



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 05:48 PM UTC

PDB ID : 8VKI / pdb_00008vki
EMDB ID : EMD-43317
Title : Structure of Mycobacterium smegmatis 50S ribosomal subunit bound to HflX:50S-HflX-C
Authors : Majumdar, S.; Koripella, R.K.; Sharma, M.R.; Manjari, S.R.; Banavali, N.K.; Agrawal, R.K.
Deposited on : 2024-01-09
Resolution : 2.96 Å (reported)
Based on initial models : 5O61, 6DZI

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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

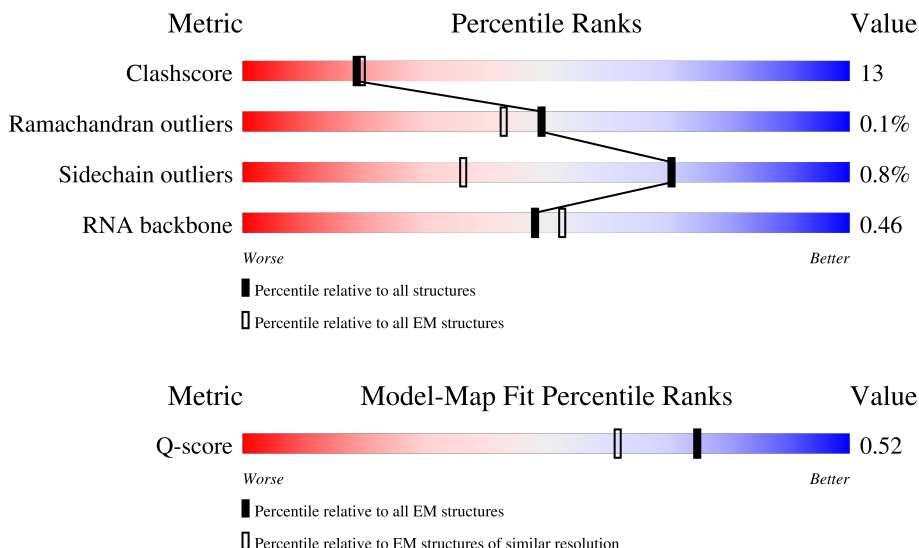
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.96 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	13155 (2.46 - 3.46)

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	2	61	
2	3	24	

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Mol	Chain	Length	Quality of chain
3	4	470	
4	B	118	
5	C	278	
6	D	217	
7	E	215	
8	F	187	
9	G	179	
10	H	151	
11	I	175	
12	J	142	
13	K	147	
14	L	122	
15	M	147	
16	N	138	
17	O	199	
18	P	127	
19	Q	113	
20	R	129	
21	S	103	
22	T	153	
23	U	100	
24	V	105	
25	W	215	
26	X	88	
27	Y	64	

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Mol	Chain	Length	Quality of chain
28	Z	77	
29	b	57	
30	c	55	
31	d	47	
32	e	64	
33	f	37	
34	A	3120	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
35	GCP	4	501	-	-	X	-

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 96565 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 L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	2	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 2 is a protein called 50S Ribosomal Protein L37.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 3 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	466	Total	C	N	O	S	0	0
			3516	2171	649	689	7		

- Molecule 4 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 5 is a protein called 50S ribosomal protein L2.

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

- Molecule 6 is a protein called 50S ribosomal protein L3.

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

- Molecule 7 is a protein called 50S Ribosomal Protein L4.

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

- Molecule 8 is a protein called 50S Ribosomal Protein L5.

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

- Molecule 9 is a protein called 50S ribosomal protein L6.

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

- Molecule 10 is a protein called 50S ribosomal protein L9.

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

- Molecule 11 is a protein called 50S ribosomal protein L10.

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

- Molecule 12 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	132	Total	C	N	O	S	0	0
			958	602	172	181	3		

- Molecule 13 is a protein called 50S Ribosomal Protein L13.

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

- Molecule 14 is a protein called 50S ribosomal protein L14.

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

- Molecule 15 is a protein called 50S ribosomal protein L15.

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

- Molecule 16 is a protein called Large ribosomal subunit protein uL16.

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

- Molecule 17 is a protein called 50S ribosomal protein L17.

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

- Molecule 18 is a protein called 50S Ribosomal Protein L18.

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

- Molecule 19 is a protein called 50S ribosomal protein L19.

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

- Molecule 20 is a protein called 50S Ribosomal Protein L20.

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

- Molecule 21 is a protein called 50S Ribosomal Protein L21.

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

- Molecule 22 is a protein called 50S Ribosomal Protein L22.

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

- Molecule 23 is a protein called 50S Ribosomal Protein L23.

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

- Molecule 24 is a protein called 50S ribosomal protein L24.

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

- Molecule 25 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	W	95	Total	C	N	O	0	0
			735	452	149	134		

- Molecule 26 is a protein called 50S ribosomal protein L27.

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

- Molecule 27 is a protein called 50S Ribosomal Protein L28.

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

- Molecule 28 is a protein called 50S ribosomal protein L29.

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

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

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

- Molecule 30 is a protein called 50S Ribosomal Protein L33.

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

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

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

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

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

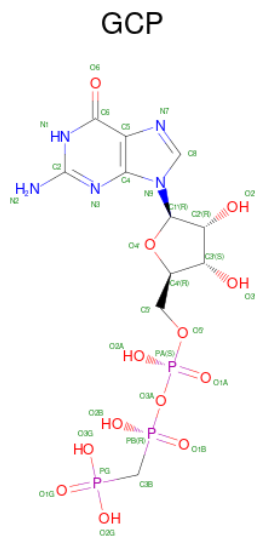
- Molecule 33 is a protein called 50S ribosomal protein L36.

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

- Molecule 34 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	A	2952	Total	C	N	O	P	0	0
			63419	28264	11675	20528	2952		

- Molecule 35 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).

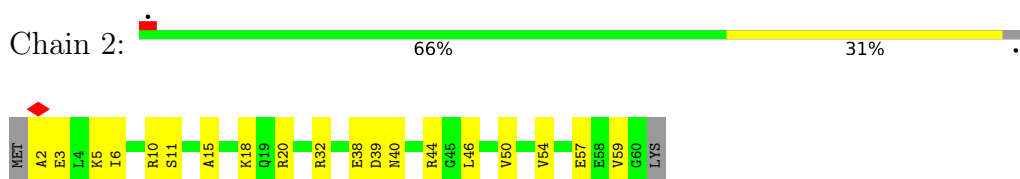


Mol	Chain	Residues	Atoms					AltConf
35	4	1	Total	C	N	O	P	0
			32	11	5	13	3	

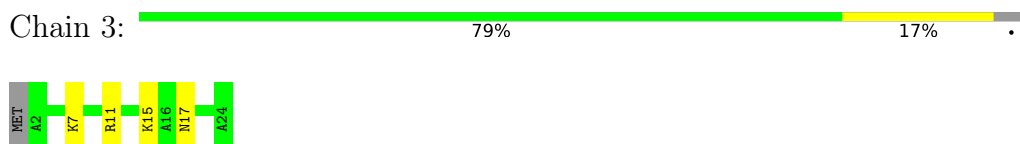
3 Residue-property plots

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

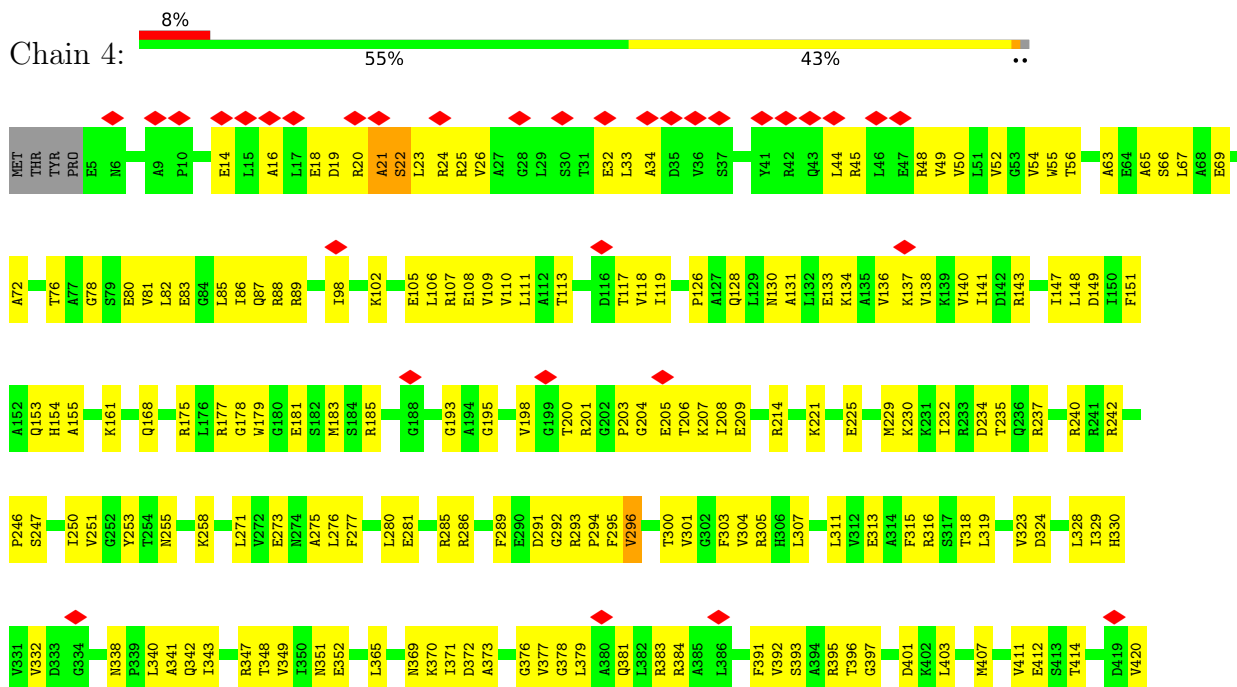
- Molecule 1: 50S ribosomal protein L30



- Molecule 2: 50S Ribosomal Protein L37

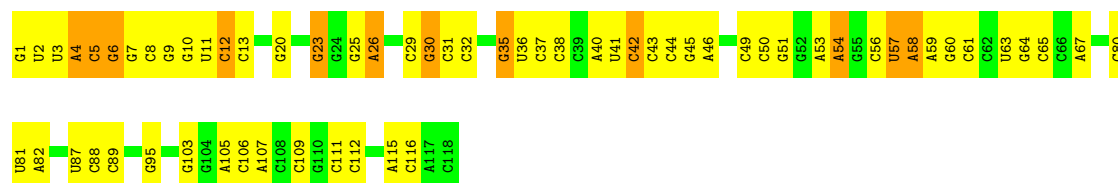


- Molecule 3: GTPase HflX

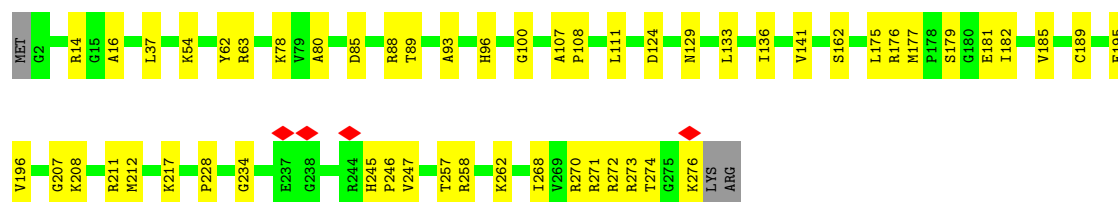
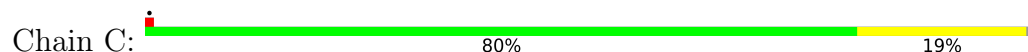




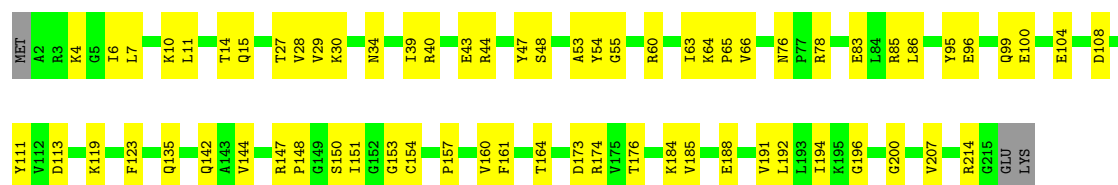
• Molecule 4: 5S ribosomal RNA



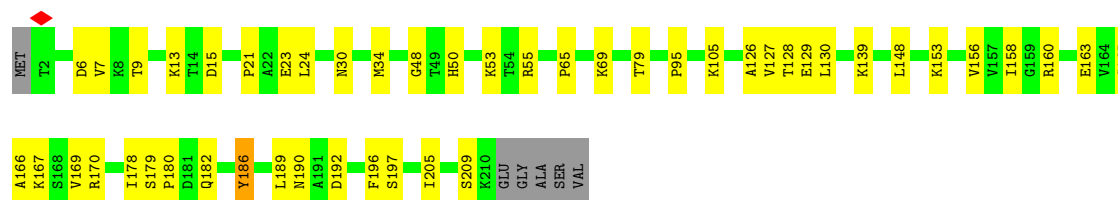
• Molecule 5: 50S ribosomal protein L2



• Molecule 6: 50S ribosomal protein L3

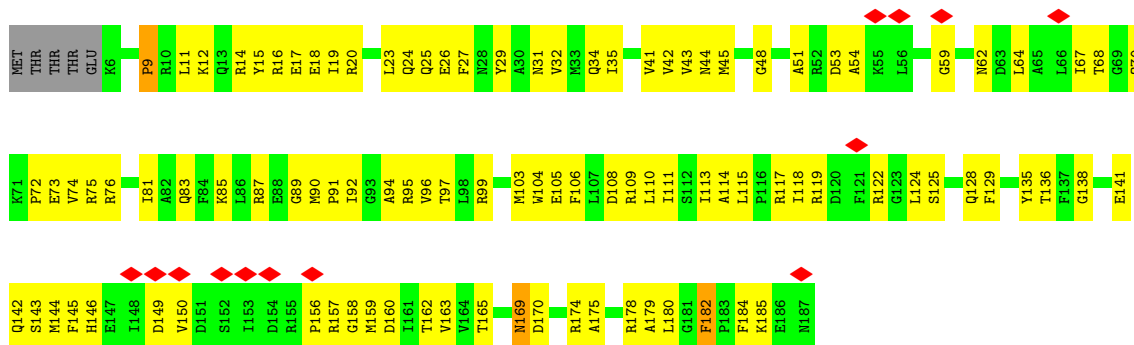


• Molecule 7: 50S Ribosomal Protein L4

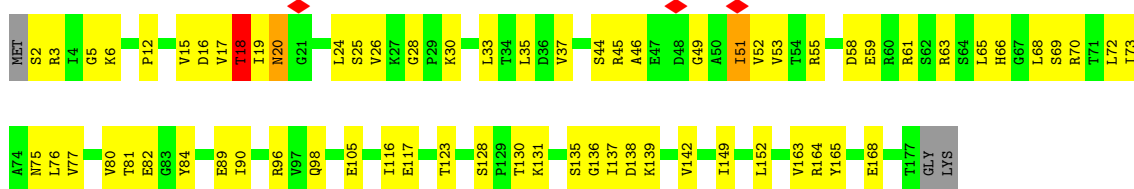


• Molecule 8: 50S Ribosomal Protein L5

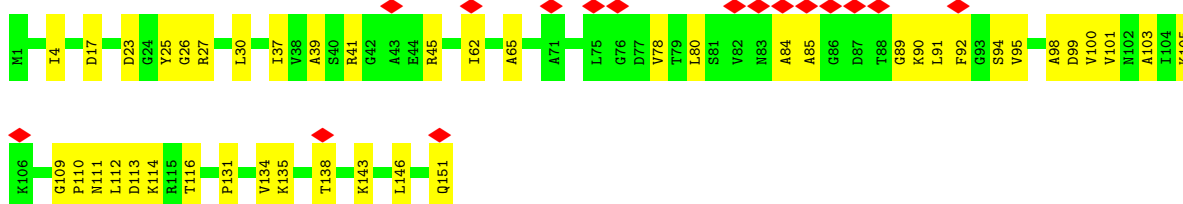




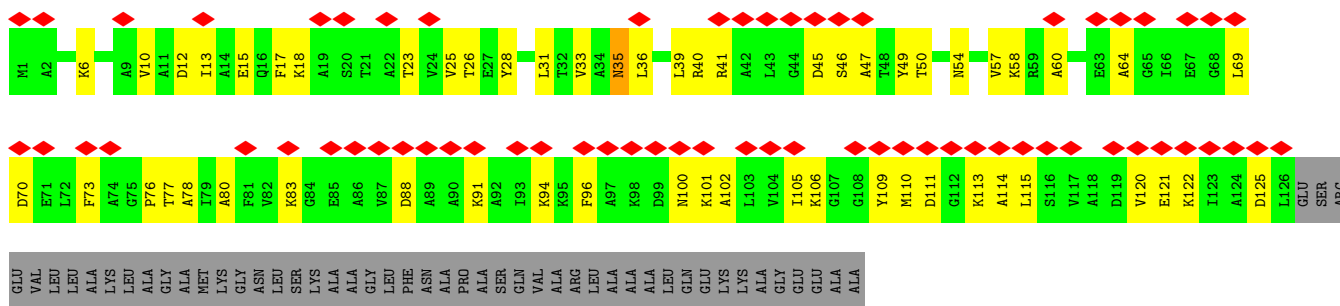
• Molecule 9: 50S ribosomal protein L6



• Molecule 10: 50S ribosomal protein L9

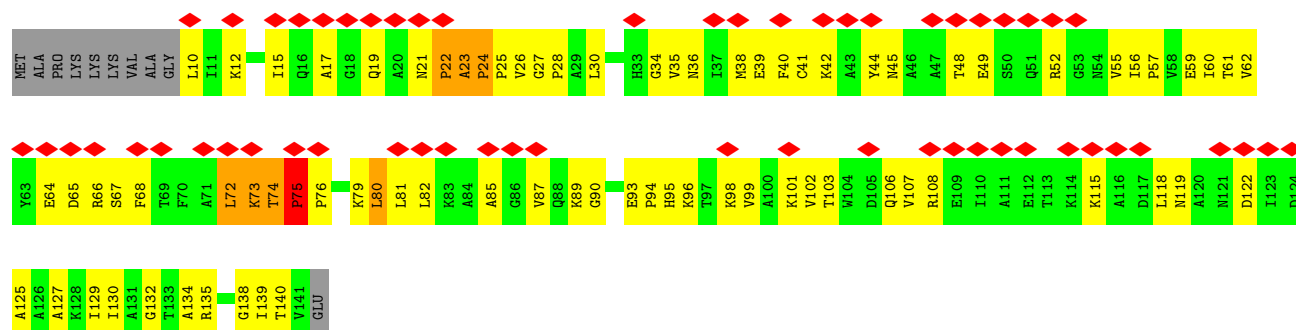


• Molecule 11: 50S ribosomal protein L10



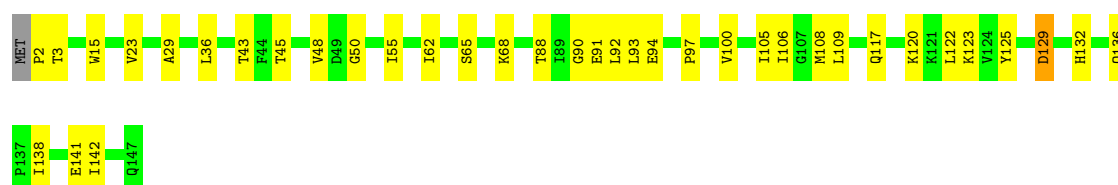
• Molecule 12: 50S ribosomal protein L11





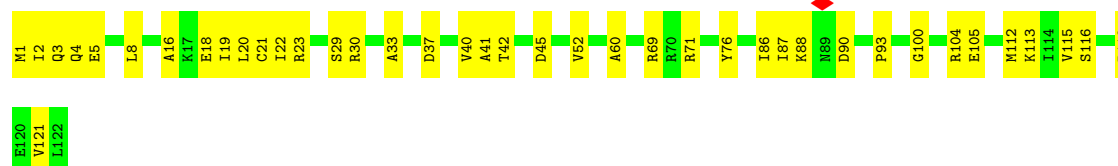
• Molecule 13: 50S Ribosomal Protein L13

Chain K: 74% 24%



• Molecule 14: 50S ribosomal protein L14

Chain L: 67% 33%



• Molecule 15: 50S ribosomal protein L15

Chain M: 63% 36%

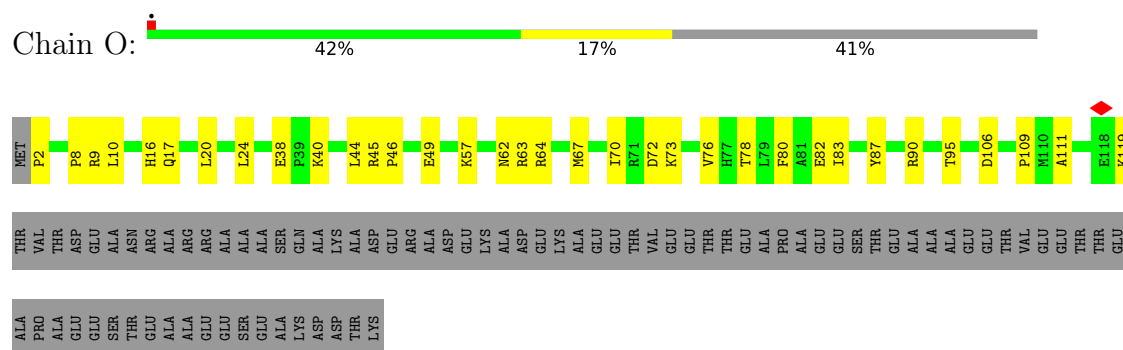


• Molecule 16: Large ribosomal subunit protein uL16

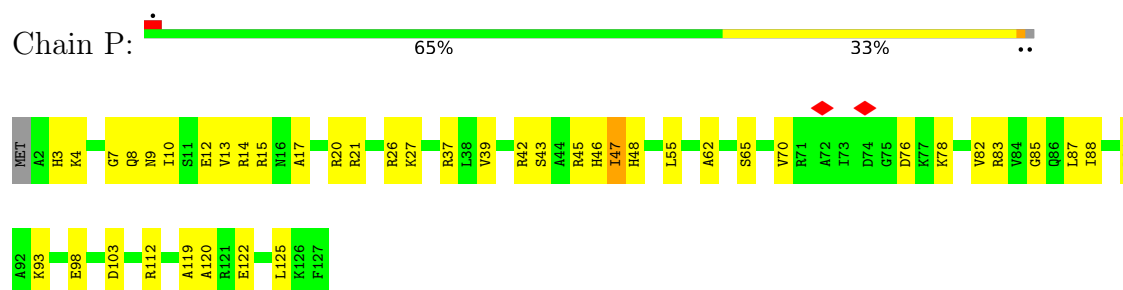
Chain N: 77% 22%



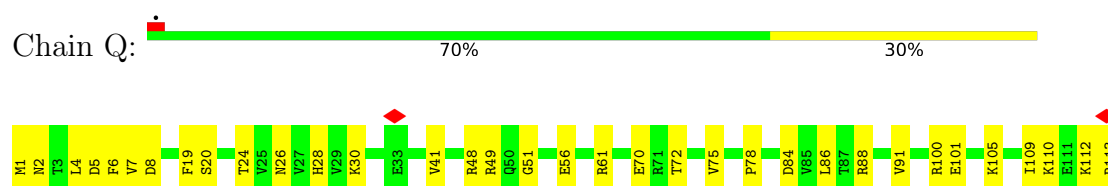
• Molecule 17: 50S ribosomal protein L17



