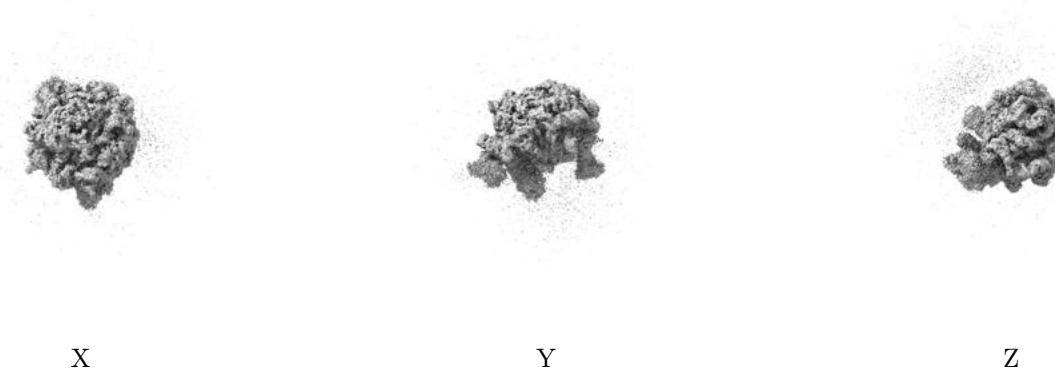


Z

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.

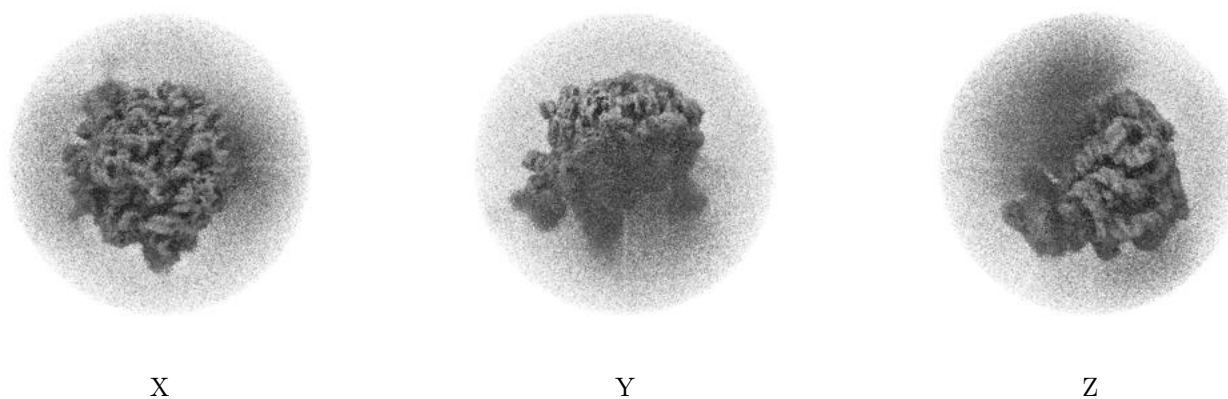
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. 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.

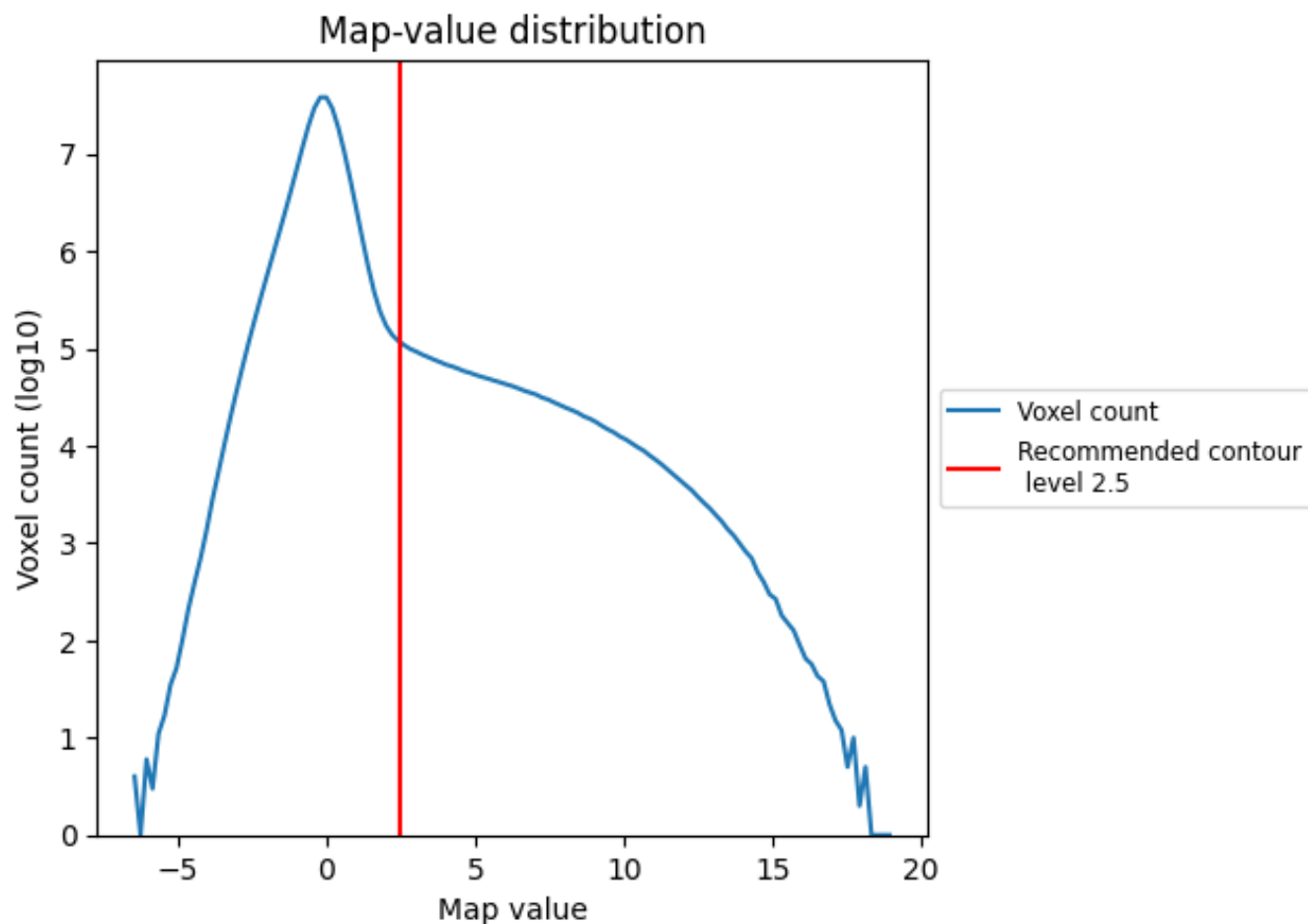
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