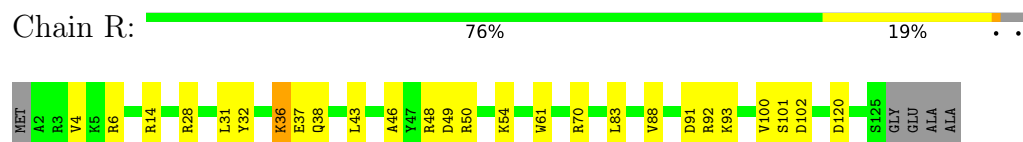
• Molecule 18: 50S Ribosomal Protein L18



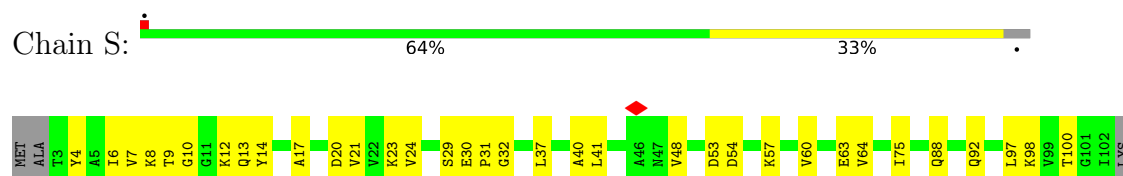
• Molecule 19: 50S ribosomal protein L19



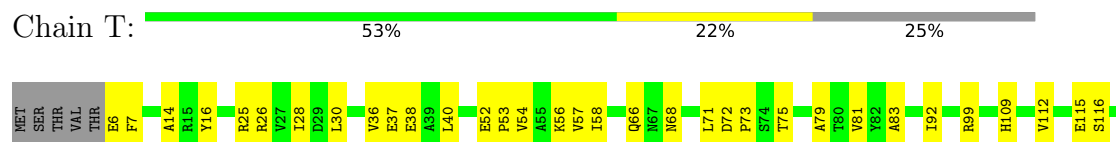
• Molecule 20: 50S Ribosomal Protein L20



• Molecule 21: 50S Ribosomal Protein L21



• Molecule 22: 50S Ribosomal Protein L22





- Molecule 29: 50S ribosomal protein L32

Chain b: 68% 26% 5%



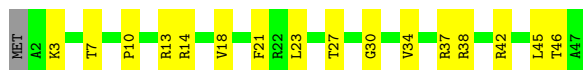
- Molecule 30: 50S Ribosomal Protein L33

Chain c: 60% 29% 11%



- Molecule 31: 50S ribosomal protein L34

Chain d: 64% 34% .



- Molecule 32: 50S ribosomal protein L35

Chain e: 69% 30% .



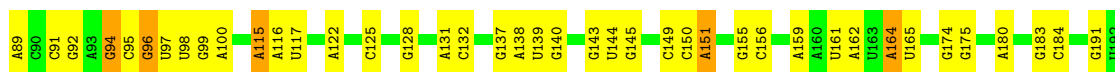
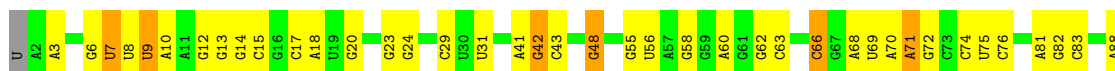
- Molecule 33: 50S ribosomal protein L36

Chain f: 78% 22%



- Molecule 34: 23S ribosomal RNA

Chain A: 49% 36% 10% 5%



G1411	U1316	G1225	G1152	G1073	G971	G853	U767	G695	C614	U519	G437	C346	A282	G193
A1415	G1317	U1226	G1156	A1074	A972	A854	G768	A696	C614	U519	U438	U347	U283	A194
A1416	C1318	C1227	G1157	U1075	A973	G872	U769	G697	U617	U524	C618	G348	G284	A196
A1417	A1319	A1228	U1158	A1076	G974	G877	G771	G698	C618	C523	U440	G349	U285	A196
G1418	G1323	A1229	C1159	A1077	G978	G878	U772	U699	C619	A527	U441	A350	G286	C197
A1419	G1324	G1230	G1160	G1078	A978	A879	G773	C704	G620	G528	U442	G351	A287	A198
	U1325	U1231	C1161	G1085	G979	G885	G774	G705	C621		U443	G352	U288	A206
G1424	G1326	U1234	G1162	G1086	G980	G886	U782	G706	G622	A531	U444	G356	A289	C207
G1425	U1235	G1235	G1165	U1087	A981	G890	G783	G707	A625	A535	U445	G357	C291	A212
G1426	G1236	U1237	A1166	U1088	A982	G891	G789	G708	G626		U446	G358	C292	G213
U1428	U1237		A1169	G1089	G993	G892		U709		C539	U447	G359	C293	G214
G1429	G1330	G1243	A1174	G1090	A994	G893	U801	C718	U630		U448	A363	G294	G214
U1431	G1335	A1244	G1175	A1091	U995	A897	C802	G719	G631	U643	U449	A364	U295	A215
	G1337		G1176	G1092	G996	A898		C720	C632	U644	U450	G366	A296	A216
G1434	A1340	U1250	A1177	A1098	G997	G899	A808	A721	U644	U645	U451	G367	G297	G217
C1435	U1178	G1252	U1179	C1100	G998	G900		A722	C634	A545	U452	U368	G298	A218
C1436	G1343	C1253	G1180	A1101	C999		C813	G723	C634	G555	U453	G369	G299	G219
	A1344	G1254	G1181	G1102	C1000	A904		G724	U636	G556	U454	U370	G300	A220
G1443	G1345	G1255	C1182	C1103	C1001	A907	U818	A725	G637	G557	U455	G371	U301	A221
U1444	U1346	G1256	U1183	C1104	C1002	G920	A821	A726	U638	A558	U456	U302	U302	A222
C1445	G1347		U1184	A1105	C1003	G921	G822	A727	U639	U560	U457	G303	G303	A227
	G1351	U1259	U1185	G1106	C1004	G922	G823	C728	G642		U458	G376	U304	A227
G1449	A1352	C1260	U1186	G1107	A1005	G923	G824	G730	G643	G564	U459	C377	G305	U229
G1456	G1353	A1261	A1187	A1108	A1006	G924	G825	A731	G644	A565	U460	G378	G306	G230
	G1355		G1188	U1109	C1007	G925	G826	G732	G645	A566	U461	G379	G307	U231
G1465	G1365	C1272	A1189	C1110	G1008	G926	G827	G733	G651	A567	U462	A380	U232	A233
C1466	A1366	G1278	G1190	G1111	U1009	U927	G828	C734	U654	G569	U463	A381	A234	U234
U1467	G1367	G1279	A1191	C1112	C927	U928	G829	A737	G655	U570	U464	A382	U235	U235
A1468	A1368		G1192	G1113	U929	U929	G830	A738	U658	A571	U465	A383	G242	
	G1369	C1283	C1193	G1114	C930	U930	G831	A739	U658	C572	U466	A384	U318	U246
G1473	U1370	A1284	C1194	U1115	C931	G931	G832	G740	G665	G576	U467	A385	G319	U246
G1475	G1371	G1285	A1195	U1116	C932	C932	G833	G741	A666	G577	U468	A386	G247	G248
G1476		C1286	C1196	U1117	G933	G933	G834	G742	A667	G578	U469	A387	G249	C249
C1477	U1378	C1287	C1197	C934	U934	G934	G835	G743	U668	G582	U470	A388	G250	G250
G1478	G1379	A1288	U935	G836	U941	G941	G837	C744	U669	G587	U471	A389	G254	
A1480	A1380	A1289	U942	G838	U942	G942	G839	G745	G672	G587	U472	A390	C322	G263
A1481	G1385	G1290	U943	U839	U943	G943	G840	A746	C673	G590	U473	A391	U325	G264
A1482	C1385	G1291	A944	G841	A944	G944	G842	U748	U674	A590	U474	A392	U326	A266
	G1386	U1292	G945	A842	G945	G945	A843			G591	U475	A393	U327	U266
U1487	A1387	G1293	G946	G843	U947	G947	G844	A751		G592	U476	A394	G328	G268
A1488		U1294	G948	G844	C1030	G948	G845	A752	A678	G593	U477	A401	U329	
	G1398	U1295	C949	G845	C1030	G949	G846	C754	G679	G594	U478	A402	U330	G264
A1493	A1399	G1296	A950	G846	A1033	A950	C847	A755	U680	G595	U479	A403	U331	A266
U1494	U1400	G1297	U954	G848	U1034	A954	G849	A756	A682	C596	U480	A404	U332	G267
	A1401		C955	G849	G1035	U955	A849	G757	G683	G597	U481	U410	U333	G268
A1499	G1402	G1301	G960	C853	A1042	G960	C853	G759	U688	G599	U482	A411	G334	
A1500	C1403	A1214	U963	U857	A1047	U963	U857	U760	A688	A600	U483	A412	G335	A271
C1501	A1404	A1304	G964	A858	A1048	G964	A858	A761	U689	G604	U484	A413	U336	A272
G1502	U1405	G1305	U965	U861	G1049	U965	U861	U762	G690	G605	U485	A414	U337	A273
	U1406	G1306	U966	U862	G1063	U966	U862	G763	G691		U486	A415	U338	C274
U1509	C1407	U1313	U967	U863	G1064	U967	U863	G764	G692		U487	A416	U339	C275
A1510	U1408	C1314	G967	U864	A1064	U967	U864	G765	G693	G609	U488	A417	U340	U277
U1512	U1512	G1315	C1065	U865	C1065	G967	U865	G766	C694	C610	U489	A418	U341	A278

G2581	G2495	C2397	A2337	G	U2044	G1936	G1736	G1642	C	G1513
G2585	U2496	C2398	G2338	A	G2045	U1937	A1737	G1645	C	C1514
G2586	A2497	A2399	G2339	A	A2046	G1938	G1746	U1646	U	A1518
G2587	A2498	C2400	A2340	U	U2051	C1944	C1752	G1647	U	G1524
G2588	G2503	C2401	U2341	U	G2052	U1945	C1753	A1648	C	U1525
G2589	C2507	U2402	A2342	A	C2053	U1946	G1754	C1649	G	G1528
A2590	G2508	U2403	G2343	A	C2054	U1947	G1755	G1650	G	U1529
A2593	C2509	G2404	A2344	G	C2055	G1951	U1756	C1651	G	G1530
A2597	A2510	A2405	U2345	C	C2056	G1952	U1757	G1652	U	C1531
C2598	G2511	G2278	G2346	C	G2057	A1955	G1758	G1653	G	G1532
G2599	A2512	C2279	G2347	C	G2058	A1956	A1759	U1654	U	U1533
A2600	G2514	A2281	G2348	U	U2059	G1959	G1760	C1658	G	C1534
G2603	G2515	C2282	A2349	C	G2060	U1960	G1761	U1671	C	C1535
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G2606	G2413	A2286	C2353	C	A	U1964	U1767	G1675	G	G1541
G2607	G2414	C2287	U2354	U	A	C1977	C1768	U1676	U	A1542
G2608	G2415	C2288	G2355	G	G2064	U1977	G1769	A1680	G	A1543
G2610	G2416	C2289	G2356	C	G2065	U1981	G1770	U1681	G	U1544
A2609	C2417	A2294	U2357	A	A	U1985	A1778	A1689	C	C1545
G2613	U2418	C2295	U2358	C	A	A1990	U1779	A1691	U	A
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G2615	A2420	C2299	G2360	G	A	A2000	C1784	G1696	C	C
G2618	A2421	C2300	U2361	A	G	U1999	C1785	U1703	U	G
A2623	G2427	G2301	C2362	G	G	A2001	G1786	U1704	C	G
C2624	C2431	C2307	U2363	A	A	G2007	U1787	C1705	U	G
C2625	U2436	U2308	A2363	C	C	A2008	A1788	A1706	C	C
U2626	A2436	G2309	G2364	G	C	G2014	G1789	U1709	C	C
G2627	G2447	C2310	C2365	A	A	U2015	A1790	A1710	U	A
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G2629	A2449	U2312	G2367	U	C	C2017	U1798	G1712	C	U
A2630	G2453	U2315	U2368	A	G	A2018	A1799	U1713	U	A
A2635	G2462	G2316	C2369	A	U	A2019	U1800	A1714	C	U
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G2637	G2466	U2318	G2371	C	C	G2025	A1802	G1622	C	C
U2641	U2467	G2319	C2372	A	U	A2026	A1803	U1623	C	A
C2644	U2468	C2320	U2373	C	C	A2027	A1804	U1624	C	A
A2649	U2469	G2321	G2374	C	C	G2028	G1805	G1625	C	A
A2650	A2470	C2322	U2375	A	U	C2028	A1806	G1626	C	A
A2651	A2471	A2323	G2376	C	U	G2028	C1807	U1627	C	C
C2652	G2472	U2324	U2377	A	G	G2031	A1808	A1628	A	A
G2653	U2473	G2325	C2378	C	G	G2032	A1809	G1629	C	C
A2654	G2474	C2326	U2379	A	G	U2033	U1810	U1630	C	C
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	A2491	U2334	G2387	C	C	G2040	A1825	U1638	C	A
		G2335	U2388	C	C	G2040	A1826	U1639	C	A
		U2336	U2389	C	C	G2040	A1827	U1640	C	A
			U2390	C	C	G2040		U1641	C	A
			G2391	C	C	G2040			C	A
			A2392	C	C	G2040			C	A
			A2393	C	C	G2040			C	A
			A2394	C	C	G2040			C	A
			U2395	C	C	G2040			C	A
			A2396	C	C	G2040			C	A

G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3098	G3078	G3087	G3
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	132147	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51.85	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	64000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.399	Depositor
Minimum map value	-1.560	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.111	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	430.4, 430.4, 430.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.076, 1.076, 1.076	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	2	0.36	0/477	0.45	0/640
2	3	0.37	0/191	0.40	0/247
3	4	0.36	2/3558 (0.1%)	0.69	7/4822 (0.1%)
4	B	0.32	0/2821	0.32	0/4396
5	C	0.36	0/2153	0.38	0/2895
6	D	0.38	0/1609	0.44	0/2165
7	E	0.35	0/1592	0.39	0/2153
8	F	0.36	2/1467 (0.1%)	0.68	2/1973 (0.1%)
9	G	0.29	0/1369	0.52	1/1848 (0.1%)
10	H	0.28	0/1027	0.48	0/1398
11	I	0.18	0/925	0.48	0/1246
12	J	0.43	1/971 (0.1%)	1.26	12/1315 (0.9%)
13	K	0.35	0/1157	0.40	0/1567
14	L	0.35	0/946	0.46	0/1268
15	M	0.34	0/1091	0.41	0/1457
16	N	0.35	0/1118	0.39	0/1506
17	O	0.36	0/945	0.38	0/1267
18	P	0.29	0/966	0.39	0/1298
19	Q	0.31	0/921	0.45	0/1236
20	R	0.41	0/1000	0.42	0/1341
21	S	0.39	1/764 (0.1%)	0.45	0/1030
22	T	0.36	0/887	0.41	0/1204
23	U	0.33	0/766	0.37	0/1030
24	V	0.27	0/738	0.47	0/987
25	W	0.25	0/745	0.39	0/1008
26	X	0.37	0/595	0.38	0/798
27	Y	0.44	0/478	0.38	0/641
28	Z	0.28	0/534	0.42	0/713
29	b	0.38	0/427	0.38	0/572
30	c	0.35	0/413	0.40	0/553
31	d	0.40	0/380	0.42	0/500
32	e	0.39	0/507	0.39	0/672

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.37	0/303	0.39	0/401
34	A	0.42	0/71013	0.36	2/110798 (0.0%)
All	All	0.40	6/104854 (0.0%)	0.41	24/156945 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
12	J	0	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	4	458	PRO	CG-CD	-11.14	1.12	1.50
3	4	458	PRO	CB-CG	-6.34	1.18	1.49
21	S	29	SER	C-N	-5.71	1.21	1.33
8	F	9	PRO	CG-CD	-5.53	1.31	1.50
12	J	21	ASN	N-CA	5.52	1.53	1.46
8	F	9	PRO	N-CD	5.12	1.54	1.47

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	4	458	PRO	N-CD-CG	-21.18	71.43	103.20
3	4	458	PRO	CA-CB-CG	-15.88	74.33	104.50
12	J	74	THR	CA-C-N	15.83	136.68	120.38
12	J	74	THR	C-N-CA	15.83	136.68	120.38
8	F	9	PRO	CA-N-CD	-12.70	94.22	112.00
3	4	21	ALA	N-CA-C	11.18	123.16	110.97
3	4	458	PRO	CB-CG-CD	10.17	138.63	106.10
8	F	9	PRO	N-CD-CG	-9.26	89.31	103.20
12	J	23	ALA	CA-C-N	-9.20	110.91	120.38
12	J	23	ALA	C-N-CA	-9.20	110.91	120.38
12	J	80	LEU	N-CA-C	-9.03	101.52	111.36
9	G	18	THR	N-CA-C	8.06	119.84	111.14
12	J	73	LYS	N-CA-C	-7.95	95.31	108.34
12	J	74	THR	N-CA-C	7.70	119.95	109.24
12	J	24	PRO	CA-C-N	7.08	126.57	118.85
12	J	24	PRO	C-N-CA	7.08	126.57	118.85
3	4	19	ASP	CA-C-N	-6.27	112.10	120.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	4	19	ASP	C-N-CA	-6.27	112.10	120.63
12	J	21	ASN	N-CA-C	5.94	122.94	109.81
3	4	458	PRO	CA-N-CD	-5.94	103.68	112.00
34	A	2123	A	C4'-C3'-O3'	-5.66	100.91	109.40
12	J	22	PRO	N-CA-C	5.41	122.88	114.98
34	A	2123	A	C2'-C3'-O3'	5.39	117.59	109.50
12	J	75	PRO	N-CA-C	5.11	116.93	110.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	J	72	LEU	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	474	0	500	16	0
2	3	189	0	205	4	0
3	4	3516	0	3564	205	0
4	B	2522	0	1285	45	0
5	C	2110	0	2165	40	0
6	D	1587	0	1630	60	0
7	E	1569	0	1607	37	0
8	F	1445	0	1476	97	0
9	G	1348	0	1399	59	0
10	H	1018	0	988	34	0
11	I	918	0	959	49	0
12	J	958	0	961	137	0
13	K	1130	0	1167	26	0
14	L	938	0	1000	27	0
15	M	1078	0	1151	40	0
16	N	1092	0	1128	23	0
17	O	928	0	972	26	0
18	P	956	0	991	39	0
19	Q	907	0	938	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	R	988	0	1038	24	0
21	S	754	0	802	24	0
22	T	873	0	909	22	0
23	U	756	0	802	22	0
24	V	732	0	782	33	0
25	W	735	0	756	18	0
26	X	586	0	601	14	0
27	Y	470	0	484	5	0
28	Z	531	0	541	15	0
29	b	423	0	463	12	0
30	c	405	0	411	13	0
31	d	377	0	411	12	0
32	e	502	0	541	13	0
33	f	299	0	324	7	0
34	A	63419	0	31905	1035	0
35	4	32	0	14	11	0
All	All	96565	0	64870	2038	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 13.