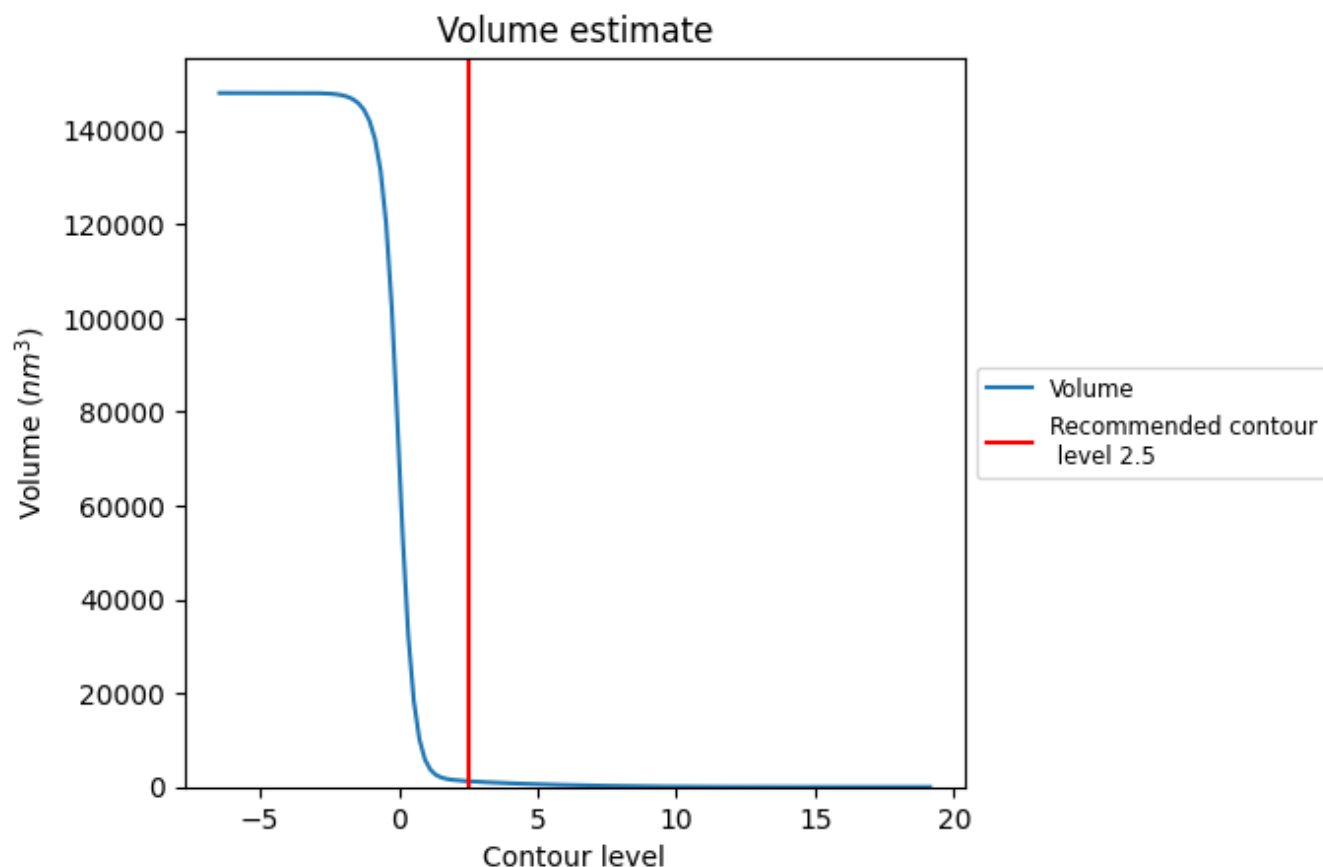
This section contains the results of statistical analysis of the map.

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.