All (2038) 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)
12:J:56:ILE:CD1	12:J:74:THR:HG22	1.48	1.39
12:J:56:ILE:HD13	12:J:74:THR:CG2	1.49	1.39
12:J:56:ILE:HD12	12:J:74:THR:CA	1.52	1.37
12:J:56:ILE:CD1	12:J:74:THR:HA	1.58	1.31
12:J:24:PRO:HG2	12:J:25:PRO:CD	1.58	1.30
12:J:99:VAL:O	12:J:139:ILE:HG22	1.16	1.28
12:J:59:GLU:HB2	12:J:73:LYS:NZ	1.50	1.25
12:J:24:PRO:O	12:J:28:PRO:HD2	1.36	1.25
12:J:24:PRO:O	12:J:28:PRO:CD	1.84	1.24
3:4:444:HIS:CE1	12:J:24:PRO:CB	2.22	1.22
12:J:56:ILE:CD1	12:J:74:THR:CG2	2.11	1.22
3:4:21:ALA:HB1	3:4:88:ARG:HB3	1.23	1.21
12:J:24:PRO:CG	12:J:25:PRO:HD3	1.69	1.21
3:4:444:HIS:ND1	12:J:24:PRO:HB3	1.56	1.19
12:J:56:ILE:CD1	12:J:74:THR:CA	2.16	1.18
3:4:21:ALA:CB	3:4:88:ARG:HB3	1.75	1.17
12:J:98:LYS:HG2	12:J:138:GLY:O	1.45	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:99:VAL:O	12:J:139:ILE:CG2	1.94	1.15
3:4:444:HIS:CE1	12:J:24:PRO:HB3	1.84	1.11
12:J:59:GLU:CB	12:J:73:LYS:HZ1	1.63	1.09
34:A:273:A:H62	34:A:313:G:N2	1.51	1.06
34:A:2055:C:H41	34:A:2145:C:H5'	1.17	1.04
12:J:24:PRO:HG2	12:J:25:PRO:HD3	1.05	1.02
3:4:21:ALA:HB1	3:4:88:ARG:CB	1.90	1.02
9:G:18:THR:OG1	9:G:25:SER:N	1.93	0.99
34:A:1938:G:H21	34:A:1956:A:H62	1.05	0.98
12:J:98:LYS:CG	12:J:138:GLY:O	2.12	0.97
3:4:18:GLU:HB2	3:4:22:SER:H	1.29	0.97
12:J:24:PRO:CG	12:J:25:PRO:CD	2.34	0.95
12:J:24:PRO:HG2	12:J:25:PRO:HD2	1.49	0.94
12:J:24:PRO:CB	12:J:25:PRO:HD3	1.98	0.92
3:4:444:HIS:NE2	12:J:24:PRO:HB2	1.86	0.91
12:J:56:ILE:CD1	12:J:74:THR:CB	2.48	0.90
30:c:18:CYS:SG	30:c:44:ASN:ND2	2.43	0.90
10:H:105:LYS:HD2	10:H:111:ASN:HB2	1.50	0.90
12:J:23:ALA:O	12:J:26:VAL:N	2.07	0.88
3:4:444:HIS:CE1	12:J:24:PRO:HB2	2.06	0.87
12:J:76:PRO:O	12:J:80:LEU:N	2.07	0.87
34:A:2129:C:H4'	34:A:2130:G:H8	1.40	0.86
3:4:444:HIS:CD2	12:J:24:PRO:HB2	2.10	0.86
12:J:23:ALA:O	12:J:24:PRO:C	2.17	0.86
34:A:2127:G:H3'	34:A:2128:G:H8	1.39	0.86
3:4:255:ASN:H	35:4:501:GCP:H3B1	1.39	0.86
34:A:2129:C:H4'	34:A:2130:G:H5'	1.58	0.85
34:A:2354:G:H5''	34:A:2356:G:H4'	1.55	0.85
34:A:285:U:H3'	34:A:286:G:H4'	1.58	0.85
34:A:273:A:N6	34:A:313:G:H21	1.75	0.85
34:A:273:A:N6	34:A:313:G:N2	2.24	0.85
3:4:201:ARG:HD2	3:4:205:GLU:HG2	1.57	0.84
3:4:198:VAL:HG21	3:4:203:PRO:HD2	1.59	0.84
9:G:18:THR:HG1	9:G:25:SER:H	1.25	0.84
12:J:79:LYS:HB2	12:J:82:LEU:HB2	1.60	0.84
34:A:297:G:H2'	34:A:298:G:H8	1.40	0.84
21:S:7:VAL:HG12	21:S:60:VAL:HG11	1.57	0.83
12:J:59:GLU:HB2	12:J:73:LYS:HZ1	0.72	0.83
20:R:6:ARG:HD2	34:A:1365:G:H5''	1.61	0.82
3:4:18:GLU:CB	3:4:22:SER:H	1.92	0.82
34:A:1181:G:N1	34:A:1193:C:N3	2.28	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:119:LYS:NZ	34:A:2905:C:OP2	2.13	0.82
3:4:141:ILE:HG22	3:4:179:TRP:HZ2	1.44	0.82
12:J:23:ALA:O	12:J:27:GLY:N	2.13	0.82
12:J:56:ILE:HD11	12:J:74:THR:CG2	2.08	0.81
12:J:56:ILE:HD11	12:J:73:LYS:C	2.05	0.81
34:A:329:U:HO2'	34:A:446:G:H1	1.28	0.81
34:A:2133:G:H3'	34:A:2134:G:H8	1.42	0.81
8:F:41:VAL:HG22	8:F:103:MET:HG3	1.63	0.81
3:4:21:ALA:HB2	3:4:88:ARG:HB3	1.63	0.81
14:L:30:ARG:NH1	14:L:37:ASP:OD2	2.14	0.80
34:A:1181:G:N2	34:A:1193:C:O2	2.14	0.80
12:J:17:ALA:HB2	12:J:55:VAL:CA	2.12	0.80
26:X:64:PRO:HB3	34:A:759:G:H1	1.47	0.80
9:G:18:THR:HG21	9:G:25:SER:HB3	1.63	0.80
22:T:68:ASN:ND2	34:A:582:G:N3	2.31	0.79
12:J:98:LYS:NZ	12:J:140:THR:HG22	1.97	0.79
15:M:55:MET:HE3	15:M:59:MET:HB3	1.65	0.79
5:C:85:ASP:OD2	5:C:88:ARG:NH1	2.16	0.79
3:4:426:ARG:HB3	3:4:429:LEU:HD13	1.65	0.79
24:V:104:ASP:OD2	24:V:105:ILE:N	2.16	0.79
6:D:104:GLU:N	6:D:104:GLU:OE1	2.17	0.78
12:J:56:ILE:HD11	12:J:74:THR:N	1.99	0.78
27:Y:18:VAL:HG12	27:Y:24:ARG:HG2	1.65	0.77
34:A:347:U:H2'	34:A:348:G:H8	1.47	0.77
34:A:273:A:H62	34:A:313:G:H21	1.27	0.77
12:J:17:ALA:HB2	12:J:55:VAL:N	1.99	0.77
8:F:142:GLN:HE21	8:F:156:PRO:HA	1.49	0.77
34:A:293:G:H2'	34:A:294:G:C8	2.20	0.77
9:G:17:VAL:HA	9:G:26:VAL:HG12	1.66	0.76
26:X:14:ARG:NH1	34:A:2503:G:N7	2.32	0.76
5:C:177:MET:HA	5:C:177:MET:HE3	1.66	0.76
32:e:28:ASN:O	32:e:36:LYS:NZ	2.18	0.76
12:J:55:VAL:O	12:J:75:PRO:CB	2.34	0.76
34:A:2131:G:H3'	34:A:2132:U:H6	1.50	0.76
7:E:186:TYR:O	7:E:190:ASN:HB2	1.85	0.76
3:4:18:GLU:HB2	3:4:22:SER:N	2.00	0.75
20:R:36:LYS:NZ	34:A:1367:G:N7	2.34	0.75
12:J:24:PRO:O	12:J:28:PRO:HD3	1.86	0.75
12:J:56:ILE:CD1	12:J:74:THR:N	2.50	0.75
3:4:237:ARG:HG2	3:4:240:ARG:HH12	1.51	0.75
14:L:1:MET:HE1	34:A:2950:C:H4'	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:2358:A:HO2'	34:A:2383:U:HO2'	1.35	0.74
9:G:35:LEU:HB2	9:G:76:LEU:HD22	1.70	0.74
10:H:4:ILE:HG13	10:H:45:ARG:HA	1.69	0.74
34:A:297:G:H2'	34:A:298:G:C8	2.22	0.74
3:4:444:HIS:CE1	12:J:24:PRO:CA	2.69	0.74
31:d:14:ARG:NH2	34:A:885:G:OP2	2.19	0.74
34:A:960:G:OP2	34:A:960:G:N2	2.15	0.74
22:T:81:VAL:HG12	22:T:112:VAL:HG22	1.68	0.74
34:A:1157:G:O6	34:A:1234:U:O2	2.05	0.73
33:f:8:LYS:NZ	34:A:2691:C:OP1	2.21	0.73
3:4:444:HIS:ND1	12:J:24:PRO:CB	2.34	0.73
17:O:10:LEU:HD21	17:O:40:LYS:HG2	1.71	0.73
17:O:106:ASP:OD2	34:A:1867:G:O2'	2.06	0.73
34:A:1938:G:N2	34:A:1956:A:H62	1.85	0.73
34:A:2317:G:H1	34:A:2418:U:H3	1.32	0.73
3:4:23:LEU:HA	3:4:102:LYS:HE2	1.70	0.73
3:4:300:THR:HB	3:4:318:THR:HG23	1.70	0.73
34:A:2055:C:N4	34:A:2145:C:H5'	1.99	0.73
34:A:2361:U:H3	34:A:2376:G:H1	1.36	0.73
21:S:30:GLU:OE2	21:S:32:GLY:N	2.16	0.73
8:F:23:LEU:HD11	8:F:175:ALA:HB1	1.70	0.73
9:G:96:ARG:HH22	9:G:98:GLN:HB3	1.53	0.73
24:V:10:LEU:HD13	24:V:80:PRO:HG3	1.70	0.73
29:b:16:ARG:NH2	34:A:1379:G:OP1	2.13	0.73
12:J:56:ILE:CD1	12:J:73:LYS:C	2.61	0.72
34:A:1996:U:OP2	34:A:2001:A:N6	2.22	0.72
34:A:2255:A:N3	34:A:2679:G:O2'	2.22	0.72
34:A:2055:C:H42	34:A:2122:U:H2'	1.54	0.72
12:J:56:ILE:HD13	12:J:74:THR:CB	2.14	0.72
27:Y:41:ARG:HG2	27:Y:42:PRO:HD2	1.70	0.72
3:4:330:HIS:ND1	3:4:330:HIS:O	2.20	0.72
10:H:84:ALA:HB3	10:H:94:SER:H	1.54	0.72
34:A:2474:G:O2'	34:A:2720:C:OP1	2.08	0.72
34:A:298:G:N2	34:A:300:G:O2'	2.22	0.71
9:G:2:SER:HA	9:G:55:ARG:HH12	1.54	0.71
34:A:2158:C:H4'	34:A:2159:G:H2'	1.70	0.71
3:4:420:VAL:HG11	3:4:463:LEU:HB3	1.71	0.71
34:A:3023:G:H2'	34:A:3024:A:H8	1.55	0.71
25:W:37:LEU:HB3	25:W:45:GLN:HB2	1.71	0.71
3:4:21:ALA:CB	3:4:88:ARG:CB	2.54	0.71
20:R:49:ASP:OD2	34:A:651:G:N2	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:1411:G:OP1	34:A:2933:G:O2'	2.08	0.71
8:F:20:ARG:HG3	8:F:35:ILE:HG21	1.71	0.71
14:L:3:GLN:NE2	34:A:2219:U:O2	2.23	0.71
20:R:92:ARG:NH2	34:A:1272:C:OP1	2.24	0.71
34:A:2123:A:N7	34:A:2145:C:C4	2.59	0.71
18:P:43:SER:O	18:P:112:ARG:NH2	2.24	0.70
31:d:10:PRO:HB2	34:A:1424:G:H4'	1.72	0.70
3:4:376:GLY:HA3	3:4:379:LEU:HG	1.73	0.70
20:R:37:GLU:OE2	34:A:1367:G:N2	2.19	0.70
3:4:24:ARG:HD2	3:4:88:ARG:HE	1.57	0.70
9:G:2:SER:N	34:A:2973:A:OP1	2.24	0.70
18:P:9:ASN:OD1	18:P:10:ILE:N	2.25	0.70
24:V:15:LYS:NZ	34:A:390:G:O2'	2.25	0.70
9:G:12:PRO:HG3	9:G:81:THR:HG22	1.73	0.70
3:4:395:ARG:HB2	35:4:501:GCP:N1	2.07	0.70
34:A:1181:G:O6	34:A:1193:C:N4	2.25	0.70
4:B:26:A:H2	4:B:115:A:H1'	1.57	0.69
8:F:15:TYR:HA	8:F:19:ILE:HG12	1.74	0.69
3:4:76:THR:HG21	3:4:276:LEU:HB2	1.72	0.69
34:A:3023:G:H2'	34:A:3024:A:C8	2.27	0.69
8:F:138:GLY:HA2	8:F:160:ASP:HA	1.74	0.69
34:A:2127:G:H3'	34:A:2128:G:C8	2.26	0.69
8:F:29:TYR:CD1	8:F:34:GLN:HB2	2.28	0.69
12:J:119:ASN:ND2	34:A:1176:G:N3	2.38	0.69
34:A:1415:A:H4'	34:A:1416:A:H5''	1.75	0.69
5:C:175:LEU:HD11	5:C:185:VAL:HG12	1.75	0.69
34:A:2123:A:N7	34:A:2145:C:C5	2.61	0.69
22:T:56:LYS:NZ	34:A:576:G:O2'	2.21	0.68
34:A:2051:U:H4'	34:A:2160:A:H62	1.58	0.68
32:e:45:ASP:OD1	32:e:46:GLY:N	2.26	0.68
34:A:7:U:O2'	34:A:8:U:O4'	2.12	0.68
34:A:289:A:H2'	34:A:290:C:H5	1.59	0.68
34:A:2851:G:N2	34:A:3001:G:OP2	2.27	0.68
8:F:53:ASP:OD1	8:F:54:ALA:N	2.27	0.68
34:A:737:A:N1	34:A:2593:A:O2'	2.25	0.68
12:J:81:LEU:HD21	12:J:102:VAL:HG21	1.74	0.68
31:d:3:LYS:NZ	34:A:853:C:OP1	2.22	0.68
9:G:17:VAL:O	9:G:45:ARG:NH1	2.27	0.68
23:U:34:HIS:ND1	23:U:36:ASP:OD1	2.25	0.68
14:L:69:ARG:HE	14:L:105:GLU:HG2	1.59	0.68
15:M:94:GLY:HA2	15:M:125:THR:HG22	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:1754:G:H1	34:A:1759:A:H2	1.40	0.68
5:C:257:THR:OG1	34:A:2014:G:O2'	2.12	0.68
3:4:444:HIS:CG	12:J:24:PRO:CB	2.77	0.68
14:L:4:GLN:NE2	14:L:22:ILE:O	2.25	0.68
4:B:3:U:O2'	4:B:5:C:OP2	2.10	0.67
6:D:144:VAL:HA	6:D:147:ARG:HG3	1.76	0.67
20:R:48:ARG:NH1	20:R:49:ASP:OD1	2.26	0.67
34:A:1756:G:H1'	34:A:1758:G:H22	1.59	0.67
3:4:371:ILE:HG21	3:4:391:PHE:HD1	1.57	0.67
34:A:1195:A:H2	34:A:1206:A:H8	1.42	0.67
12:J:56:ILE:HG12	12:J:72:LEU:HB3	1.76	0.67
34:A:499:G:OP2	34:A:2630:A:O2'	2.13	0.67
34:A:587:G:N1	34:A:590:A:OP2	2.28	0.67
8:F:108:ASP:HA	8:F:111:ILE:HG22	1.76	0.67
6:D:27:THR:OG1	6:D:196:GLY:O	2.13	0.67
16:N:118:LEU:HD12	16:N:131:ILE:HG23	1.77	0.67
34:A:978:A:H2'	34:A:979:G:H8	1.58	0.67
13:K:141:GLU:OE1	13:K:142:ILE:N	2.28	0.67
34:A:2527:G:O6	34:A:2538:A:N6	2.27	0.67
17:O:90:ARG:NH2	34:A:3101:C:O2'	2.27	0.67
34:A:2123:A:C8	34:A:2145:C:C2	2.82	0.67
12:J:24:PRO:CB	12:J:25:PRO:CD	2.70	0.67
15:M:99:VAL:HG13	15:M:104:VAL:HG23	1.76	0.67
18:P:8:GLN:HG2	18:P:12:GLU:OE2	1.95	0.67
12:J:129:ILE:HD11	34:A:1199:U:H1'	1.77	0.67
34:A:1864:U:O2	34:A:1865:A:N6	2.27	0.67
34:A:2350:G:H2'	34:A:2351:A:C8	2.30	0.66
6:D:148:PRO:O	34:A:2735:U:O2'	2.13	0.66
18:P:46:HIS:HB3	18:P:65:SER:HB3	1.76	0.66
3:4:21:ALA:HB2	3:4:88:ARG:HD2	1.75	0.66
3:4:291:ASP:OD1	3:4:292:GLY:N	2.29	0.66
8:F:68:THR:HG23	8:F:70:GLN:H	1.58	0.66
26:X:11:ARG:O	26:X:14:ARG:NH2	2.23	0.66
34:A:1478:C:O2'	34:A:2026:A:N3	2.27	0.66
3:4:234:ASP:OD1	3:4:235:THR:N	2.28	0.66
34:A:2399:A:HO2'	34:A:2400:C:H6	1.43	0.66
3:4:85:LEU:HD21	3:4:109:VAL:HG21	1.78	0.66
11:I:69:LEU:HB3	11:I:109:TYR:HB3	1.77	0.66
12:J:23:ALA:HA	12:J:26:VAL:HB	1.78	0.66
34:A:286:G:H2'	34:A:287:A:H8	1.59	0.66
34:A:1758:G:O2'	34:A:1759:A:OP2	2.11	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:1212:U:H3'	34:A:1213:A:H5''	1.78	0.66
6:D:39:ILE:O	6:D:44:ARG:NH2	2.26	0.66
30:c:8:ARG:NH1	34:A:2509:C:OP2	2.29	0.66
34:A:263:G:O2'	34:A:517:A:N3	2.26	0.66
34:A:289:A:N7	34:A:298:G:N1	2.39	0.66
3:4:195:GLY:HA2	3:4:204:GLY:HA2	1.78	0.65
10:H:114:LYS:NZ	34:A:282:A:OP1	2.28	0.65
32:e:24:ARG:NH1	32:e:25:GLN:O	2.29	0.65
6:D:39:ILE:HD11	6:D:95:TYR:HB2	1.78	0.65
12:J:22:PRO:HG2	12:J:41:CYS:SG	2.36	0.65
11:I:47:ALA:HB1	11:I:80:ALA:HB1	1.78	0.65
8:F:17:GLU:N	8:F:17:GLU:OE2	2.27	0.65
34:A:137:G:H21	34:A:1524:G:H1'	1.62	0.65
34:A:944:A:N7	34:A:2471:A:O2'	2.29	0.65
34:A:2051:U:O2	34:A:2194:A:O2'	2.13	0.65
34:A:2121:G:H5'	34:A:2145:C:P	2.37	0.65
34:A:2123:A:C8	34:A:2145:C:N3	2.65	0.65
3:4:289:PHE:CE1	3:4:295:PHE:HB3	2.32	0.65
34:A:2394:A:OP1	34:A:2397:C:N4	2.29	0.65
17:O:70:ILE:HG23	17:O:72:ASP:H	1.61	0.65
12:J:24:PRO:O	12:J:28:PRO:CG	2.44	0.65
17:O:38:GLU:HG3	17:O:111:ALA:HB2	1.79	0.65
33:f:6:SER:HB3	34:A:2690:C:H5''	1.78	0.65
34:A:1184:U:N3	34:A:1187:A:OP2	2.27	0.65
7:E:105:LYS:NZ	34:A:699:U:OP2	2.29	0.65
34:A:2528:G:H22	34:A:2536:U:H3	1.44	0.65
24:V:45:THR:O	34:A:571:A:O2'	2.14	0.64
4:B:53:A:N7	18:P:45:ARG:NH2	2.45	0.64
8:F:14:ARG:O	8:F:18:GLU:HG3	1.96	0.64
9:G:165:TYR:HB2	9:G:168:GLU:HG2	1.79	0.64
13:K:3:THR:HG21	20:R:61:TRP:HE1	1.62	0.64
32:e:19:THR:OG1	34:A:745:G:OP1	2.15	0.64
34:A:1122:C:H2'	34:A:1129:G:H2'	1.78	0.64
34:A:1202:A:O3'	34:A:1223:U:O2'	2.13	0.64
3:4:444:HIS:CG	12:J:24:PRO:HB3	2.29	0.64
12:J:82:LEU:HD11	12:J:90:GLY:HA2	1.80	0.64
34:A:523:U:H2'	34:A:524:C:H5'	1.79	0.64
3:4:108:GLU:HA	3:4:111:LEU:HG	1.79	0.64
3:4:136:VAL:HG13	3:4:138:VAL:H	1.63	0.64
34:A:2390:U:H2'	34:A:2392:A:N7	2.12	0.64
12:J:56:ILE:HD11	12:J:74:THR:CA	2.24	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:83:LEU:HD22	20:R:88:VAL:HG21	1.79	0.64
30:c:6:ASP:O	30:c:29:ARG:NH1	2.31	0.64
34:A:2158:C:H5'	34:A:2159:G:C4	2.33	0.64
1:2:6:ILE:HD11	1:2:54:VAL:HG21	1.80	0.64
3:4:143:ARG:NH1	3:4:305:ARG:O	2.29	0.64
34:A:1696:G:O2'	34:A:1736:G:O6	2.15	0.64
34:A:2054:C:O2	34:A:2145:C:C2	2.51	0.63
8:F:27:PHE:CZ	8:F:35:ILE:HG13	2.33	0.63
12:J:24:PRO:HB2	12:J:25:PRO:HD3	1.80	0.63
34:A:634:C:H3'	34:A:635:G:H5''	1.80	0.63
34:A:2129:C:H4'	34:A:2130:G:C8	2.29	0.63
3:4:178:GLY:O	3:4:181:GLU:HG3	1.98	0.63
8:F:27:PHE:HZ	8:F:35:ILE:HG13	1.63	0.63
34:A:2123:A:C8	34:A:2145:C:C4	2.86	0.63
3:4:286:ARG:HG3	34:A:2697:U:H1'	1.80	0.63
7:E:127:VAL:HG11	7:E:148:LEU:HD11	1.80	0.63
12:J:10:LEU:N	12:J:60:ILE:O	2.32	0.63
3:4:285:ARG:NH2	34:A:2695:A:OP1	2.30	0.63
5:C:124:ASP:OD1	5:C:129:ASN:ND2	2.32	0.63
26:X:15:ASP:OD1	34:A:2487:C:N4	2.31	0.63
34:A:66:C:O2	34:A:70:A:O2'	2.16	0.63
34:A:242:G:O2'	34:A:254:G:O6	2.13	0.63
1:2:11:SER:OG	34:A:1107:G:OP2	2.11	0.63
6:D:40:ARG:HD2	6:D:83:GLU:OE1	1.99	0.63
9:G:20:ASN:N	9:G:20:ASN:OD1	2.30	0.63
32:e:47:ARG:NH2	34:A:724:G:OP1	2.32	0.63
34:A:279:U:H2'	34:A:280:G:H8	1.64	0.63
34:A:2575:G:O2'	34:A:2590:A:N6	2.30	0.63
17:O:57:LYS:O	17:O:62:ASN:ND2	2.32	0.63
34:A:453:U:H1'	34:A:454:U:H5	1.63	0.63
34:A:978:A:H2'	34:A:979:G:C8	2.34	0.63
34:A:2872:G:H2'	34:A:2873:U:C6	2.33	0.63
3:4:107:ARG:NH2	3:4:136:VAL:O	2.32	0.63
5:C:37:LEU:HD13	5:C:62:TYR:HB2	1.81	0.63
34:A:273:A:N6	34:A:313:G:C2	2.66	0.63
14:L:93:PRO:HD2	14:L:113:LYS:HE3	1.81	0.62
17:O:38:GLU:OE2	29:b:42:ARG:NH2	2.31	0.62
3:4:332:VAL:HB	3:4:343:ILE:HD11	1.81	0.62
4:B:111:C:H2'	4:B:112:C:C6	2.34	0.62
23:U:85:LYS:NZ	34:A:1514:C:OP1	2.27	0.62
34:A:1195:A:H2	34:A:1206:A:C8	2.16	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:X:19:GLN:NE2	34:A:2486:U:OP2	2.32	0.62
1:2:57:GLU:N	1:2:57:GLU:OE1	2.32	0.62
34:A:1625:G:N1	34:A:1626:G:O6	2.31	0.62
11:I:58:LYS:HA	11:I:73:PHE:HE2	1.64	0.62
13:K:125:TYR:OH	13:K:132:HIS:NE2	2.32	0.62
22:T:71:LEU:HD21	22:T:116:SER:HB2	1.80	0.62
34:A:1313:U:H2'	34:A:1314:C:H6	1.65	0.62
5:C:208:LYS:HG3	5:C:211:ARG:HB2	1.81	0.62
9:G:35:LEU:HD13	9:G:76:LEU:HD13	1.80	0.62
10:H:131:PRO:HB2	10:H:143:LYS:NZ	2.15	0.62
13:K:90:GLY:O	13:K:94:GLU:HG3	1.99	0.62
34:A:277:U:H2'	34:A:278:A:C8	2.35	0.62
2:3:17:ASN:ND2	34:A:1103:C:O2	2.31	0.62
11:I:58:LYS:HD2	11:I:70:ASP:HB3	1.81	0.62
8:F:111:ILE:HA	8:F:115:LEU:HD12	1.80	0.62
34:A:2294:A:H2'	34:A:2295:C:C6	2.35	0.62
34:A:1201:G:N2	34:A:1204:A:OP2	2.33	0.62
34:A:2131:G:H3'	34:A:2132:U:C6	2.32	0.62
6:D:160:VAL:HG21	34:A:2842:G:H21	1.65	0.62
34:A:1479:G:N2	34:A:1482:A:OP2	2.29	0.62
5:C:89:THR:HG21	34:A:2038:A:H5''	1.82	0.61
6:D:64:LYS:HG2	34:A:3011:C:H4'	1.80	0.61
34:A:2410:A:H2'	34:A:2411:U:C6	2.35	0.61
15:M:65:LYS:NZ	34:A:2641:U:OP1	2.28	0.61
26:X:75:ARG:HD2	34:A:2558:C:H42	1.65	0.61
34:A:326:A:N6	34:A:450:G:H21	1.98	0.61
34:A:823:C:H2'	34:A:824:G:H8	1.65	0.61
12:J:62:VAL:HA	12:J:67:SER:HB2	1.81	0.61
30:c:35:ARG:NH2	30:c:53:GLU:O	2.34	0.61
34:A:997:G:H2'	34:A:998:G:H5'	1.83	0.61
15:M:80:VAL:HG22	15:M:114:GLY:HA2	1.83	0.61
34:A:1199:U:H2'	34:A:1200:U:C6	2.35	0.61
34:A:2055:C:H5''	34:A:2149:C:C5	2.35	0.61
3:4:370:LYS:HG2	35:4:501:GCP:C5	2.31	0.61
12:J:57:PRO:N	12:J:73:LYS:O	2.33	0.61
34:A:450:G:O2'	34:A:451:U:H5'	2.01	0.61
3:4:379:LEU:N	3:4:383:ARG:HB2	2.16	0.61
18:P:42:ARG:HA	18:P:47:ILE:HG13	1.83	0.61
34:A:1770:G:OP1	34:A:1937:U:O2'	2.13	0.61
34:A:2125:A:H2'	34:A:2125:A:N3	2.16	0.61
10:H:100:VAL:HG21	10:H:146:LEU:HD21	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:115:VAL:HG13	14:L:121:VAL:HG21	1.82	0.61
8:F:125:SER:H	8:F:185:LYS:NZ	1.98	0.61
34:A:742:G:O2'	34:A:2575:G:OP1	2.17	0.61
34:A:1223:U:H2'	34:A:1224:G:H8	1.66	0.61
25:W:21:LYS:O	25:W:25:ARG:HG3	2.01	0.61
34:A:2336:U:O2'	34:A:2337:A:O5'	2.18	0.61
7:E:189:LEU:HD13	15:M:9:LEU:HD11	1.83	0.60
34:A:920:G:N2	34:A:944:A:OP1	2.34	0.60
34:A:1710:A:H62	34:A:1716:A:H5''	1.66	0.60
34:A:2133:G:H5''	34:A:2134:G:N7	2.16	0.60
4:B:59:A:N3	18:P:9:ASN:ND2	2.49	0.60
11:I:111:ASP:O	11:I:113:LYS:NZ	2.33	0.60
34:A:2412:U:H2'	34:A:2413:G:C8	2.36	0.60
8:F:125:SER:H	8:F:185:LYS:HZ3	1.48	0.60
18:P:62:ALA:O	18:P:91:ARG:NH1	2.34	0.60
25:W:32:LYS:NZ	25:W:48:GLU:OE1	2.30	0.60
31:d:27:THR:HG23	31:d:30:GLY:H	1.67	0.60
34:A:2339:G:O6	34:A:2394:A:N6	2.33	0.60
34:A:2359:G:C2	34:A:2360:C:H1'	2.36	0.60
34:A:3115:A:H2'	34:A:3116:C:C6	2.36	0.60
6:D:83:GLU:OE2	34:A:2860:U:H4'	2.01	0.60
17:O:67:MET:HG2	17:O:76:VAL:HG21	1.84	0.60
34:A:1003:A:N3	34:A:1004:C:O2'	2.30	0.60
12:J:59:GLU:CB	12:J:73:LYS:NZ	2.42	0.60
8:F:29:TYR:HD1	8:F:34:GLN:HB2	1.65	0.60
11:I:88:ASP:OD1	11:I:88:ASP:N	2.32	0.60
34:A:289:A:H2'	34:A:290:C:C5	2.36	0.60
34:A:2062:G:H21	34:A:2119:C:H5	1.49	0.60
34:A:2726:G:H5''	34:A:2727:A:H5''	1.84	0.60
3:4:348:THR:O	3:4:352:GLU:HG2	2.00	0.60
34:A:1728:U:H5'	34:A:1729:A:O5'	2.02	0.60
34:A:2552:A:H2'	34:A:2553:G:C8	2.37	0.60
8:F:95:ARG:NH2	34:A:2537:C:OP1	2.34	0.60
22:T:54:VAL:O	22:T:58:ILE:HG13	2.02	0.60
34:A:353:G:H1	34:A:442:U:H3	1.47	0.60
3:4:63:ALA:O	3:4:66:SER:OG	2.15	0.60
3:4:50:VAL:HG12	3:4:83:GLU:HB3	1.84	0.59
11:I:25:VAL:HG12	11:I:106:LYS:HG3	1.84	0.59
12:J:56:ILE:HD13	12:J:74:THR:HG22	0.67	0.59
13:K:129:ASP:OD1	13:K:129:ASP:N	2.34	0.59
14:L:5:GLU:HA	14:L:20:LEU:HD21	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:d:42:ARG:NH2	34:A:556:G:N7	2.48	0.59
34:A:292:G:OP1	34:A:344:G:N2	2.35	0.59
34:A:747:A:N6	34:A:768:G:O2'	2.35	0.59
3:4:280:LEU:HA	3:4:301:VAL:HG13	1.83	0.59
14:L:2:ILE:HG13	14:L:8:LEU:HD21	1.84	0.59
34:A:2054:C:O2	34:A:2145:C:C4	2.55	0.59
11:I:26:THR:HG22	11:I:105:ILE:HG23	1.85	0.59
12:J:76:PRO:CB	12:J:79:LYS:HG3	2.32	0.59
14:L:112:MET:O	14:L:116:SER:OG	2.19	0.59
34:A:292:G:H2'	34:A:293:G:C8	2.37	0.59
34:A:747:A:H2'	34:A:748:U:O4'	2.03	0.59
4:B:31:C:OP1	18:P:14:ARG:NH1	2.35	0.59
9:G:19:ILE:O	9:G:19:ILE:HG22	2.02	0.59
20:R:50:ARG:O	20:R:54:LYS:NZ	2.36	0.59
34:A:279:U:H3	34:A:307:G:H1	1.51	0.59
13:K:108:MET:SD	34:A:1256:G:N2	2.70	0.59
34:A:1938:G:H21	34:A:1956:A:N6	1.87	0.59
28:Z:25:SER:HB2	28:Z:54:ILE:HD11	1.84	0.59
34:A:1003:A:H1'	34:A:1004:C:H2'	1.84	0.59
34:A:2382:G:O2'	34:A:2383:U:O4'	2.21	0.59
12:J:135:ARG:HH22	34:A:1206:A:N6	2.00	0.59
34:A:1063:G:O6	34:A:1090:G:N2	2.36	0.59
34:A:808:A:O2'	34:A:1468:A:N3	2.31	0.59
34:A:993:G:N2	34:A:1015:A:OP2	2.30	0.59
25:W:37:LEU:HB2	25:W:47:LEU:HD11	1.85	0.58
34:A:271:A:OP2	34:A:314:G:N1	2.27	0.58
34:A:473:C:O2'	34:A:476:G:N2	2.36	0.58
34:A:2331:U:H4'	34:A:2374:U:H5'	1.84	0.58
34:A:1160:G:H1	34:A:1231:U:H3	1.51	0.58
12:J:44:TYR:OH	12:J:56:ILE:O	2.20	0.58
30:c:11:ILE:HG21	30:c:27:LYS:HE2	1.84	0.58
34:A:996:G:C4	34:A:997:G:C8	2.91	0.58
34:A:1530:G:H2'	34:A:1531:C:C6	2.38	0.58
34:A:2127:G:H5'	34:A:2153:G:H2'	1.84	0.58
3:4:148:LEU:HB3	3:4:168:GLN:HG2	1.85	0.58
7:E:178:ILE:HD12	34:A:708:G:H1	1.67	0.58
21:S:75:ILE:HB	21:S:88:GLN:HB3	1.84	0.58
34:A:2872:G:H2'	34:A:2873:U:H6	1.69	0.58
3:4:24:ARG:HG3	3:4:26:VAL:HG13	1.84	0.58
7:E:153:LYS:NZ	34:A:1319:A:OP1	2.27	0.58
16:N:47:ILE:HD12	16:N:70:PRO:HG3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:2364:C:H2'	34:A:2365:A:H8	1.68	0.58
12:J:26:VAL:HG13	12:J:30:LEU:HD23	1.85	0.58
16:N:44:ASN:OD1	16:N:44:ASN:N	2.37	0.58
34:A:1011:A:C6	34:A:1012:C:H1'	2.39	0.58
34:A:2061:U:H2'	34:A:2062:G:H4'	1.85	0.58
6:D:48:SER:OG	6:D:86:LEU:O	2.18	0.58
8:F:11:LEU:HD11	8:F:111:ILE:HG21	1.86	0.58
12:J:98:LYS:HG2	12:J:138:GLY:C	2.23	0.58
34:A:1704:U:H2'	34:A:1705:C:C6	2.38	0.58
34:A:2869:C:H3'	34:A:2870:C:H5'	1.85	0.58
3:4:141:ILE:HG22	3:4:179:TRP:CZ2	2.33	0.58
6:D:135:GLN:HE21	34:A:2802:G:H21	1.52	0.58
9:G:58:ASP:O	9:G:63:ARG:NH1	2.36	0.58
12:J:12:LYS:H	12:J:12:LYS:HD3	1.68	0.58
34:A:1205:G:O2'	34:A:1207:G:O4'	2.21	0.58
3:4:24:ARG:H	3:4:87:GLN:CD	2.12	0.58
34:A:635:G:O2'	34:A:636:U:O5'	2.20	0.58
4:B:49:C:OP1	18:P:42:ARG:NH1	2.31	0.57
19:Q:101:GLU:N	19:Q:101:GLU:OE1	2.36	0.57
34:A:248:G:H5'	34:A:250:G:N7	2.19	0.57
34:A:389:G:N1	34:A:392:A:OP2	2.31	0.57
12:J:95:HIS:HB2	34:A:1195:A:H4'	1.85	0.57
15:M:82:ASP:HA	15:M:85:LYS:HG2	1.86	0.57
3:4:214:ARG:NH1	34:A:2684:U:O2'	2.37	0.57
3:4:315:PHE:O	3:4:319:LEU:HG	2.04	0.57
34:A:56:U:O2'	34:A:71:A:OP2	2.21	0.57
34:A:1204:A:O2'	34:A:1205:G:N7	2.37	0.57
18:P:20:ARG:NH1	34:A:2558:C:OP2	2.37	0.57
34:A:3078:G:N2	34:A:3081:A:OP2	2.29	0.57
12:J:129:ILE:HA	34:A:1198:C:H1'	1.87	0.57
28:Z:52:GLN:O	28:Z:56:ARG:HG3	2.04	0.57
34:A:284:G:H21	34:A:286:G:H22	1.50	0.57
34:A:996:G:H3'	34:A:997:G:H8	1.70	0.57
34:A:347:U:H2'	34:A:348:G:C8	2.35	0.57
34:A:1537:U:H2'	34:A:1538:G:C8	2.39	0.57
34:A:2238:A:H2'	34:A:2239:A:C8	2.40	0.57
12:J:24:PRO:C	12:J:28:PRO:HD2	2.26	0.57
34:A:29:C:N4	34:A:535:A:OP2	2.38	0.57
34:A:2053:C:P	34:A:2134:G:H22	2.28	0.57
34:A:2125:A:H3'	34:A:2126:C:C5	2.39	0.57
34:A:2402:C:H2'	34:A:2403:U:C2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:71:ASP:OD1	16:N:71:ASP:N	2.33	0.57
21:S:9:THR:HG21	21:S:37:LEU:HD22	1.86	0.57
5:C:177:MET:HG2	5:C:181:GLU:O	2.05	0.57
9:G:149:ILE:O	9:G:163:VAL:HG11	2.05	0.57
23:U:4:ILE:HD12	28:Z:19:LYS:NZ	2.19	0.57
34:A:757:G:OP2	34:A:757:G:N2	2.23	0.57
3:4:246:PRO:HG3	3:4:293:ARG:HD3	1.86	0.56
3:4:424:TYR:CE1	3:4:444:HIS:HE1	2.23	0.56
12:J:38:MET:HA	12:J:38:MET:HE3	1.86	0.56
12:J:93:GLU:HA	12:J:96:LYS:HE3	1.87	0.56
12:J:129:ILE:HG22	12:J:130:ILE:HD13	1.87	0.56
29:b:45:LYS:NZ	34:A:3103:A:OP1	2.38	0.56
34:A:995:U:H2'	34:A:996:G:H8	1.69	0.56
34:A:2358:A:H3'	34:A:2359:G:H8	1.70	0.56
34:A:2358:A:O2'	34:A:2383:U:O2'	2.12	0.56
34:A:2362:C:H2'	34:A:2363:A:C8	2.40	0.56
34:A:2761:U:H2'	34:A:2762:C:C6	2.40	0.56
34:A:3115:A:H2'	34:A:3116:C:H6	1.70	0.56
3:4:285:ARG:NH1	34:A:2696:G:OP2	2.38	0.56
3:4:392:VAL:HG21	3:4:403:LEU:HD22	1.87	0.56
8:F:111:ILE:HD11	8:F:182:PHE:HA	1.86	0.56
12:J:89:LYS:NZ	34:A:1183:U:OP1	2.38	0.56
26:X:64:PRO:HB3	34:A:759:G:N1	2.18	0.56
32:e:29:ARG:NH1	32:e:41:THR:O	2.37	0.56
34:A:1671:U:O2	34:A:1673:A:N6	2.37	0.56
34:A:2326:A:C5	34:A:2410:A:C2	2.94	0.56
34:A:2332:U:N3	34:A:2404:G:N3	2.52	0.56
6:D:29:VAL:HG21	6:D:194:ILE:HD12	1.87	0.56
9:G:3:ARG:HB3	34:A:2975:G:C8	2.41	0.56
12:J:107:VAL:HG23	12:J:108:ARG:HD3	1.87	0.56
23:U:57:VAL:HG13	23:U:84:VAL:HG22	1.87	0.56
29:b:45:LYS:O	29:b:49:LEU:HG	2.04	0.56
30:c:18:CYS:SG	30:c:20:HIS:ND1	2.76	0.56
34:A:327:U:H2'	34:A:328:C:C6	2.40	0.56
11:I:109:TYR:HA	11:I:115:LEU:HA	1.86	0.56
34:A:1000:C:H2'	34:A:1001:C:H6	1.70	0.56
34:A:3014:A:H62	34:A:3113:A:H2	1.53	0.56
3:4:251:VAL:HG12	3:4:300:THR:HG21	1.86	0.56
10:H:62:ILE:H	10:H:65:ALA:HB3	1.69	0.56
30:c:34:ASP:OD1	30:c:34:ASP:N	2.37	0.56
31:d:34:VAL:HG13	31:d:45:LEU:HD12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:159:A:N3	34:A:2431:C:O2'	2.36	0.56
34:A:2163:U:H1'	34:A:2198:C:H4'	1.87	0.56
3:4:444:HIS:CG	12:J:24:PRO:HB2	2.40	0.56
11:I:31:LEU:HD23	11:I:35:ASN:ND2	2.21	0.56
11:I:40:ARG:HH21	11:I:50:THR:HA	1.69	0.56
12:J:56:ILE:HD12	12:J:74:THR:HA	0.69	0.56
34:A:1118:A:H2'	34:A:1119:A:C8	2.41	0.56
3:4:381:GLN:HA	3:4:384:ARG:HB2	1.88	0.56
3:4:424:TYR:HB3	12:J:28:PRO:HA	1.86	0.56
7:E:158:ILE:HD13	7:E:197:SER:HB3	1.87	0.56
34:A:2357:A:O2'	34:A:2382:G:N3	2.31	0.56
3:4:55:TRP:N	3:4:87:GLN:O	2.35	0.56
8:F:45:MET:HE1	8:F:64:LEU:HD12	1.87	0.56
14:L:16:ALA:HB2	14:L:52:VAL:HG21	1.86	0.56
24:V:82:ARG:NH2	34:A:382:A:OP2	2.37	0.56
34:A:1178:U:H3	34:A:1206:A:H2	1.52	0.56
34:A:1188:A:H2'	34:A:1215:U:OP1	2.04	0.56
34:A:1907:A:H2'	34:A:1908:A:C8	2.40	0.56
11:I:28:TYR:OH	34:A:1225:G:OP1	2.21	0.56
12:J:23:ALA:O	12:J:25:PRO:N	2.38	0.56
24:V:1:MET:HG2	24:V:2:LYS:O	2.06	0.56
34:A:1203:A:H2'	34:A:1204:A:C4	2.41	0.56
34:A:1755:A:N3	34:A:1755:A:H2'	2.20	0.56
34:A:1825:C:N4	34:A:1840:G:OP2	2.35	0.56
3:4:370:LYS:HE2	35:4:501:GCP:N9	2.21	0.56
9:G:33:LEU:HD11	9:G:137:ILE:HG22	1.87	0.56
9:G:75:ASN:ND2	34:A:2971:G:OP1	2.37	0.55
17:O:8:PRO:HG2	34:A:1870:U:C4	2.41	0.55
19:Q:28:HIS:HD2	19:Q:41:VAL:HG22	1.71	0.55
20:R:28:ARG:NH1	20:R:38:GLN:OE1	2.39	0.55
34:A:2053:C:N4	34:A:2158:C:OP1	2.39	0.55
34:A:2121:G:H8	34:A:2121:G:O5'	1.88	0.55
34:A:2341:U:H5'	34:A:2371:G:O2'	2.06	0.55
34:A:2805:G:OP2	34:A:2805:G:N2	2.33	0.55
13:K:106:ILE:HD12	13:K:109:LEU:HD12	1.89	0.55
22:T:66:GLN:HG3	22:T:73:PRO:HG3	1.88	0.55
34:A:2382:G:H2'	34:A:2383:U:C6	2.40	0.55