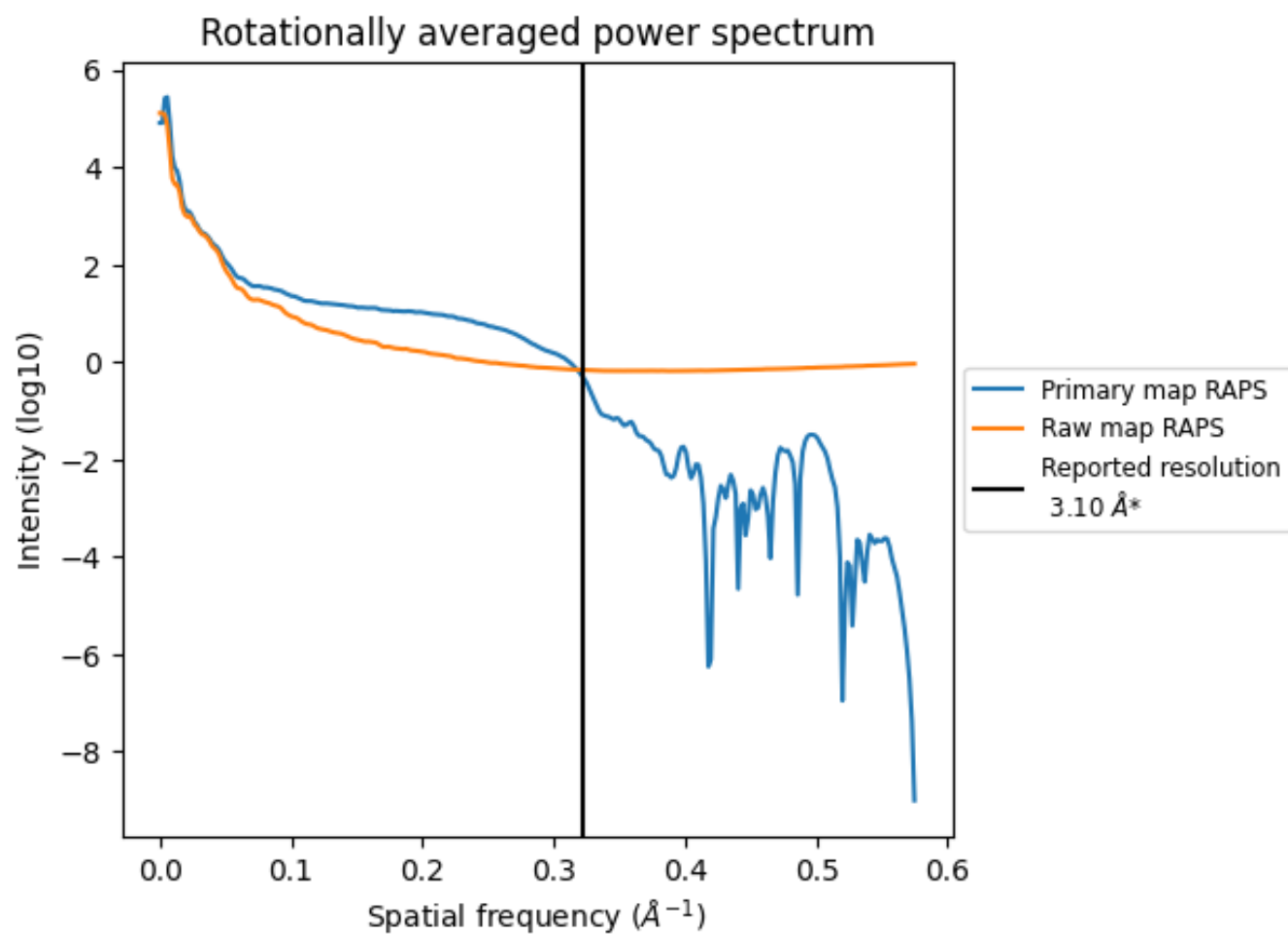
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1232 nm^3 ; this corresponds to an approximate mass of 1112 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 ⓘ