3:4:195:GLY:HA2	3:4:204:GLY:CA	2.37	0.55
5:C:141:VAL:HG13	5:C:162:SER:HB2	1.87	0.55
12:J:30:LEU:HD12	12:J:35:VAL:HB	1.86	0.55
14:L:21:CYS:HA	14:L:41:ALA:HA	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:217:G:H22	34:A:235:U:H4'	1.70	0.55
4:B:5:C:HO2'	4:B:6:G:H8	1.54	0.55
21:S:8:LYS:HG3	21:S:40:ALA:HB2	1.88	0.55
22:T:79:ALA:HB2	22:T:115:GLU:HB2	1.89	0.55
34:A:1530:G:H21	34:A:1805:G:H1	1.53	0.55
34:A:1536:A:H2'	34:A:1537:U:O4'	2.07	0.55
8:F:14:ARG:HH22	8:F:180:LEU:HD23	1.71	0.55
9:G:55:ARG:HD3	9:G:63:ARG:HA	1.89	0.55
11:I:54:ASN:HA	11:I:57:VAL:HG12	1.88	0.55
11:I:88:ASP:O	11:I:91:LYS:NZ	2.33	0.55
12:J:76:PRO:O	12:J:80:LEU:CA	2.55	0.55
21:S:10:GLY:O	21:S:12:LYS:NZ	2.39	0.55
34:A:1305:G:H2'	34:A:1306:G:H8	1.72	0.55
23:U:11:ILE:O	28:Z:33:ARG:NH2	2.40	0.55
34:A:365:U:H2'	34:A:366:G:H8	1.72	0.55
34:A:681:C:H2'	34:A:682:A:C8	2.42	0.55
34:A:858:A:O2'	34:A:1877:U:OP1	2.23	0.55
34:A:965:U:H2'	34:A:966:U:C6	2.42	0.55
34:A:6:G:O2'	34:A:3114:A:N6	2.40	0.55
34:A:2146:A:H3'	34:A:2146:A:OP2	2.07	0.55
34:A:2777:G:N1	34:A:2779:U:C5	2.75	0.55
4:B:26:A:C2	4:B:115:A:H1'	2.41	0.55
5:C:258:ARG:NE	5:C:262:LYS:HZ3	2.05	0.55
7:E:50:HIS:O	7:E:50:HIS:ND1	2.40	0.55
7:E:130:LEU:HD23	7:E:130:LEU:H	1.71	0.55
8:F:19:ILE:HD12	8:F:179:ALA:HB1	1.89	0.55
34:A:2054:C:H4'	34:A:2055:C:OP2	2.06	0.55
1:2:18:LYS:NZ	34:A:1035:G:OP1	2.34	0.55
4:B:42:C:H2'	8:F:73:GLU:HG3	1.89	0.55
12:J:96:LYS:HE2	34:A:1194:C:H4'	1.89	0.55
34:A:491:U:H4'	34:A:492:C:H5'	1.89	0.55
34:A:1201:G:N2	34:A:1203:A:H3'	2.22	0.55
3:4:34:ALA:HB2	3:4:80:GLU:HG3	1.89	0.54
3:4:255:ASN:N	35:4:501:GCP:H3B1	2.16	0.54
19:Q:30:LYS:NZ	19:Q:78:PRO:O	2.31	0.54
34:A:1291:G:C2	34:A:1292:U:H1'	2.43	0.54
34:A:3117:U:H2'	34:A:3118:U:C6	2.42	0.54
6:D:10:LYS:NZ	6:D:200:GLY:O	2.36	0.54
6:D:188:GLU:H	6:D:188:GLU:CD	2.15	0.54
34:A:285:U:H2'	34:A:287:A:H5'	1.89	0.54
3:4:379:LEU:H	3:4:383:ARG:HB2	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:18:LYS:HB3	11:I:64:ALA:HB1	1.89	0.54
13:K:43:THR:HG22	20:R:100:VAL:HG13	1.90	0.54
34:A:2051:U:H4'	34:A:2160:A:N6	2.22	0.54
34:A:2857:A:H2'	34:A:2858:G:C8	2.43	0.54
9:G:44:SER:HB3	9:G:52:VAL:O	2.07	0.54
34:A:733:U:H2'	34:A:734:C:C6	2.43	0.54
34:A:1955:A:H3'	34:A:1956:A:H8	1.72	0.54
34:A:3024:A:H2'	34:A:3025:G:O4'	2.08	0.54
5:C:133:LEU:HD23	5:C:136:ILE:HD12	1.89	0.54
9:G:53:VAL:HG21	9:G:70:ARG:HB2	1.90	0.54
34:A:823:C:H2'	34:A:824:G:C8	2.43	0.54
34:A:997:G:H3'	34:A:998:G:H8	1.73	0.54
34:A:2054:C:O2	34:A:2145:C:C6	2.60	0.54
34:A:2411:U:H2'	34:A:2412:U:O4'	2.08	0.54
34:A:2780:C:H2'	34:A:2781:G:O4'	2.07	0.54
5:C:258:ARG:HE	5:C:262:LYS:HZ3	1.56	0.54
6:D:30:LYS:HA	6:D:191:VAL:HG12	1.89	0.54
33:f:12:ASP:OD1	33:f:12:ASP:N	2.32	0.54
34:A:206:A:H2'	34:A:207:C:O4'	2.08	0.54
34:A:2129:C:C4'	34:A:2130:G:H5'	2.33	0.54
34:A:2532:G:N2	34:A:2534:A:O2'	2.40	0.54
8:F:128:GLN:HB3	8:F:135:TYR:CE1	2.43	0.54
25:W:63:THR:O	25:W:80:THR:OG1	2.26	0.54
34:A:88:A:H1'	34:A:89:A:C8	2.42	0.54
34:A:998:G:N2	34:A:1010:U:O4	2.40	0.54
34:A:2356:G:H2'	34:A:2380:G:C5	2.42	0.54
6:D:40:ARG:HH21	34:A:3008:C:H1'	1.72	0.54
19:Q:19:PHE:O	19:Q:49:ARG:NH1	2.40	0.54
25:W:11:LEU:HD11	25:W:57:VAL:HG11	1.89	0.54
29:b:44:LEU:HD22	29:b:48:ARG:HH21	1.73	0.54
3:4:148:LEU:HD13	3:4:168:GLN:HA	1.89	0.54
6:D:142:GLN:NE2	34:A:861:U:O4	2.41	0.54
10:H:84:ALA:HB1	10:H:92:PHE:CE2	2.43	0.54
11:I:70:ASP:HA	11:I:73:PHE:CE2	2.42	0.54
22:T:25:ARG:NH1	22:T:83:ALA:O	2.41	0.54
25:W:56:ALA:O	25:W:60:SER:OG	2.21	0.54
34:A:669:G:O2'	34:A:1369:A:OP1	2.24	0.54
34:A:1000:C:H2'	34:A:1001:C:C6	2.43	0.54
34:A:1291:G:H1'	34:A:1293:G:N2	2.23	0.54
8:F:73:GLU:O	8:F:94:ALA:HA	2.08	0.54
10:H:89:GLY:C	10:H:90:LYS:HD3	2.34	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:56:ILE:HD11	12:J:74:THR:HG23	1.88	0.54
12:J:103:THR:HB	12:J:106:GLN:HG3	1.89	0.54
16:N:85:SER:O	16:N:85:SER:OG	2.20	0.54
3:4:369:ASN:OD1	3:4:370:LYS:N	2.42	0.53
34:A:380:A:N3	34:A:401:C:O2'	2.40	0.53
3:4:271:LEU:HD12	3:4:273:GLU:HG3	1.90	0.53
15:M:12:ALA:HB3	15:M:15:GLU:HB2	1.89	0.53
18:P:98:GLU:HB3	18:P:125:LEU:HA	1.90	0.53
34:A:1198:C:H2'	34:A:1199:U:H6	1.73	0.53
34:A:1690:A:H2'	34:A:1691:A:C8	2.43	0.53
12:J:101:LYS:HA	12:J:101:LYS:HE2	1.90	0.53
21:S:30:GLU:OE1	21:S:31:PRO:HD2	2.08	0.53
25:W:39:GLY:HA3	25:W:99:VAL:HG12	1.90	0.53
34:A:1430:C:H2'	34:A:1431:U:C6	2.43	0.53
13:K:93:LEU:HD23	13:K:97:PRO:HA	1.91	0.53
21:S:41:LEU:HD11	21:S:48:VAL:HG13	1.89	0.53
25:W:41:GLY:H	25:W:99:VAL:HG11	1.73	0.53
34:A:678:A:N1	34:A:924:G:O2'	2.36	0.53
12:J:102:VAL:HG12	12:J:106:GLN:HE21	1.73	0.53
15:M:89:GLN:H	15:M:89:GLN:CD	2.17	0.53
34:A:762:U:H2'	34:A:763:G:C8	2.43	0.53
34:A:2470:A:H2'	34:A:2471:A:C8	2.43	0.53
1:2:15:ALA:O	1:2:20:ARG:NH1	2.41	0.53
3:4:377:VAL:HB	3:4:383:ARG:HH21	1.74	0.53
10:H:101:VAL:HG21	10:H:114:LYS:HA	1.90	0.53
12:J:94:PRO:HD2	34:A:1194:C:H1'	1.90	0.53
20:R:91:ASP:OD2	21:S:13:GLN:HG3	2.07	0.53
34:A:1223:U:C2	34:A:1224:G:C8	2.96	0.53
34:A:1758:G:HO2'	34:A:1759:A:P	2.30	0.53
34:A:2497:A:H2'	34:A:2498:A:C8	2.44	0.53
7:E:156:VAL:HG12	7:E:158:ILE:HG12	1.90	0.53
26:X:50:ASN:HB2	26:X:80:ILE:HB	1.91	0.53
34:A:1146:A:H2'	34:A:1147:A:C8	2.43	0.53
34:A:1473:G:N1	34:A:1487:U:OP2	2.27	0.53
34:A:2054:C:O2	34:A:2145:C:C5	2.61	0.53
34:A:2122:U:H4'	34:A:2125:A:N7	2.23	0.53
34:A:2133:G:H5''	34:A:2134:G:C8	2.44	0.53
34:A:2288:C:H2'	34:A:2289:C:C6	2.44	0.53
3:4:24:ARG:NH1	3:4:86:ILE:HG22	2.24	0.53
5:C:176:ARG:HH12	5:C:182:ILE:HD11	1.73	0.53
9:G:63:ARG:HG2	34:A:2973:A:H4'	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:51:GLU:OE2	32:e:57:ARG:NH1	2.42	0.53
19:Q:110:LYS:HD3	19:Q:113:ARG:HH22	1.72	0.53
34:A:1198:C:H2'	34:A:1199:U:C6	2.44	0.53
3:4:54:VAL:HB	3:4:56:THR:HG23	1.91	0.53
3:4:67:LEU:HG	3:4:86:ILE:HD11	1.89	0.53
18:P:7:GLY:HA2	34:A:2540:G:H5''	1.90	0.53
23:U:31:PHE:CE2	23:U:96:PHE:HZ	2.27	0.53
24:V:15:LYS:HZ1	34:A:411:G:H22	1.56	0.53
28:Z:7:PRO:HD3	28:Z:56:ARG:HD2	1.90	0.53
28:Z:51:ARG:NH2	34:A:58:G:OP2	2.42	0.53
34:A:2053:C:H5'	34:A:2134:G:N2	2.24	0.53
34:A:2948:C:H2'	34:A:2949:A:C8	2.44	0.53
3:4:395:ARG:HB2	35:4:501:GCP:C6	2.39	0.53
4:B:81:U:H2'	4:B:82:A:C8	2.44	0.53
11:I:28:TYR:HD2	11:I:78:ALA:HB2	1.73	0.53
18:P:27:LYS:HD3	34:A:2558:C:H1'	1.90	0.53
34:A:388:U:H2'	34:A:389:G:O4'	2.08	0.53
34:A:1165:G:O2'	34:A:1228:A:N6	2.36	0.53
34:A:2123:A:H8	34:A:2145:C:C2	2.26	0.53
34:A:2346:G:H1'	34:A:2347:G:H5'	1.90	0.53
34:A:2407:C:H2'	34:A:2408:G:C8	2.43	0.53
34:A:2626:U:O2'	34:A:2627:C:H5'	2.09	0.53
4:B:56:C:O3'	8:F:31:ASN:ND2	2.42	0.52
6:D:7:LEU:HD22	6:D:207:VAL:HG22	1.90	0.52
6:D:47:TYR:OH	34:A:2860:U:O2'	2.24	0.52
10:H:80:LEU:HD21	10:H:99:ASP:OD2	2.09	0.52
10:H:84:ALA:HB3	10:H:94:SER:N	2.21	0.52
13:K:48:VAL:HG12	13:K:50:GLY:H	1.74	0.52
18:P:26:ARG:HH12	18:P:37:ARG:CD	2.21	0.52
34:A:221:A:N6	34:A:232:G:H1'	2.24	0.52
34:A:365:U:H2'	34:A:366:G:C8	2.44	0.52
34:A:1156:A:H2'	34:A:1157:G:O4'	2.09	0.52
34:A:2756:G:N2	34:A:2887:G:O2'	2.42	0.52
7:E:55:ARG:NH2	34:A:789:G:OP1	2.42	0.52
8:F:142:GLN:NE2	8:F:156:PRO:HA	2.20	0.52
34:A:1889:U:O2'	34:A:1891:G:N7	2.31	0.52
8:F:12:LYS:HG3	8:F:104:TRP:CD1	2.45	0.52
18:P:83:ARG:HD3	18:P:87:LEU:HD23	1.92	0.52
24:V:75:ASP:C	24:V:77:ASP:H	2.17	0.52
34:A:1201:G:H21	34:A:1203:A:H3'	1.74	0.52
34:A:1287:C:H2'	34:A:1288:A:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:2146:A:OP2	34:A:2146:A:C8	2.63	0.52
6:D:63:ILE:HG13	6:D:66:VAL:HG22	1.90	0.52
16:N:67:ASN:ND2	16:N:105:GLU:OE2	2.37	0.52
34:A:441:G:H2'	34:A:442:U:C6	2.44	0.52
34:A:448:U:H2'	34:A:449:G:H8	1.74	0.52
3:4:24:ARG:CG	3:4:26:VAL:HG13	2.39	0.52
12:J:24:PRO:CG	12:J:25:PRO:HD2	2.22	0.52
24:V:89:ASP:N	24:V:89:ASP:OD1	2.37	0.52
34:A:747:A:H61	34:A:768:G:H1'	1.74	0.52
34:A:1001:C:C5	34:A:1002:C:H1'	2.45	0.52
34:A:1343:G:H2'	34:A:1345:G:C8	2.45	0.52
3:4:72:ALA:O	3:4:76:THR:HG22	2.09	0.52
3:4:437:GLY:HA2	3:4:456:PRO:HD3	1.90	0.52
4:B:2:U:H2'	4:B:3:U:C6	2.45	0.52
16:N:74:LEU:HB2	16:N:92:TRP:HB2	1.91	0.52
34:A:196:A:N6	34:A:2654:A:O2'	2.43	0.52
34:A:1291:G:H5'	34:A:1292:U:OP2	2.10	0.52
12:J:132:GLY:O	12:J:135:ARG:NH2	2.43	0.52
20:R:4:VAL:HG22	34:A:1314:C:H1'	1.92	0.52
24:V:88:ASP:OD1	24:V:91:THR:OG1	2.22	0.52
34:A:2404:G:H2'	34:A:2405:A:C4	2.45	0.52
3:4:126:PRO:HG3	3:4:175:ARG:HB3	1.92	0.52
9:G:128:SER:HB3	9:G:131:LYS:HB2	1.92	0.52
18:P:76:ASP:OD2	18:P:78:LYS:N	2.35	0.52
32:e:26:LYS:NZ	32:e:48:THR:HG23	2.25	0.52
34:A:325:U:O4'	34:A:450:G:N2	2.39	0.52
34:A:751:A:H2'	34:A:752:C:C6	2.45	0.52
34:A:2133:G:H3'	34:A:2134:G:C8	2.33	0.52
34:A:2417:C:H2'	34:A:2418:U:O4'	2.10	0.52
13:K:136:GLN:N	13:K:136:GLN:OE1	2.42	0.52
19:Q:51:GLY:HA2	19:Q:56:GLU:CD	2.35	0.52
20:R:14:ARG:HA	20:R:32:TYR:CE1	2.43	0.52
34:A:993:G:O2'	34:A:1015:A:N6	2.43	0.52
34:A:995:U:C2	34:A:996:G:C8	2.98	0.52
3:4:251:VAL:N	3:4:329:ILE:O	2.35	0.51
5:C:228:PRO:HA	5:C:234:GLY:HA3	1.92	0.51
8:F:42:VAL:HG11	34:A:2538:A:H5'	1.90	0.51
34:A:523:U:C2'	34:A:524:C:H5'	2.40	0.51
34:A:1098:A:N3	34:A:2261:U:O2'	2.40	0.51
8:F:45:MET:HE3	8:F:159:MET:SD	2.49	0.51
8:F:110:LEU:HA	8:F:114:ALA:HB3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:66:ARG:HB3	12:J:68:PHE:CZ	2.45	0.51
34:A:502:C:H2'	34:A:503:A:C8	2.45	0.51
34:A:718:C:O2'	34:A:772:U:OP1	2.26	0.51
34:A:1398:G:O2'	34:A:1400:G:N7	2.37	0.51
34:A:1642:G:O2'	34:A:1713:U:O4	2.22	0.51
34:A:2124:A:N6	34:A:2155:U:O2'	2.43	0.51
9:G:59:GLU:HG3	9:G:61:ARG:H	1.76	0.51
30:c:38:ILE:HG13	30:c:40:LYS:HG2	1.91	0.51
31:d:18:VAL:O	31:d:23:LEU:HD22	2.10	0.51
34:A:349:G:H3'	34:A:350:A:H8	1.76	0.51
34:A:2704:C:H2'	34:A:2705:G:O4'	2.11	0.51
34:A:3055:G:H2'	34:A:3100:A:H61	1.75	0.51
6:D:111:TYR:CD1	6:D:214:ARG:HD3	2.46	0.51
11:I:73:PHE:HD1	11:I:77:THR:HG21	1.75	0.51
12:J:98:LYS:HZ2	12:J:140:THR:HG22	1.72	0.51
34:A:1294:U:H2'	34:A:1295:U:C6	2.45	0.51
34:A:1425:G:N2	34:A:1428:U:C4	2.79	0.51
34:A:2339:G:H1	34:A:2387:U:H3	1.57	0.51
34:A:2345:U:N3	34:A:2346:G:O6	2.44	0.51
34:A:2538:A:H2'	34:A:2539:G:C8	2.46	0.51
3:4:193:GLY:O	3:4:207:LYS:HG3	2.10	0.51
3:4:300:THR:HB	3:4:318:THR:CG2	2.38	0.51
3:4:393:SER:OG	3:4:396:THR:OG1	2.26	0.51
6:D:96:GLU:HG2	6:D:99:GLN:HB2	1.92	0.51
14:L:71:ARG:NH1	14:L:104:ARG:HB3	2.25	0.51
34:A:1195:A:C2	34:A:1206:A:H2'	2.45	0.51
3:4:25:ARG:NH1	3:4:85:LEU:HD11	2.26	0.51
3:4:44:LEU:HD23	3:4:45:ARG:H	1.75	0.51
3:4:106:LEU:HD23	3:4:136:VAL:HB	1.92	0.51
3:4:407:MET:O	3:4:411:VAL:HG23	2.11	0.51
34:A:1076:A:H2'	34:A:1077:A:C8	2.45	0.51
34:A:1174:G:H4'	34:A:1204:A:H8	1.76	0.51
34:A:1199:U:H2'	34:A:1200:U:H6	1.76	0.51
34:A:1223:U:H2'	34:A:1224:G:C8	2.45	0.51
34:A:2778:U:H2'	34:A:2780:C:C4	2.46	0.51
3:4:65:ALA:O	3:4:69:GLU:HG2	2.11	0.51
11:I:54:ASN:OD1	11:I:77:THR:OG1	2.28	0.51
18:P:12:GLU:OE2	18:P:13:VAL:HG23	2.11	0.51
22:T:52:GLU:HB3	22:T:53:PRO:HD3	1.93	0.51
31:d:38:ARG:HB2	31:d:45:LEU:HD11	1.92	0.51
34:A:1754:G:H2'	34:A:1755:A:O2'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:118:VAL:O	3:4:119:ILE:HD12	2.11	0.51
17:O:49:GLU:OE2	17:O:95:THR:OG1	2.28	0.51
31:d:7:THR:HG22	34:A:802:C:H1'	1.92	0.51
34:A:346:C:H2'	34:A:347:U:O4'	2.10	0.51
34:A:681:C:H2'	34:A:682:A:H8	1.75	0.51
34:A:764:U:H3'	34:A:765:G:H8	1.74	0.51
34:A:1284:A:H2'	34:A:1285:G:C8	2.46	0.51
34:A:1729:A:H2'	34:A:1731:A:C8	2.46	0.51
34:A:2007:C:H2'	34:A:2008:A:C8	2.45	0.51
3:4:395:ARG:HB2	35:4:501:GCP:C2	2.41	0.51
12:J:44:TYR:O	12:J:48:THR:HG23	2.10	0.51
12:J:94:PRO:O	34:A:1194:C:O2'	2.17	0.51
22:T:37:GLU:HG3	22:T:38:GLU:N	2.26	0.51
34:A:298:G:H3'	34:A:299:G:H8	1.75	0.51
34:A:672:C:H2'	34:A:673:C:C6	2.46	0.51
34:A:980:C:O2'	34:A:981:U:O5'	2.27	0.51
34:A:2127:G:H21	34:A:2150:U:H2'	1.74	0.51
3:4:106:LEU:O	3:4:110:VAL:HG13	2.11	0.51
6:D:108:ASP:OD1	6:D:184:LYS:HA	2.11	0.51
12:J:115:LYS:HG2	12:J:118:LEU:HD12	1.93	0.51
34:A:979:G:H2'	34:A:980:C:C6	2.46	0.51
34:A:2693:A:H2'	34:A:2694:G:O4'	2.11	0.51
34:A:3070:G:H4'	34:A:3071:A:H5'	1.93	0.51
3:4:151:PHE:HE2	3:4:311:LEU:HD13	1.76	0.50
9:G:24:LEU:HD13	9:G:73:ILE:HD12	1.93	0.50
11:I:31:LEU:HD23	11:I:35:ASN:HD22	1.75	0.50
14:L:88:LYS:HG3	14:L:90:ASP:H	1.76	0.50
15:M:87:PHE:CE1	15:M:101:LYS:HE2	2.46	0.50
18:P:87:LEU:HD12	18:P:91:ARG:HH21	1.76	0.50
34:A:380:A:N1	34:A:404:A:O2'	2.38	0.50
34:A:2847:G:OP1	34:A:3047:A:O2'	2.22	0.50
34:A:2857:A:H2'	34:A:2858:G:H8	1.75	0.50
3:4:119:ILE:HG13	3:4:141:ILE:HD12	1.93	0.50
9:G:17:VAL:HG11	9:G:51:ILE:HG12	1.92	0.50
12:J:85:ALA:HB3	12:J:87:VAL:HG22	1.93	0.50
19:Q:48:ARG:NH1	34:A:2909:G:OP1	2.45	0.50
34:A:2407:C:N4	34:A:2408:G:O6	2.44	0.50
3:4:45:ARG:HB3	3:4:48:ARG:HH21	1.75	0.50
12:J:56:ILE:CD1	12:J:73:LYS:O	2.60	0.50
30:c:31:ASN:ND2	34:A:2510:A:OP1	2.44	0.50
34:A:410:U:O2	34:A:414:A:N7	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:1284:A:H2'	34:A:1285:G:H8	1.76	0.50
34:A:2654:A:N3	34:A:2654:A:H2'	2.26	0.50
34:A:2781:G:H2'	34:A:2782:C:H6	1.76	0.50
3:4:225:GLU:HB3	3:4:229:MET:HE3	1.93	0.50
8:F:11:LEU:HA	8:F:14:ARG:HH11	1.76	0.50
13:K:92:LEU:HD23	13:K:100:VAL:HG22	1.94	0.50
34:A:1428:U:H2'	34:A:1828:A:C2	2.46	0.50
34:A:2879:G:O2'	34:A:2888:G:O6	2.21	0.50
8:F:44:ASN:ND2	8:F:94:ALA:H	2.09	0.50
24:V:15:LYS:NZ	34:A:411:G:H22	2.09	0.50
25:W:11:LEU:HD11	25:W:57:VAL:HG21	1.94	0.50
34:A:818:U:H2'	34:A:819:G:O4'	2.12	0.50
34:A:1533:U:OP2	34:A:1535:C:N4	2.44	0.50
7:E:24:LEU:HG	7:E:209:SER:HB2	1.92	0.50
25:W:82:ALA:HB3	25:W:96:ASP:HB2	1.94	0.50
34:A:2399:A:O2'	34:A:2400:C:H6	1.94	0.50
34:A:2777:G:N1	34:A:2779:U:C4	2.80	0.50
7:E:165:GLY:O	7:E:169:VAL:HG22	2.12	0.50
9:G:65:LEU:O	9:G:68:LEU:HD23	2.12	0.50
34:A:1047:A:OP1	34:A:1297:G:N2	2.30	0.50
34:A:1201:G:H21	34:A:1203:A:H8	1.59	0.50
34:A:1291:G:N2	34:A:1292:U:H1'	2.27	0.50
34:A:1653:G:H2'	34:A:1654:G:O4'	2.12	0.50
34:A:2394:A:P	34:A:2397:C:H41	2.34	0.50
7:E:65:PRO:HG3	7:E:79:THR:HG23	1.93	0.50
8:F:169:ASN:N	8:F:169:ASN:OD1	2.44	0.50
34:A:277:U:H2'	34:A:278:A:H8	1.77	0.50
34:A:928:U:H2'	34:A:929:C:C6	2.46	0.50
34:A:2122:U:H3'	34:A:2122:U:OP2	2.12	0.50
3:4:21:ALA:O	3:4:22:SER:C	2.55	0.50
8:F:74:VAL:HG13	8:F:91:PRO:HB3	1.93	0.50
18:P:120:ALA:O	18:P:125:LEU:HB2	2.12	0.50
34:A:633:A:H2'	34:A:634:C:O4'	2.11	0.50
34:A:1529:U:H3'	34:A:1530:G:C8	2.47	0.50
34:A:1815:G:H5''	34:A:1816:C:H5'	1.94	0.50
2:3:15:LYS:HA	4:B:87:U:O2	2.13	0.49
9:G:46:ALA:HB2	9:G:52:VAL:HG23	1.92	0.49
9:G:89:GLU:O	9:G:90:ILE:HD13	2.12	0.49
12:J:57:PRO:CB	12:J:73:LYS:O	2.60	0.49
1:2:2:ALA:HB1	1:2:59:VAL:HG21	1.94	0.49
6:D:76:ASN:N	6:D:76:ASN:OD1	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:81:ILE:HG13	8:F:83:GLN:HG2	1.94	0.49
12:J:98:LYS:HZ1	12:J:140:THR:HG22	1.74	0.49
15:M:113:LEU:HD23	15:M:130:SER:HB2	1.94	0.49
34:A:55:G:O2'	34:A:70:A:N1	2.33	0.49
34:A:502:C:H2'	34:A:503:A:H8	1.77	0.49
34:A:981:U:H4'	34:A:982:A:O5'	2.12	0.49
34:A:2156:A:H1'	34:A:2159:G:OP1	2.12	0.49
34:A:2529:A:H2'	34:A:2530:C:C6	2.47	0.49
34:A:644:G:H2'	34:A:645:G:H8	1.77	0.49
34:A:2121:G:C5'	34:A:2121:G:C8	2.95	0.49
34:A:2613:G:H5''	34:A:2614:U:O4'	2.12	0.49
3:4:130:ASN:OD1	3:4:131:ALA:N	2.45	0.49
12:J:15:ILE:O	12:J:44:TYR:OH	2.18	0.49
15:M:72:ARG:HE	15:M:74:GLU:HG2	1.77	0.49
34:A:1675:U:O2'	34:A:1676:G:N7	2.44	0.49
34:A:2121:G:H3'	34:A:2122:U:H6	1.76	0.49
34:A:2343:G:H2'	34:A:2344:G:O4'	2.12	0.49
6:D:176:THR:OG1	34:A:2997:C:OP1	2.30	0.49
7:E:69:LYS:NZ	34:A:2285:G:OP1	2.38	0.49
9:G:77:VAL:O	9:G:81:THR:HG23	2.11	0.49
16:N:42:ILE:HD12	16:N:97:VAL:HG11	1.94	0.49
34:A:1290:C:H2'	34:A:1291:G:O4'	2.12	0.49
34:A:1703:G:C6	34:A:1727:A:C2	3.00	0.49
3:4:250:ILE:O	3:4:300:THR:HG23	2.13	0.49
3:4:411:VAL:O	3:4:412:GLU:HB3	2.12	0.49
14:L:112:MET:HE2	14:L:112:MET:HA	1.93	0.49
34:A:150:C:H2'	34:A:151:A:H8	1.77	0.49
34:A:857:U:H2'	34:A:858:A:C8	2.46	0.49
34:A:2528:G:N2	34:A:2536:U:H3	2.08	0.49
34:A:2580:G:H2'	34:A:2581:G:O4'	2.13	0.49
28:Z:7:PRO:HD3	28:Z:56:ARG:CD	2.43	0.49
34:A:844:G:O2'	34:A:878:G:H4'	2.13	0.49
34:A:2235:C:H2'	34:A:2236:G:O4'	2.13	0.49
34:A:2404:G:H8	34:A:2405:A:C2	2.30	0.49
3:4:237:ARG:HG2	3:4:240:ARG:NH1	2.25	0.49
3:4:338:ASN:ND2	3:4:341:ALA:HB2	2.28	0.49
8:F:76:ARG:HG3	8:F:89:GLY:HA2	1.94	0.49
8:F:115:LEU:HA	8:F:118:ILE:HG13	1.94	0.49
9:G:5:GLY:HA3	9:G:66:HIS:NE2	2.28	0.49
21:S:30:GLU:HG3	21:S:32:GLY:O	2.13	0.49
34:A:828:G:H2'	34:A:829:U:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:1735:U:H2'	34:A:1736:G:O4'	2.13	0.49
34:A:2354:G:C5	34:A:2381:A:H1'	2.48	0.49
3:4:247:SER:HA	3:4:296:VAL:HG12	1.95	0.49
8:F:15:TYR:HA	8:F:19:ILE:CG1	2.40	0.49
8:F:48:GLY:H	8:F:92:ILE:HG23	1.76	0.49
15:M:77:VAL:HG11	34:A:730:G:N1	2.28	0.49
16:N:59:LYS:O	16:N:60:ARG:HD2	2.13	0.49
34:A:729:C:O2'	34:A:733:U:OP1	2.31	0.49
34:A:782:U:H2'	34:A:783:G:O4'	2.13	0.49
34:A:821:A:H2'	34:A:822:G:O4'	2.13	0.49
34:A:1673:A:H2'	34:A:1673:A:N3	2.27	0.49
34:A:2163:U:O2	34:A:2198:C:O2'	2.22	0.49
34:A:3017:C:H2'	34:A:3018:U:C6	2.48	0.49
34:A:3071:A:P	34:A:3087:G:H22	2.35	0.49
8:F:141:GLU:HG3	8:F:143:SER:H	1.78	0.49
8:F:149:ASP:OD1	8:F:150:VAL:N	2.45	0.49
10:H:80:LEU:HD22	10:H:100:VAL:HG23	1.95	0.49
23:U:24:ILE:HG12	23:U:29:TYR:CD1	2.47	0.49
26:X:19:GLN:HB2	26:X:21:LEU:HG	1.93	0.49
34:A:1532:G:H2'	34:A:1533:U:H6	1.78	0.49
34:A:2019:A:H2'	34:A:2020:A:C8	2.47	0.49
34:A:2420:U:H1'	34:A:2421:A:C8	2.48	0.49
4:B:29:C:O2'	4:B:60:G:N2	2.46	0.48
6:D:14:THR:HG22	6:D:15:GLN:H	1.78	0.48
9:G:117:GLU:N	9:G:117:GLU:OE2	2.46	0.48
10:H:131:PRO:HB3	10:H:146:LEU:H	1.77	0.48
12:J:98:LYS:HA	12:J:138:GLY:O	2.13	0.48
34:A:621:U:H2'	34:A:622:C:C6	2.47	0.48
34:A:1529:U:H3'	34:A:1530:G:H8	1.78	0.48
34:A:1532:G:O2'	34:A:1803:A:N1	2.41	0.48
3:4:442:THR:HB	3:4:451:ILE:HA	1.95	0.48
15:M:75:TYR:CD2	15:M:109:LEU:HB3	2.48	0.48
34:A:429:A:H2'	34:A:430:A:C8	2.48	0.48
34:A:443:C:H2'	34:A:444:U:O4'	2.13	0.48
34:A:672:C:H2'	34:A:673:C:H6	1.79	0.48
34:A:1177:G:H2'	34:A:1178:U:C6	2.48	0.48
34:A:1999:U:H1'	34:A:2833:U:H5''	1.95	0.48
34:A:3046:C:H2'	34:A:3047:A:O4'	2.13	0.48
4:B:58:A:H1'	8:F:34:GLN:HG3	1.94	0.48
8:F:129:PHE:HE1	8:F:174:ARG:HG3	1.78	0.48
10:H:131:PRO:HB2	10:H:143:LYS:HZ2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:28:TYR:CE2	11:I:76:PRO:HB2	2.47	0.48
34:A:193:G:H2'	34:A:194:A:O4'	2.12	0.48
34:A:288:U:O2	34:A:299:G:N2	2.46	0.48
34:A:1334:C:H2'	34:A:1335:G:O4'	2.13	0.48
34:A:1630:U:H2'	34:A:1631:A:O4'	2.13	0.48
34:A:2044:U:H2'	34:A:2045:G:O4'	2.13	0.48
34:A:2054:C:H41	34:A:2135:U:H3	1.61	0.48
5:C:63:ARG:NH1	34:A:1788:G:OP1	2.47	0.48
5:C:268:ILE:HG21	5:C:271:ARG:HE	1.78	0.48
10:H:91:LEU:HD13	10:H:94:SER:HB2	1.94	0.48
12:J:81:LEU:HD13	12:J:134:ALA:HB2	1.95	0.48
12:J:122:ASP:CG	12:J:125:ALA:HB3	2.39	0.48
17:O:24:LEU:HB3	17:O:44:LEU:HD22	1.96	0.48
34:A:377:C:H2'	34:A:378:G:H8	1.78	0.48
34:A:625:A:H2'	34:A:626:G:O4'	2.14	0.48
34:A:1719:C:C2	34:A:1720:G:C8	3.01	0.48
34:A:2122:U:O2	34:A:2126:C:N4	2.47	0.48
3:4:207:LYS:HG2	3:4:208:ILE:HG12	1.95	0.48
10:H:98:ALA:HB2	10:H:114:LYS:HE3	1.94	0.48
21:S:54:ASP:HA	21:S:57:LYS:HG3	1.95	0.48
24:V:97:ILE:HA	24:V:104:ASP:HA	1.96	0.48
34:A:58:G:C6	34:A:92:G:N2	2.81	0.48
34:A:834:C:H2'	34:A:835:C:C6	2.48	0.48
3:4:45:ARG:NE	3:4:78:GLY:O	2.46	0.48
3:4:423:PRO:HD2	3:4:466:TYR:CE2	2.49	0.48
4:B:49:C:P	18:P:42:ARG:HH12	2.37	0.48
5:C:108:PRO:HA	5:C:196:VAL:HA	1.96	0.48
17:O:72:ASP:OD1	17:O:73:LYS:N	2.47	0.48
34:A:332:C:H2'	34:A:333:C:C6	2.48	0.48
34:A:337:U:H1'	34:A:345:G:C2	2.49	0.48
34:A:994:A:H3'	34:A:995:U:H6	1.79	0.48
34:A:1229:A:H1'	34:A:1230:G:H1'	1.95	0.48
34:A:3037:C:O2	34:A:3104:A:O2'	2.30	0.48
4:B:25:G:O6	4:B:57:U:O2'	2.28	0.48
12:J:64:GLU:HG2	12:J:65:ASP:OD1	2.13	0.48
16:N:75:THR:HA	16:N:90:PRO:HA	1.95	0.48
17:O:82:GLU:HG3	17:O:83:ILE:N	2.29	0.48
19:Q:100:ARG:HG2	19:Q:101:GLU:OE1	2.13	0.48
22:T:36:VAL:O	22:T:40:LEU:HG	2.13	0.48
28:Z:16:ASP:N	28:Z:16:ASP:OD1	2.43	0.48
6:D:154:CYS:O	6:D:157:PRO:HD2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:160:ARG:HG3	7:E:179:SER:OG	2.14	0.48
10:H:4:ILE:HG23	10:H:17:ASP:O	2.14	0.48
12:J:36:ASN:HB3	12:J:39:GLU:HB3	1.95	0.48
15:M:104:VAL:HG11	15:M:110:VAL:HG12	1.96	0.48
34:A:665:G:N2	34:A:2255:A:OP1	2.43	0.48
34:A:1208:U:C4	34:A:1220:C:C2	3.02	0.48
18:P:4:LYS:HD3	18:P:4:LYS:N	2.28	0.48
34:A:334:G:O6	34:A:347:U:O2	2.31	0.48
34:A:1295:U:H2'	34:A:1296:G:H8	1.77	0.48
34:A:1400:G:N2	34:A:1443:G:H5''	2.29	0.48
34:A:1944:C:H2'	34:A:1945:U:O4'	2.13	0.48
3:4:32:GLU:O	3:4:81:VAL:HG23	2.13	0.48
3:4:444:HIS:CE1	12:J:24:PRO:HA	2.48	0.48
5:C:16:ALA:HB2	5:C:207:GLY:HA3	1.96	0.48
20:R:54:LYS:HE3	34:A:1113:C:OP2	2.13	0.48
34:A:2134:G:C2'	34:A:2135:U:H2'	2.44	0.48
3:4:444:HIS:HA	3:4:449:THR:HG22	1.96	0.47
7:E:186:TYR:O	7:E:190:ASN:CB	2.59	0.47
24:V:16:ASP:OD1	24:V:16:ASP:N	2.47	0.47
34:A:2383:U:C4	34:A:2384:C:H1'	2.49	0.47
3:4:154:HIS:ND1	3:4:277:PHE:O	2.46	0.47
3:4:201:ARG:C	3:4:204:GLY:H	2.21	0.47
3:4:286:ARG:HH21	3:4:294:PRO:HB3	1.79	0.47
14:L:90:ASP:O	14:L:90:ASP:OD1	2.32	0.47
20:R:70:ARG:NH2	34:A:1130:C:OP1	2.48	0.47
34:A:1203:A:O2'	34:A:1204:A:O4'	2.12	0.47
34:A:1535:C:H2'	34:A:1536:A:O4'	2.14	0.47
34:A:1542:A:H1'	34:A:1628:A:C6	2.49	0.47
34:A:2326:A:H2'	34:A:2327:C:H5'	1.96	0.47
3:4:98:ILE:HD11	3:4:106:LEU:HD13	1.95	0.47
3:4:393:SER:O	3:4:397:GLY:N	2.45	0.47
11:I:94:LYS:NZ	11:I:125:ASP:OD2	2.43	0.47
13:K:29:ALA:HA	13:K:105:ILE:HG12	1.97	0.47
15:M:24:ARG:HA	34:A:926:U:H2'	1.96	0.47
24:V:15:LYS:NZ	34:A:411:G:H1	2.12	0.47
27:Y:15:GLY:HA3	27:Y:29:TRP:HZ3	1.78	0.47
29:b:4:PRO:HG2	34:A:2240:U:O2	2.15	0.47
34:A:997:G:H3'	34:A:998:G:C8	2.50	0.47
34:A:2055:C:H4'	34:A:2056:G:H8	1.80	0.47
34:A:2351:A:H1'	34:A:2396:A:H1'	1.95	0.47
6:D:6:ILE:HD11	6:D:34:ASN:OD1	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:9:THR:HG21	7:E:13:LYS:HD2	1.96	0.47
24:V:57:GLY:HA3	34:A:571:A:O2'	2.13	0.47
9:G:30:LYS:HE2	9:G:82:GLU:HA	1.96	0.47
9:G:59:GLU:HG3	9:G:61:ARG:N	2.30	0.47
11:I:10:VAL:HG13	11:I:60:ALA:HB2	1.96	0.47
12:J:23:ALA:N	12:J:24:PRO:HD2	2.29	0.47
12:J:98:LYS:HE3	12:J:98:LYS:HB2	1.44	0.47
14:L:76:TYR:HB2	19:Q:72:THR:HB	1.95	0.47
34:A:2031:G:OP2	34:A:2032:A:O2'	2.30	0.47
34:A:2791:G:H2'	34:A:2792:C:C6	2.50	0.47
4:B:46:A:H1'	8:F:99:ARG:HH21	1.80	0.47
24:V:74:VAL:HG23	24:V:76:SER:H	1.80	0.47
34:A:76:C:O2'	34:A:428:A:N3	2.40	0.47
34:A:827:G:H2'	34:A:828:G:C8	2.50	0.47
34:A:971:G:H2'	34:A:972:A:C8	2.49	0.47
34:A:2056:G:O2'	34:A:2057:G:O5'	2.32	0.47
34:A:2311:G:H2'	34:A:2312:U:O4'	2.15	0.47
3:4:24:ARG:HH12	3:4:86:ILE:HG22	1.78	0.47
3:4:55:TRP:HB3	3:4:88:ARG:HA	1.97	0.47
3:4:424:TYR:OH	3:4:445:THR:O	2.32	0.47
4:B:7:G:OP1	18:P:15:ARG:NH1	2.41	0.47
4:B:41:U:N3	4:B:45:G:OP2	2.35	0.47
4:B:81:U:O2'	34:A:1033:A:N3	2.45	0.47
8:F:85:LYS:O	8:F:85:LYS:HD3	2.14	0.47
12:J:15:ILE:HB	12:J:44:TYR:CZ	2.50	0.47
14:L:60:ALA:HB2	14:L:86:ILE:HD13	1.95	0.47
15:M:93:VAL:HB	15:M:124:VAL:HA	1.96	0.47
28:Z:45:ARG:HG2	34:A:94:G:O2'	2.13	0.47
34:A:600:A:H5''	34:A:1330:C:O2'	2.14	0.47
34:A:1798:U:H2'	34:A:1799:A:H8	1.80	0.47
34:A:2322:C:H2'	34:A:2323:G:O4'	2.15	0.47
4:B:29:C:OP1	18:P:48:HIS:NE2	2.35	0.47
4:B:49:C:H2'	4:B:50:C:O4'	2.15	0.47
5:C:245:HIS:HB3	5:C:246:PRO:HD2	1.97	0.47
7:E:7:VAL:O	7:E:15:ASP:N	2.46	0.47
15:M:95:VAL:O	15:M:99:VAL:HG22	2.15	0.47
34:A:994:A:H3'	34:A:995:U:C6	2.50	0.47
34:A:1161:C:H2'	34:A:1162:G:C8	2.50	0.47
34:A:1182:C:H2'	34:A:1183:U:O4'	2.14	0.47
34:A:1326:G:H1'	34:A:1351:G:N2	2.30	0.47
34:A:2058:U:O5'	34:A:2151:A:N6	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:370:LYS:HG2	35:4:501:GCP:C6	2.44	0.47
3:4:443:GLU:HG3	3:4:450:ARG:HG2	1.97	0.47
6:D:28:VAL:HG11	19:Q:7:VAL:HG21	1.97	0.47
8:F:32:VAL:HA	8:F:35:ILE:HD13	1.97	0.47
8:F:43:VAL:HA	8:F:160:ASP:O	2.15	0.47
9:G:65:LEU:O	9:G:69:SER:OG	2.23	0.47
16:N:29:PHE:HB2	16:N:105:GLU:OE1	2.15	0.47
16:N:40:ALA:HB2	16:N:127:ILE:HG21	1.97	0.47
16:N:77:LYS:N	34:A:1074:A:OP1	2.46	0.47
29:b:3:VAL:HG12	34:A:2239:A:C2	2.50	0.47
34:A:503:A:H2'	34:A:504:C:C6	2.50	0.47
34:A:1015:A:H2'	34:A:1016:C:O4'	2.14	0.47