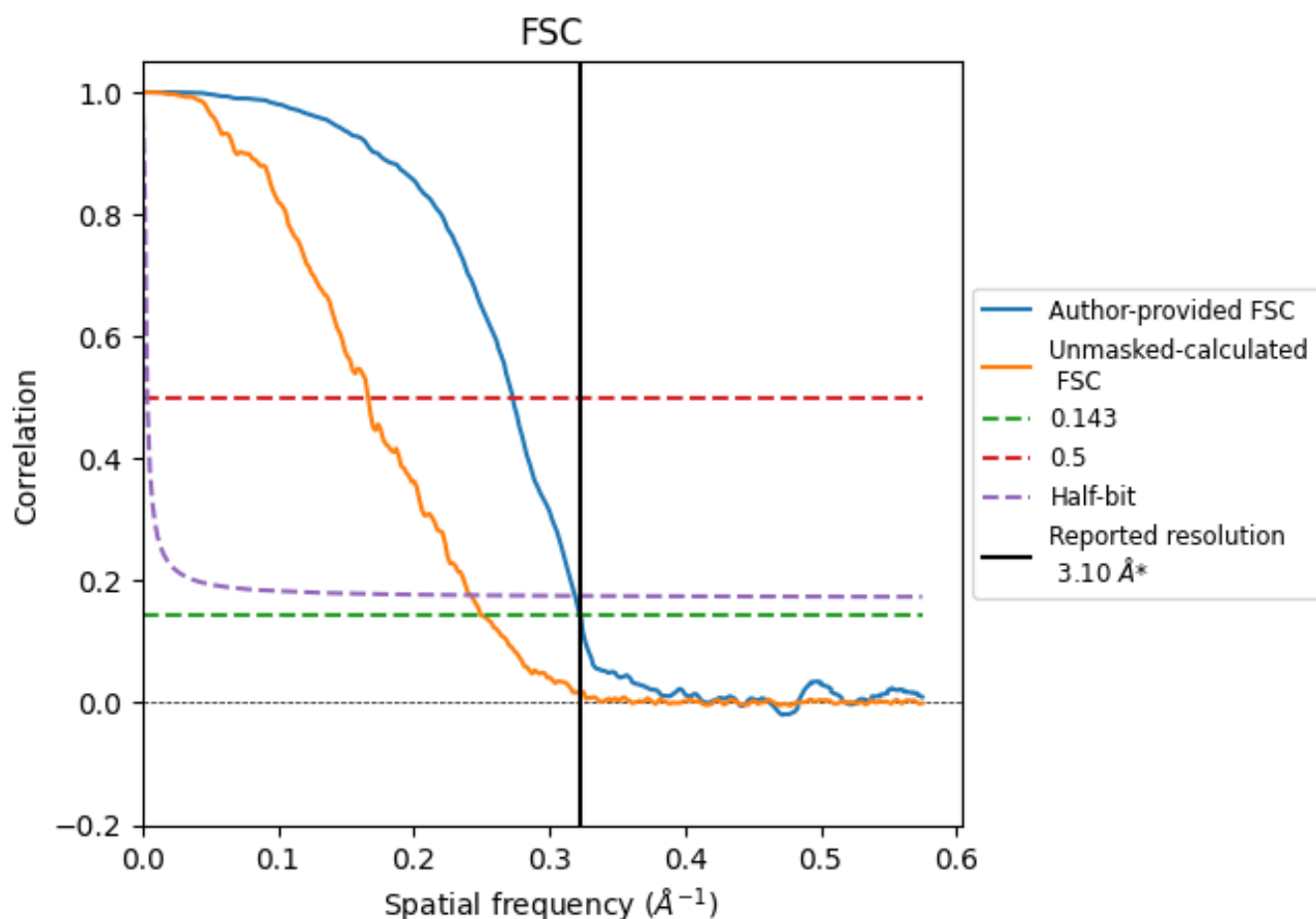


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

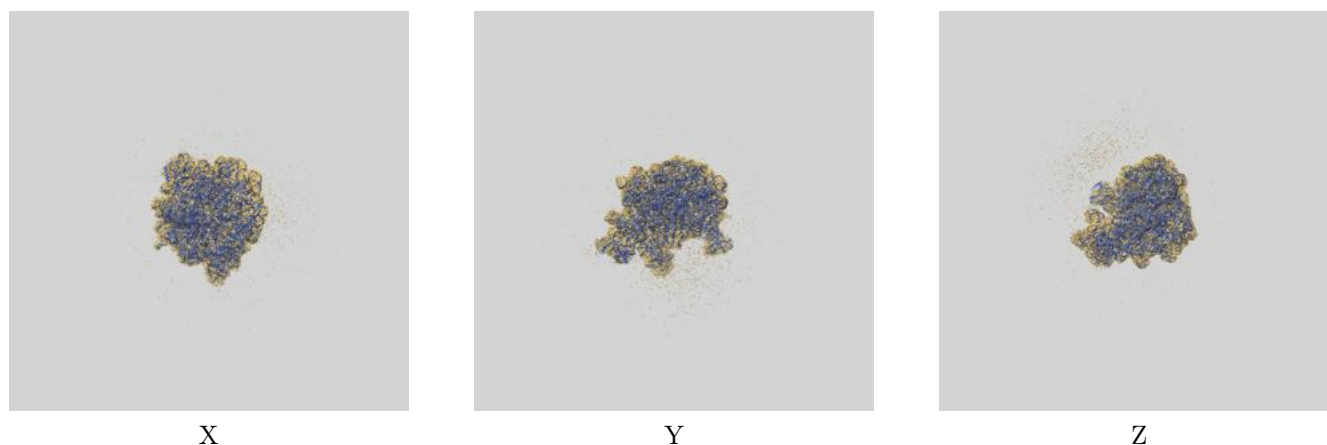
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.10	3.66	3.14
Unmasked-calculated*	4.00	6.01	4.13

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.00 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

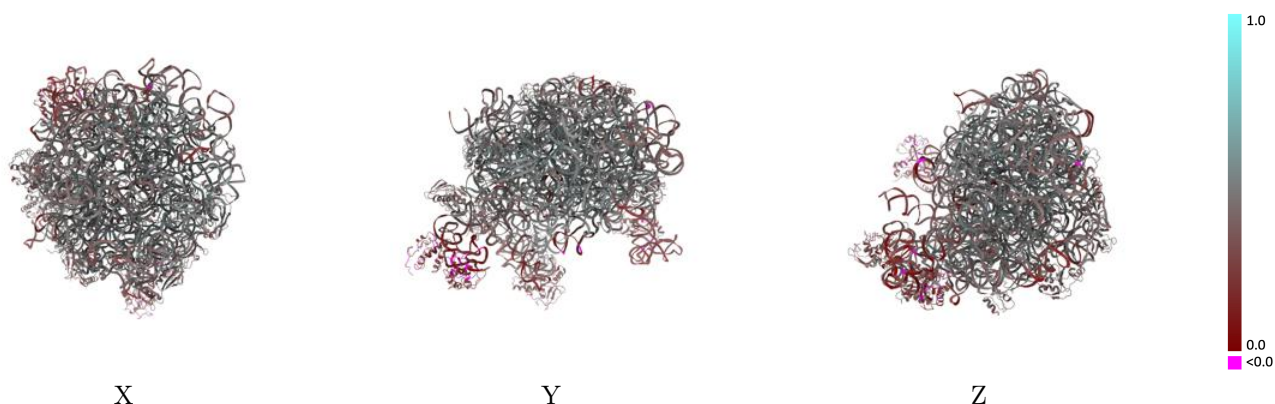
This section contains information regarding the fit between EMDB map EMD-21856 and PDB model 6WNT. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



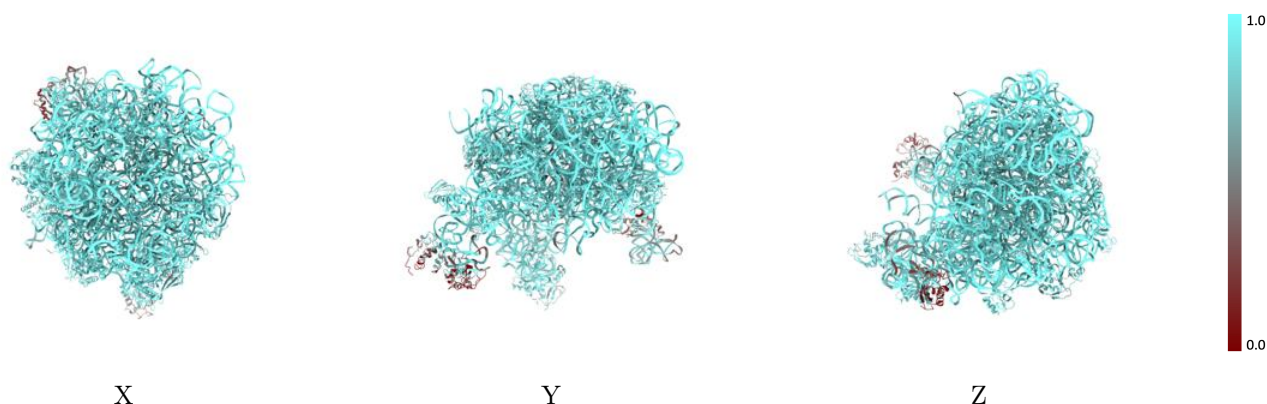
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