34:A:1189:G:H1'	34:A:1207:G:H2'	1.97	0.47
34:A:1900:C:H2'	34:A:1901:C:C6	2.50	0.47
34:A:2055:C:C5	34:A:2146:A:OP1	2.67	0.47
34:A:2298:U:H4'	34:A:2820:U:O2	2.15	0.47
34:A:2414:G:H2'	34:A:2415:G:H8	1.79	0.47
6:D:151:ILE:HG21	6:D:160:VAL:HG22	1.96	0.47
7:E:130:LEU:HD22	7:E:158:ILE:HD11	1.97	0.47
10:H:4:ILE:HG12	10:H:39:ALA:HB2	1.96	0.47
10:H:37:ILE:HD12	10:H:37:ILE:HA	1.79	0.47
11:I:12:ASP:O	11:I:15:GLU:HG3	2.14	0.47
21:S:4:TYR:HA	21:S:17:ALA:HA	1.96	0.47
22:T:53:PRO:O	22:T:57:VAL:HG23	2.15	0.47
24:V:56:SER:HA	34:A:572:C:H4'	1.96	0.47
34:A:1189:G:N3	34:A:1207:G:O2'	2.34	0.47
34:A:1898:U:H2'	34:A:1899:G:O4'	2.15	0.47
34:A:2510:A:H4'	34:A:2511:A:O4'	2.15	0.47
3:4:432:ARG:HH21	3:4:462:THR:HG21	1.78	0.46
33:f:7:VAL:HG23	33:f:34:GLN:HB2	1.96	0.46
34:A:824:G:H2'	34:A:825:C:H6	1.80	0.46
34:A:911:U:H2'	34:A:912:C:C6	2.50	0.46
34:A:993:G:N2	34:A:1014:G:H2'	2.30	0.46
34:A:1278:C:C2	34:A:1279:G:C8	3.04	0.46
34:A:1316:U:H2'	34:A:1317:G:H8	1.80	0.46
20:R:14:ARG:HA	20:R:32:TYR:CD1	2.50	0.46
28:Z:49:THR:O	28:Z:53:GLU:HG3	2.15	0.46
34:A:452:G:H2'	34:A:453:U:N1	2.30	0.46
34:A:979:G:H2'	34:A:980:C:H6	1.79	0.46
34:A:1177:G:H2'	34:A:1178:U:C5	2.50	0.46
34:A:2629:G:O2'	34:A:2635:A:N6	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:200:THR:HG23	16:N:45:ARG:HH22	1.81	0.46
3:4:232:ILE:HD13	34:A:2704:C:H4'	1.97	0.46
3:4:340:LEU:HD12	3:4:343:ILE:HB	1.98	0.46
18:P:12:GLU:HA	18:P:15:ARG:HB3	1.96	0.46
21:S:23:LYS:HE3	21:S:23:LYS:HB2	1.59	0.46
34:A:304:U:H2'	34:A:305:G:C8	2.51	0.46
34:A:931:C:H2'	34:A:932:C:H6	1.80	0.46
34:A:1856:C:O2	34:A:2922:U:O2'	2.31	0.46
3:4:183:MET:HB3	3:4:207:LYS:NZ	2.31	0.46
5:C:272:ARG:NH1	34:A:2015:U:OP2	2.45	0.46
6:D:123:PHE:HB2	34:A:3044:A:OP1	2.15	0.46
21:S:97:LEU:HD23	21:S:97:LEU:HA	1.78	0.46
24:V:1:MET:HE2	24:V:28:PRO:HB3	1.97	0.46
24:V:9:VAL:HB	24:V:71:VAL:HG13	1.97	0.46
34:A:138:A:H2'	34:A:139:U:O2	2.14	0.46
34:A:285:U:O2'	34:A:287:A:OP1	2.31	0.46
34:A:325:U:O2'	34:A:326:A:OP1	2.29	0.46
34:A:2127:G:H2'	34:A:2127:G:N3	2.30	0.46
34:A:2148:C:OP2	34:A:2149:C:N4	2.49	0.46
8:F:119:ARG:NH1	8:F:119:ARG:O	2.49	0.46
8:F:141:GLU:OE1	8:F:143:SER:OG	2.19	0.46
10:H:135:LYS:NZ	10:H:138:THR:O	2.37	0.46
14:L:18:GLU:HG2	14:L:45:ASP:HB2	1.96	0.46
34:A:1169:A:N3	34:A:2975:G:N2	2.62	0.46
34:A:1476:G:H2'	34:A:1477:C:C6	2.50	0.46
34:A:1928:C:H4'	34:A:3079:U:H3	1.80	0.46
3:4:155:ALA:HA	3:4:280:LEU:HD11	1.97	0.46
7:E:205:ILE:O	7:E:209:SER:HB3	2.15	0.46
9:G:17:VAL:HG12	9:G:19:ILE:HG12	1.98	0.46
12:J:76:PRO:O	12:J:79:LYS:C	2.57	0.46
12:J:98:LYS:HD2	12:J:140:THR:HA	1.97	0.46
13:K:15:TRP:O	13:K:138:ILE:HD12	2.16	0.46
20:R:91:ASP:OD1	20:R:93:LYS:N	2.48	0.46
25:W:60:SER:HB2	25:W:61:HIS:CE1	2.51	0.46
34:A:827:G:C2'	34:A:828:G:H5'	2.45	0.46
34:A:944:A:C8	34:A:2472:C:H5'	2.50	0.46
3:4:242:ARG:NE	34:A:2755:A:OP1	2.49	0.46
8:F:34:GLN:HB3	18:P:3:HIS:CD2	2.50	0.46
8:F:117:ARG:HG3	8:F:144:MET:HA	1.98	0.46
34:A:567:A:N3	34:A:569:G:H5''	2.30	0.46
34:A:752:C:H2'	34:A:753:A:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:965:U:H2'	34:A:966:U:H6	1.79	0.46
34:A:1138:A:N1	34:A:1259:U:H2'	2.31	0.46
34:A:1175:A:N7	34:A:1204:A:H2'	2.30	0.46
34:A:1313:U:H2'	34:A:1314:C:C6	2.49	0.46
34:A:2686:U:H2'	34:A:2687:U:C6	2.50	0.46
3:4:23:LEU:HG	3:4:102:LYS:HG3	1.97	0.46
3:4:347:ARG:O	3:4:351:ASN:OD1	2.33	0.46
4:B:35:G:N3	4:B:37:C:N4	2.64	0.46
4:B:80:C:H2'	4:B:81:U:O4'	2.15	0.46
5:C:80:ALA:HB2	5:C:96:HIS:CD2	2.51	0.46
6:D:95:TYR:HA	6:D:99:GLN:OE1	2.15	0.46
6:D:157:PRO:HD3	34:A:2795:C:O2'	2.16	0.46
13:K:23:VAL:O	13:K:62:ILE:HG13	2.16	0.46
18:P:17:ALA:O	18:P:21:ARG:HG3	2.15	0.46
34:A:448:U:H2'	34:A:449:G:C8	2.51	0.46
34:A:828:G:N1	34:A:832:G:OP2	2.49	0.46
34:A:1473:G:O2'	34:A:1488:A:N6	2.48	0.46
34:A:1963:G:H2'	34:A:1964:U:C6	2.51	0.46
34:A:2157:G:H5'	34:A:2158:C:H5''	1.96	0.46
3:4:242:ARG:HH22	34:A:2757:C:N4	2.14	0.46
4:B:1:G:H2'	4:B:2:U:C6	2.50	0.46
4:B:63:U:H2'	4:B:64:G:H8	1.81	0.46
8:F:118:ILE:HG12	8:F:144:MET:HG2	1.98	0.46
9:G:98:GLN:OE1	9:G:98:GLN:N	2.49	0.46
12:J:34:GLY:C	12:J:66:ARG:HH21	2.24	0.46
15:M:72:ARG:HG2	34:A:727:A:OP1	2.16	0.46
34:A:1174:G:H4'	34:A:1204:A:C8	2.51	0.46
34:A:1545:C:O2'	34:A:1625:G:O6	2.33	0.46
34:A:1668:C:O2'	34:A:1764:A:N3	2.45	0.46
34:A:2344:G:H5'	34:A:2392:A:O2'	2.15	0.46
34:A:3022:G:H2'	34:A:3023:G:H1'	1.98	0.46
5:C:212:MET:HG3	34:A:2008:A:H5''	1.98	0.46
30:c:27:LYS:HG2	30:c:28:ASN:O	2.16	0.46
34:A:1090:G:OP2	34:A:1091:A:O2'	2.27	0.46
34:A:1296:G:H2'	34:A:1297:G:C8	2.51	0.46
34:A:2331:U:C4'	34:A:2374:U:H5'	2.46	0.46
3:4:253:TYR:CZ	3:4:304:VAL:HA	2.51	0.45
4:B:11:U:H3'	4:B:12:C:H5''	1.98	0.45
34:A:944:A:N7	34:A:2472:C:H5'	2.32	0.45
34:A:2600:A:H8	34:A:2600:A:OP1	1.99	0.45
34:A:2781:G:H2'	34:A:2782:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:2922:U:H2'	34:A:2923:C:C6	2.51	0.45
3:4:149:ASP:OD1	3:4:153:GLN:NE2	2.50	0.45
8:F:12:LYS:HG3	8:F:104:TRP:NE1	2.31	0.45
11:I:57:VAL:HA	11:I:60:ALA:HB3	1.98	0.45
16:N:40:ALA:HB2	16:N:127:ILE:CG2	2.47	0.45
26:X:41:ARG:NE	26:X:41:ARG:HA	2.31	0.45
34:A:328:C:H2'	34:A:329:U:O4'	2.16	0.45
34:A:1157:G:O6	34:A:1234:U:C2	2.69	0.45
34:A:1187:A:H5'	34:A:1188:A:OP1	2.16	0.45
34:A:1524:G:H2'	34:A:1525:U:C6	2.50	0.45
34:A:2873:U:H2'	34:A:2874:C:H6	1.81	0.45
34:A:3017:C:H2'	34:A:3018:U:H6	1.81	0.45
3:4:258:LYS:H	35:4:501:GCP:PB	2.39	0.45
6:D:185:VAL:HG13	6:D:192:LEU:HD23	1.98	0.45
7:E:166:ALA:O	7:E:170:ARG:HB2	2.16	0.45
8:F:11:LEU:O	8:F:15:TYR:HB3	2.16	0.45
9:G:19:ILE:HG23	9:G:19:ILE:HD12	1.66	0.45
12:J:135:ARG:NH2	34:A:1197:C:H1'	2.30	0.45
15:M:35:ARG:NH1	15:M:42:ALA:O	2.47	0.45
15:M:88:PRO:HD2	15:M:89:GLN:NE2	2.31	0.45
19:Q:4:LEU:HD23	19:Q:4:LEU:HA	1.80	0.45
21:S:63:GLU:HB2	21:S:100:THR:HG23	1.97	0.45
34:A:754:C:H2'	34:A:755:A:O4'	2.16	0.45
34:A:1200:U:H3'	34:A:1201:G:H8	1.81	0.45
34:A:1900:C:OP2	34:A:1917:G:N2	2.45	0.45
34:A:2332:U:H2'	34:A:2333:G:C8	2.52	0.45
34:A:3030:A:H2'	34:A:3031:A:C8	2.51	0.45
1:2:39:ASP:OD2	1:2:44:ARG:NH2	2.49	0.45
3:4:16:ALA:HB3	3:4:22:SER:OG	2.16	0.45
3:4:319:LEU:O	3:4:323:VAL:HG23	2.16	0.45
6:D:53:ALA:HB1	6:D:78:ARG:HB2	1.98	0.45
8:F:16:ARG:HA	8:F:20:ARG:HH21	1.80	0.45
8:F:48:GLY:HA3	34:A:2531:G:O6	2.16	0.45
8:F:72:PRO:HB2	8:F:94:ALA:HB1	1.97	0.45
10:H:23:ASP:O	10:H:27:ARG:HB2	2.17	0.45
34:A:993:G:C6	34:A:1014:G:C6	3.05	0.45
34:A:1015:A:H3'	34:A:1016:C:H6	1.81	0.45
34:A:1089:C:H2'	34:A:1090:G:O4'	2.16	0.45
34:A:1647:G:H3'	34:A:1648:A:H2'	1.98	0.45
34:A:2515:U:O2'	34:A:2598:C:O2	2.34	0.45
14:L:22:ILE:N	14:L:40:VAL:O	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:O:9:ARG:HA	17:O:9:ARG:HD3	1.64	0.45
21:S:53:ASP:N	21:S:53:ASP:OD1	2.48	0.45
32:e:7:HIS:HB3	32:e:10:ALA:HB3	1.98	0.45
34:A:729:C:H2'	34:A:730:G:O4'	2.16	0.45
34:A:842:A:OP1	34:A:1652:A:O2'	2.33	0.45
34:A:999:C:H1'	34:A:1000:C:C5	2.52	0.45
34:A:2528:G:H1	34:A:2536:U:H3	1.63	0.45
3:4:49:VAL:HG13	3:4:81:VAL:HA	1.97	0.45
3:4:414:THR:O	3:4:414:THR:OG1	2.33	0.45
9:G:98:GLN:OE1	9:G:105:GLU:HB3	2.16	0.45
21:S:6:ILE:HD12	21:S:41:LEU:HB3	1.98	0.45
24:V:46:ALA:HA	34:A:571:A:H4'	1.99	0.45
34:A:17:C:H2'	34:A:18:A:C8	2.52	0.45
34:A:377:C:H2'	34:A:378:G:C8	2.50	0.45
34:A:468:G:C2'	34:A:469:G:H5'	2.47	0.45
34:A:543:U:O2'	34:A:560:U:N3	2.43	0.45
34:A:762:U:H2'	34:A:763:G:H8	1.81	0.45
34:A:1200:U:H3'	34:A:1201:G:C8	2.52	0.45
34:A:1533:U:H3'	34:A:1534:C:H5''	1.98	0.45
34:A:2134:G:H4'	34:A:2146:A:N1	2.32	0.45
34:A:2326:A:C2'	34:A:2327:C:H5'	2.46	0.45
34:A:2651:C:H5'	34:A:2653:G:H5'	1.98	0.45
3:4:179:TRP:CE3	3:4:183:MET:HE1	2.52	0.45
3:4:371:ILE:HG12	3:4:391:PHE:HB3	1.99	0.45
4:B:4:A:H8	4:B:63:U:H1'	1.82	0.45
9:G:12:PRO:HD2	9:G:15:VAL:HG21	1.99	0.45
9:G:136:GLY:HA3	9:G:142:VAL:CG2	2.47	0.45
11:I:33:VAL:HG11	34:A:1175:A:H1'	1.98	0.45
15:M:79:ASN:O	15:M:83:ILE:HG13	2.17	0.45
23:U:53:LYS:HB3	23:U:53:LYS:HE3	1.79	0.45
24:V:98:ALA:HB3	24:V:102:GLY:O	2.16	0.45
29:b:14:ARG:HB3	34:A:13:G:H5''	1.98	0.45
34:A:81:A:C2	34:A:100:A:C5	3.04	0.45
34:A:439:C:H2'	34:A:440:U:C6	2.52	0.45
34:A:3118:U:H2'	34:A:3119:A:C8	2.52	0.45
3:4:143:ARG:O	3:4:147:ILE:HG12	2.17	0.45
3:4:370:LYS:HE2	35:4:501:GCP:C4	2.47	0.45
8:F:41:VAL:HA	8:F:162:THR:O	2.17	0.45
11:I:45:ASP:N	11:I:45:ASP:OD1	2.47	0.45
21:S:14:TYR:HE2	21:S:24:VAL:HG23	1.82	0.45
22:T:72:ASP:O	22:T:75:THR:HG22	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:d:21:PHE:HA	31:d:46:THR:HG21	1.98	0.45
34:A:410:U:H5''	34:A:411:G:OP2	2.17	0.45
34:A:451:U:H1'	34:A:452:G:N7	2.31	0.45
34:A:688:A:H2'	34:A:689:U:C6	2.52	0.45
34:A:1705:C:H2'	34:A:1706:A:H8	1.81	0.45
34:A:2054:C:N4	34:A:2135:U:H3	2.14	0.45
3:4:253:TYR:HB2	3:4:342:GLN:HB3	1.99	0.45
5:C:93:ALA:HB2	5:C:107:ALA:HB2	1.98	0.45
8:F:43:VAL:HB	8:F:159:MET:HE2	1.99	0.45
8:F:109:ARG:O	8:F:113:ILE:HB	2.17	0.45
12:J:132:GLY:CA	12:J:135:ARG:HH21	2.30	0.45
19:Q:28:HIS:CD2	19:Q:41:VAL:HG22	2.51	0.45
34:A:62:G:H2'	34:A:63:C:H6	1.82	0.45
34:A:326:A:H3'	34:A:326:A:N3	2.32	0.45
34:A:620:G:H2'	34:A:621:U:C6	2.52	0.45
34:A:753:A:C2	34:A:763:G:C2	3.05	0.45
34:A:1174:G:H5''	34:A:1175:A:H5'	1.99	0.45
34:A:1180:G:H2'	34:A:1181:G:C8	2.51	0.45
34:A:1288:A:H2'	34:A:1289:A:C8	2.52	0.45
34:A:1305:G:H2'	34:A:1306:G:C8	2.51	0.45
34:A:1518:A:O2'	34:A:1692:G:O2'	2.28	0.45
34:A:2193:A:O2'	34:A:2196:G:N3	2.36	0.45
34:A:2873:U:H2'	34:A:2874:C:C6	2.52	0.45
3:4:203:PRO:O	3:4:207:LYS:N	2.49	0.45
3:4:445:THR:HG22	3:4:446:ASP:H	1.82	0.45
16:N:2:LEU:HD23	16:N:2:LEU:HA	1.79	0.45
22:T:25:ARG:NH2	34:A:604:C:O2'	2.50	0.45
34:A:150:C:H2'	34:A:151:A:C8	2.52	0.45
34:A:429:A:H2'	34:A:430:A:H8	1.81	0.45
34:A:1146:A:N3	34:A:2710:G:O2'	2.42	0.45
34:A:1178:U:N3	34:A:1206:A:H2	2.13	0.45
34:A:1509:U:H2'	34:A:1510:A:O4'	2.17	0.45
34:A:2351:A:O2'	34:A:2352:C:O5'	2.33	0.45
34:A:2531:G:H5'	34:A:2532:G:C8	2.52	0.45
3:4:89:ARG:HD2	3:4:89:ARG:HA	1.84	0.44
4:B:4:A:N6	4:B:23:G:O2'	2.47	0.44
6:D:6:ILE:HD12	6:D:6:ILE:HA	1.76	0.44
9:G:65:LEU:HD23	9:G:65:LEU:HA	1.83	0.44
22:T:30:LEU:HD23	22:T:30:LEU:HA	1.84	0.44
23:U:28:VAL:HG22	23:U:85:LYS:HA	1.98	0.44
24:V:23:VAL:HG21	24:V:26:ALA:HB2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:8:PRO:N	25:W:10:LYS:HZ3	2.15	0.44
34:A:137:G:H22	34:A:1812:A:H2	1.65	0.44
34:A:452:G:H2'	34:A:453:U:C2	2.52	0.44
34:A:824:G:H2'	34:A:825:C:C6	2.52	0.44
34:A:1287:C:H2'	34:A:1288:A:C8	2.50	0.44
34:A:2056:G:O2'	34:A:2057:G:O4'	2.35	0.44
34:A:2058:U:H5	34:A:2059:G:C4	2.35	0.44
34:A:2154:G:N3	34:A:2155:U:N3	2.58	0.44
34:A:2523:A:H2'	34:A:2524:C:H6	1.82	0.44
5:C:108:PRO:HD2	5:C:111:LEU:HD22	1.99	0.44
8:F:59:GLY:HA2	8:F:62:ASN:OD1	2.17	0.44
17:O:90:ARG:NH1	17:O:119:LYS:O	2.50	0.44
19:Q:24:THR:HG22	19:Q:86:LEU:HD12	1.98	0.44
22:T:28:ILE:HD12	22:T:83:ALA:HB2	1.98	0.44
34:A:82:G:C6	34:A:96:G:N1	2.85	0.44
34:A:365:U:H3	34:A:437:G:H1	1.66	0.44
34:A:367:U:H2'	34:A:368:U:C6	2.52	0.44
34:A:995:U:H2'	34:A:996:G:C8	2.49	0.44
34:A:3013:C:H5'	34:A:3014:A:O5'	2.17	0.44
1:2:40:ASN:O	1:2:44:ARG:HG2	2.17	0.44
3:4:24:ARG:HB3	3:4:87:GLN:HA	2.00	0.44
5:C:14:ARG:NH1	34:A:1911:U:O2'	2.50	0.44
6:D:60:ARG:NH2	34:A:3052:A:OP1	2.50	0.44
7:E:163:GLU:O	7:E:167:LYS:HG2	2.17	0.44
7:E:179:SER:OG	7:E:180:PRO:HD2	2.17	0.44
12:J:95:HIS:HD2	12:J:138:GLY:HA2	1.82	0.44
12:J:115:LYS:HA	12:J:118:LEU:HG	1.99	0.44
24:V:41:ILE:HG22	24:V:43:LYS:H	1.82	0.44
29:b:52:VAL:HG22	29:b:54:LEU:HG	1.98	0.44
34:A:837:C:C2	34:A:838:G:C8	3.05	0.44
34:A:2026:A:H8	34:A:2026:A:OP2	2.00	0.44
34:A:3033:G:H2'	34:A:3034:C:C6	2.53	0.44
3:4:423:PRO:HD2	3:4:466:TYR:CD2	2.52	0.44
8:F:75:ARG:HD3	8:F:95:ARG:HB2	1.99	0.44
8:F:118:ILE:HA	8:F:144:MET:SD	2.57	0.44
12:J:61:THR:O	12:J:61:THR:OG1	2.31	0.44
12:J:95:HIS:CB	34:A:1195:A:H4'	2.47	0.44
18:P:39:VAL:HA	18:P:103:ASP:HB3	1.98	0.44
25:W:67:LEU:HB3	25:W:69:LEU:HG	1.99	0.44
34:A:131:A:H2'	34:A:132:C:C6	2.53	0.44
34:A:1222:C:H2'	34:A:1223:U:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:1324:G:O6	34:A:1352:A:H2'	2.17	0.44