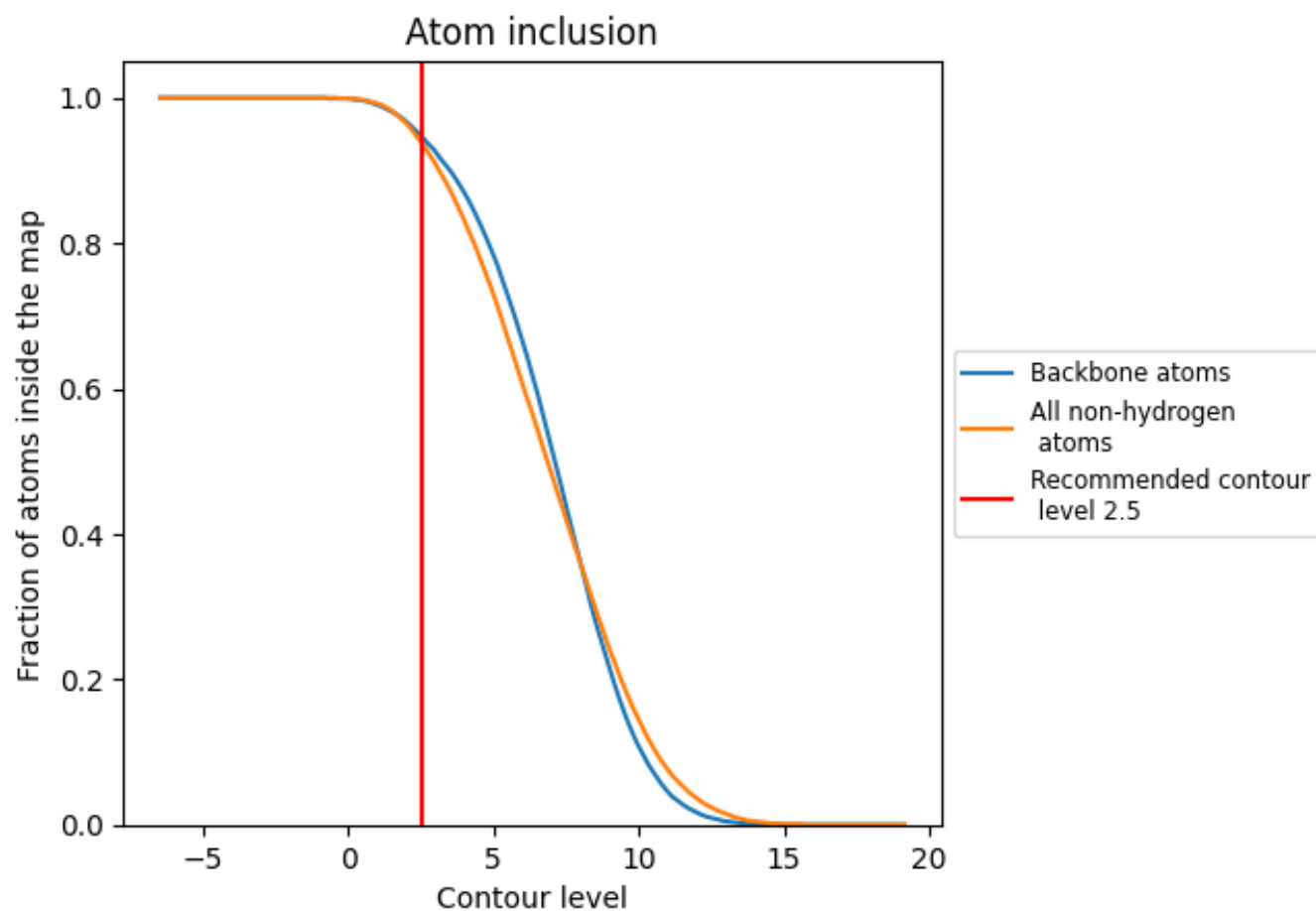
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).

9.4 Atom inclusion ⓘ



At the recommended contour level, 95% of all backbone atoms, 94% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9390	 0.4250
4	 0.9750	 0.4290
A	 0.7180	 0.3310
B	 0.9370	 0.4790
D	 0.9320	 0.4950
E	 0.9410	 0.4870
F	 0.9070	 0.4740
a	 0.3100	 0.2300
b	 0.9490	 0.4840
c	 0.9240	 0.4780
d	 0.8480	 0.4180
e	 0.8670	 0.3130
f	 0.9170	 0.3960
g	 0.8580	 0.3650
h	 0.4980	 0.2020
i	 0.3240	 0.2000
j	 0.9220	 0.4760
k	 0.9280	 0.4640
l	 0.9300	 0.4590
n	 0.9350	 0.4830
o	 0.9410	 0.3960
p	 0.9060	 0.4570
q	 0.9340	 0.4740
r	 0.9070	 0.4540
s	 0.9040	 0.4740
t	 0.9100	 0.4550
u	 0.9240	 0.4210
v	 0.8370	 0.3310
w	 0.9140	 0.4760
x	 0.9520	 0.4720
y	 0.8970	 0.3890
z	 0.9220	 0.4780