34:A:1809:U:H2'	34:A:1810:A:C8	2.52	0.44
34:A:1822:C:H2'	34:A:1823:C:H6	1.82	0.44
2:3:11:ARG:NH1	34:A:1100:C:O2	2.49	0.44
3:4:401:ASP:OD1	3:4:401:ASP:N	2.50	0.44
4:B:44:C:O2	8:F:97:THR:OG1	2.36	0.44
4:B:58:A:H1'	8:F:34:GLN:CG	2.48	0.44
5:C:133:LEU:HD23	5:C:133:LEU:HA	1.78	0.44
5:C:176:ARG:NH1	5:C:182:ILE:HD11	2.32	0.44
7:E:55:ARG:HH12	34:A:789:G:P	2.39	0.44
7:E:192:ASP:N	7:E:192:ASP:OD1	2.50	0.44
9:G:84:TYR:CE2	9:G:139:LYS:HB2	2.52	0.44
11:I:13:ILE:HB	11:I:17:PHE:CZ	2.52	0.44
12:J:45:ASN:O	12:J:49:GLU:HG3	2.17	0.44
15:M:88:PRO:HD2	15:M:89:GLN:HE22	1.81	0.44
34:A:489:A:H2'	34:A:490:A:C8	2.53	0.44
34:A:2344:G:C5	34:A:2345:U:H1'	2.52	0.44
3:4:133:GLU:OE2	3:4:134:LYS:HG2	2.18	0.44
3:4:377:VAL:HB	3:4:383:ARG:NH2	2.32	0.44
6:D:85:ARG:NH1	34:A:2861:U:H5''	2.32	0.44
11:I:28:TYR:CD2	11:I:78:ALA:HB2	2.51	0.44
11:I:105:ILE:HD13	11:I:120:VAL:HG21	1.98	0.44
13:K:136:GLN:HE22	34:A:3119:A:H5'	1.82	0.44
32:e:29:ARG:NH1	32:e:45:ASP:HB2	2.33	0.44
34:A:826:G:C2	34:A:827:G:C4	3.05	0.44
34:A:1727:A:H2'	34:A:1728:U:O4'	2.17	0.44
34:A:1900:C:H2'	34:A:1901:C:H6	1.81	0.44
34:A:2056:G:N1	34:A:2151:A:OP2	2.50	0.44
34:A:2869:C:C3'	34:A:2870:C:H5'	2.48	0.44
3:4:161:LYS:HE3	34:A:2706:A:O3'	2.18	0.44
3:4:324:ASP:N	3:4:324:ASP:OD1	2.50	0.44
3:4:445:THR:HG22	3:4:446:ASP:N	2.33	0.44
6:D:153:GLY:O	34:A:2276:G:H4'	2.18	0.44
9:G:28:GLY:HA3	9:G:80:VAL:HB	1.99	0.44
9:G:123:THR:HG23	9:G:135:SER:OG	2.18	0.44
11:I:73:PHE:CD1	11:I:77:THR:HG21	2.52	0.44
19:Q:105:LYS:HB2	19:Q:105:LYS:HE2	1.74	0.44
34:A:191:G:OP2	34:A:191:G:N2	2.43	0.44
34:A:231:U:H2'	34:A:232:G:O4'	2.18	0.44
34:A:298:G:H3'	34:A:299:G:C8	2.50	0.44
34:A:654:U:H6	34:A:654:U:H2'	1.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:857:U:H2'	34:A:858:A:H8	1.82	0.44
34:A:1805:G:H2'	34:A:1806:A:C8	2.53	0.44
34:A:2412:U:H2'	34:A:2413:G:H8	1.82	0.44
3:4:20:ARG:HB3	3:4:88:ARG:NH1	2.32	0.44
8:F:51:ALA:HA	8:F:85:LYS:HD2	1.99	0.44
8:F:105:GLU:HA	8:F:108:ASP:OD2	2.18	0.44
11:I:105:ILE:HG21	11:I:120:VAL:HG13	1.98	0.44
15:M:63:LYS:HE3	34:A:2618:C:H5''	1.99	0.44
22:T:6:GLU:OE2	22:T:7:PHE:N	2.42	0.44
23:U:4:ILE:HD12	28:Z:19:LYS:HZ3	1.83	0.44
34:A:14:G:H2'	34:A:15:C:C6	2.52	0.44
34:A:222:A:O2'	34:A:508:G:N3	2.50	0.44
34:A:564:G:N1	34:A:567:A:OP2	2.47	0.44
34:A:567:A:H1'	34:A:568:A:H5''	1.99	0.44
34:A:1784:C:H2'	34:A:1785:C:C6	2.53	0.44
34:A:2018:G:H1	34:A:2028:G:P	2.41	0.44
34:A:2777:G:C6	34:A:2778:U:H1'	2.52	0.44
1:2:5:LYS:HG3	1:2:5:LYS:O	2.17	0.44
3:4:378:GLY:HA3	3:4:383:ARG:N	2.32	0.44
4:B:32:C:O2'	4:B:54:A:N1	2.44	0.44
5:C:245:HIS:O	5:C:247:VAL:HG23	2.18	0.44
6:D:191:VAL:HG21	19:Q:7:VAL:HG11	2.00	0.44
11:I:94:LYS:HB2	11:I:120:VAL:HB	1.99	0.44
17:O:10:LEU:HD21	17:O:40:LYS:HA	1.99	0.44
17:O:87:TYR:HD2	17:O:90:ARG:HD3	1.83	0.44
25:W:11:LEU:HD13	25:W:67:LEU:HG	2.00	0.44
34:A:326:A:H2	34:A:449:G:H1	1.62	0.44
34:A:997:G:C5	34:A:998:G:C5	3.06	0.44
34:A:1754:G:O3'	34:A:1755:A:H4'	2.18	0.44
34:A:2131:G:H2'	34:A:2132:U:O4'	2.17	0.44
34:A:2213:A:H2'	34:A:2214:C:O4'	2.17	0.44
34:A:2755:A:C6	34:A:2756:G:N7	2.86	0.44
2:3:7:LYS:NZ	34:A:1252:G:N3	2.65	0.43
3:4:372:ASP:OD1	3:4:373:ALA:N	2.51	0.43
4:B:40:A:C2	4:B:45:G:C2	3.06	0.43
6:D:161:PHE:O	6:D:164:THR:OG1	2.35	0.43
8:F:124:LEU:O	8:F:184:PHE:HA	2.18	0.43
13:K:2:PRO:HA	34:A:1113:C:N3	2.33	0.43
14:L:2:ILE:HB	14:L:33:ALA:HB3	1.99	0.43
26:X:49:VAL:HG22	26:X:79:ASN:HB3	2.00	0.43
28:Z:7:PRO:HG3	34:A:74:C:H5''	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:332:C:H2'	34:A:333:C:H6	1.82	0.43
3:4:105:GLU:O	3:4:109:VAL:HG23	2.18	0.43
6:D:65:PRO:O	34:A:3010:U:O2'	2.34	0.43
11:I:23:THR:HG21	11:I:69:LEU:HD22	2.00	0.43
11:I:110:MET:N	11:I:114:ALA:O	2.27	0.43
12:J:22:PRO:HD2	12:J:41:CYS:SG	2.58	0.43
13:K:65:SER:OG	34:A:1259:U:OP2	2.22	0.43
14:L:100:GLY:O	14:L:119:PRO:HD2	2.18	0.43
15:M:37:THR:O	15:M:42:ALA:HB2	2.19	0.43
23:U:54:VAL:HG13	23:U:84:VAL:HG13	2.00	0.43
24:V:79:LYS:HA	24:V:79:LYS:HD3	1.65	0.43
29:b:9:SER:O	29:b:13:THR:HG23	2.18	0.43
34:A:150:C:O2'	34:A:151:A:H5'	2.18	0.43
34:A:394:G:H4'	34:A:413:G:C6	2.53	0.43
34:A:1160:G:N2	34:A:1231:U:O2	2.44	0.43
34:A:2134:G:C3'	34:A:2135:U:H2'	2.48	0.43
34:A:2490:A:H4'	34:A:2491:A:N3	2.33	0.43
34:A:2537:C:H2'	34:A:2538:A:H8	1.83	0.43
3:4:16:ALA:HB3	3:4:22:SER:CB	2.48	0.43
3:4:118:VAL:O	3:4:140:VAL:HG23	2.19	0.43
7:E:23:GLU:OE2	7:E:23:GLU:N	2.27	0.43
10:H:112:LEU:HD13	10:H:134:VAL:HG11	2.01	0.43
24:V:22:LYS:HE3	24:V:22:LYS:HB2	1.83	0.43
34:A:993:G:H2'	34:A:1014:G:N2	2.33	0.43
34:A:1430:C:H2'	34:A:1431:U:H6	1.82	0.43
34:A:1636:A:H2'	34:A:1637:G:O4'	2.18	0.43
34:A:3014:A:C2	34:A:3015:C:C5	3.06	0.43
1:2:38:GLU:HG2	1:2:39:ASP:N	2.32	0.43
5:C:133:LEU:N	5:C:189:CYS:O	2.46	0.43
5:C:273:ARG:HE	5:C:276:LYS:HD2	1.82	0.43
6:D:11:LEU:HB3	19:Q:4:LEU:HD21	2.00	0.43
14:L:22:ILE:HD11	14:L:42:THR:OG1	2.19	0.43
25:W:26:GLN:OE1	25:W:26:GLN:HA	2.18	0.43
34:A:1243:G:OP2	34:A:1244:A:O2'	2.22	0.43
34:A:2133:G:OP2	34:A:2133:G:H8	2.02	0.43
34:A:2368:C:H5''	34:A:2369:C:OP1	2.18	0.43
34:A:2380:G:H2'	34:A:2381:A:C2	2.53	0.43
34:A:2514:G:H4'	34:A:2605:C:O2'	2.18	0.43
34:A:2861:U:H2'	34:A:2862:G:O4'	2.17	0.43
34:A:3118:U:H2'	34:A:3119:A:H8	1.83	0.43
3:4:18:GLU:HB2	3:4:22:SER:CA	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:4:LYS:HE2	6:D:4:LYS:HB2	1.82	0.43
9:G:35:LEU:HD21	9:G:72:LEU:HB3	2.01	0.43
18:P:93:LYS:HB2	18:P:93:LYS:HE3	1.69	0.43
20:R:120:ASP:OD2	20:R:120:ASP:C	2.62	0.43
24:V:39:ASN:HD22	24:V:66:ILE:HB	1.83	0.43
34:A:1963:G:H2'	34:A:1964:U:H6	1.84	0.43
34:A:2274:C:H2'	34:A:2275:A:O4'	2.18	0.43
34:A:2538:A:H2'	34:A:2539:G:H8	1.84	0.43
34:A:2757:C:H2'	34:A:2758:A:O4'	2.19	0.43
3:4:133:GLU:O	3:4:137:LYS:N	2.35	0.43
3:4:313:GLU:OE2	3:4:316:ARG:NH1	2.51	0.43
4:B:50:C:H2'	4:B:51:G:C8	2.53	0.43
6:D:40:ARG:NH2	34:A:3008:C:O2	2.52	0.43
6:D:135:GLN:OE1	6:D:135:GLN:N	2.52	0.43
6:D:154:CYS:N	34:A:2798:G:O2'	2.45	0.43
7:E:21:PRO:HB2	7:E:24:LEU:HB2	2.00	0.43
12:J:19:GLN:OE1	12:J:19:GLN:N	2.39	0.43
12:J:135:ARG:O	12:J:135:ARG:HG2	2.17	0.43
33:f:18:ARG:HG3	34:A:1152:G:H5'	2.01	0.43
34:A:164:A:H2'	34:A:165:U:C6	2.54	0.43
34:A:1543:A:N1	34:A:1628:A:H8	2.16	0.43
34:A:1633:U:H2'	34:A:1634:C:C6	2.53	0.43
34:A:2597:A:H2'	34:A:2598:C:C6	2.54	0.43
3:4:432:ARG:HB3	3:4:459:LEU:HD21	2.00	0.43
8:F:26:GLU:OE1	8:F:26:GLU:N	2.50	0.43
9:G:49:GLY:O	9:G:51:ILE:HG13	2.18	0.43
19:Q:91:VAL:HG13	19:Q:109:ILE:HG23	2.01	0.43
23:U:46:ILE:HG23	23:U:50:PHE:HD2	1.84	0.43
25:W:16:ARG:NH2	25:W:19:THR:HA	2.34	0.43
27:Y:63:ARG:HH12	34:A:2315:U:P	2.41	0.43
30:c:11:ILE:HB	30:c:53:GLU:OE1	2.19	0.43
34:A:149:C:H2'	34:A:150:C:C6	2.54	0.43
34:A:281:C:H2'	34:A:282:A:C8	2.54	0.43
34:A:290:C:C5	34:A:303:G:H5''	2.54	0.43
34:A:1202:A:N3	34:A:1224:G:H1'	2.34	0.43
34:A:1425:G:H3'	34:A:1426:G:N2	2.34	0.43
34:A:1961:G:H3'	34:A:1962:A:H8	1.83	0.43
34:A:2124:A:N6	34:A:2157:G:O4'	2.52	0.43
3:4:82:LEU:HD22	3:4:113:THR:HG22	2.00	0.43
7:E:158:ILE:HD13	7:E:158:ILE:HA	1.89	0.43
34:A:1013:U:H2'	34:A:1014:G:O4'	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:1651:C:H2'	34:A:1652:A:C8	2.53	0.43
34:A:1790:A:H2'	34:A:1791:A:C8	2.54	0.43
34:A:2196:G:O2'	34:A:2197:G:OP2	2.30	0.43
34:A:2261:U:H2'	34:A:2262:C:C6	2.54	0.43
34:A:2375:G:H2'	34:A:2376:G:C8	2.52	0.43
34:A:2383:U:H2'	34:A:2384:C:H4'	2.00	0.43
34:A:2551:A:H2'	34:A:2552:A:C8	2.53	0.43
34:A:2623:A:H2'	34:A:2624:C:C6	2.53	0.43
1:2:46:LEU:O	1:2:50:VAL:HG22	2.18	0.43
5:C:258:ARG:HD2	34:A:2016:G:OP1	2.19	0.43
6:D:113:ASP:C	6:D:113:ASP:OD1	2.61	0.43
8:F:87:ARG:HE	8:F:87:ARG:HB2	1.59	0.43
8:F:117:ARG:O	8:F:117:ARG:NH1	2.37	0.43
9:G:18:THR:OG1	9:G:25:SER:CA	2.65	0.43
12:J:108:ARG:HD2	12:J:127:ALA:HB1	2.00	0.43
23:U:68:ARG:NH2	34:A:1449:C:H5''	2.34	0.43
30:c:35:ARG:H	30:c:35:ARG:HG2	1.66	0.43
34:A:42:G:H5'	34:A:43:C:OP1	2.18	0.43
34:A:74:C:H2'	34:A:75:U:C6	2.54	0.43
34:A:82:G:C6	34:A:83:C:C4	3.06	0.43
34:A:431:C:H2'	34:A:432:C:C6	2.54	0.43
34:A:722:G:C6	34:A:730:G:C2	3.07	0.43
34:A:954:U:H2'	34:A:955:C:C6	2.54	0.43
34:A:1214:A:OP2	34:A:1214:A:H8	2.01	0.43
34:A:1622:G:H2'	34:A:1622:G:N3	2.32	0.43
34:A:1843:C:O2'	34:A:1844:A:H5'	2.17	0.43
34:A:2193:A:C4	34:A:2197:G:H1'	2.54	0.43
34:A:2349:A:H1'	34:A:2350:G:C8	2.54	0.43
34:A:2521:C:O2	34:A:2521:C:H2'	2.19	0.43
3:4:49:VAL:HA	3:4:117:THR:HB	2.01	0.43
3:4:181:GLU:OE1	3:4:185:ARG:NH1	2.52	0.43
8:F:108:ASP:OD1	8:F:109:ARG:N	2.52	0.43
10:H:41:ARG:HD2	10:H:41:ARG:HA	1.74	0.43
20:R:43:LEU:HD23	20:R:43:LEU:HA	1.70	0.43
23:U:43:LYS:HB2	23:U:57:VAL:HG21	2.01	0.43
31:d:37:ARG:NH2	34:A:555:G:N7	2.66	0.43
34:A:600:A:H5''	34:A:1330:C:HO2'	1.83	0.43
34:A:756:A:H3'	34:A:757:G:C2	2.54	0.43
34:A:946:G:H2'	34:A:947:U:O4'	2.18	0.43
34:A:1087:G:H2'	34:A:1088:U:C6	2.53	0.43
34:A:1178:U:C2	34:A:1180:G:H5'	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:1316:U:O2'	34:A:1317:G:H5'	2.19	0.43
34:A:1401:A:H1'	34:A:1403:C:OP2	2.19	0.43
34:A:1810:A:H2'	34:A:1811:C:C6	2.53	0.43
34:A:2054:C:O2	34:A:2145:C:N3	2.52	0.43
34:A:2130:G:C2	34:A:2131:G:N7	2.87	0.43
34:A:2133:G:H2'	34:A:2133:G:N3	2.34	0.43
34:A:2300:A:H2'	34:A:2301:C:C6	2.54	0.43
34:A:2366:C:H3'	34:A:2367:G:H8	1.84	0.43
34:A:2374:U:C2	34:A:2375:G:C8	3.07	0.43
34:A:2636:A:H2'	34:A:2637:G:O4'	2.19	0.43
34:A:3018:U:H2'	34:A:3019:C:C6	2.54	0.43
3:4:76:THR:OG1	3:4:275:ALA:HB1	2.19	0.42
3:4:303:PHE:CE2	3:4:349:VAL:HG11	2.53	0.42
3:4:420:VAL:HG12	3:4:467:ALA:HA	2.00	0.42
4:B:40:A:H2'	4:B:41:U:C6	2.53	0.42
7:E:139:LYS:HB2	7:E:139:LYS:HE3	1.77	0.42
8:F:11:LEU:HG	8:F:108:ASP:HB3	2.00	0.42
13:K:93:LEU:HG	13:K:100:VAL:HG21	2.00	0.42
16:N:52:ILE:HD13	16:N:52:ILE:HA	1.82	0.42
17:O:38:GLU:HB2	17:O:109:PRO:HB2	2.01	0.42
18:P:88:ILE:HD12	18:P:88:ILE:HA	1.94	0.42
34:A:295:U:H2'	34:A:296:A:O4'	2.19	0.42
34:A:673:C:H2'	34:A:674:U:C6	2.54	0.42
34:A:696:A:N1	34:A:719:G:O2'	2.50	0.42
34:A:1012:C:C4	34:A:1013:U:C4	3.07	0.42
34:A:1202:A:C8	34:A:1203:A:N1	2.87	0.42
34:A:2336:U:H5'	34:A:2338:G:N1	2.33	0.42
34:A:3013:C:O2'	34:A:3113:A:N6	2.46	0.42
1:2:10:ARG:HE	1:2:10:ARG:HB3	1.51	0.42
3:4:128:GLN:OE1	3:4:128:GLN:N	2.52	0.42
8:F:41:VAL:HG12	8:F:163:VAL:HA	2.00	0.42
8:F:67:ILE:HG12	8:F:145:PHE:CG	2.53	0.42
8:F:142:GLN:NE2	8:F:157:ARG:H	2.17	0.42
10:H:146:LEU:HD12	10:H:146:LEU:HA	1.93	0.42
11:I:6:LYS:O	11:I:10:VAL:HG23	2.19	0.42
11:I:101:LYS:HA	11:I:101:LYS:HD3	1.82	0.42
24:V:10:LEU:HG	24:V:20:LYS:HG2	2.01	0.42
24:V:82:ARG:NH1	34:A:381:A:OP2	2.52	0.42
34:A:296:A:H2'	34:A:297:G:C8	2.54	0.42
34:A:730:G:O2'	34:A:732:G:O2'	2.33	0.42
34:A:828:G:H2'	34:A:829:U:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:864:A:H4'	34:A:1386:G:N3	2.35	0.42
34:A:1323:G:O2'	34:A:1352:A:N1	2.36	0.42
34:A:1822:C:H2'	34:A:1823:C:C6	2.54	0.42
34:A:2288:C:H2'	34:A:2289:C:H6	1.81	0.42
34:A:2350:G:H2'	34:A:2351:A:H8	1.80	0.42
34:A:2373:G:H2'	34:A:2374:U:C6	2.54	0.42
3:4:52:VAL:HA	3:4:85:LEU:O	2.19	0.42
3:4:304:VAL:HG12	3:4:307:LEU:HD12	2.02	0.42
4:B:4:A:C8	4:B:63:U:H1'	2.54	0.42
4:B:53:A:N7	18:P:45:ARG:CZ	2.82	0.42
4:B:60:G:H3'	4:B:61:C:H6	1.84	0.42
10:H:26:GLY:HA2	10:H:30:LEU:HB2	2.00	0.42
13:K:68:LYS:HE3	34:A:1140:G:N7	2.34	0.42
15:M:94:GLY:H	15:M:97:GLU:HB2	1.84	0.42
18:P:10:ILE:HD13	18:P:10:ILE:HA	1.85	0.42
21:S:92:GLN:OE1	34:A:1111:G:H1'	2.18	0.42
29:b:44:LEU:O	29:b:48:ARG:HG2	2.19	0.42
34:A:394:G:H4'	34:A:413:G:C5	2.55	0.42
34:A:401:C:H2'	34:A:402:G:O4'	2.19	0.42
34:A:1064:A:H2'	34:A:1065:C:C6	2.53	0.42
34:A:1378:U:C4	34:A:1379:G:C6	3.08	0.42
34:A:1650:G:H2'	34:A:1651:C:C6	2.54	0.42
34:A:2008:A:N6	34:A:2045:G:O2'	2.39	0.42
1:2:38:GLU:HG2	1:2:39:ASP:H	1.85	0.42
3:4:130:ASN:OD1	3:4:130:ASN:C	2.62	0.42
3:4:141:ILE:HD12	3:4:141:ILE:O	2.19	0.42
3:4:206:THR:O	3:4:209:GLU:N	2.46	0.42
3:4:276:LEU:O	3:4:277:PHE:C	2.63	0.42
3:4:280:LEU:HG	3:4:281:GLU:HG3	2.02	0.42
3:4:328:LEU:O	3:4:365:LEU:N	2.48	0.42
5:C:179:SER:OG	34:A:2016:G:N7	2.52	0.42
9:G:16:ASP:OD1	9:G:16:ASP:N	2.52	0.42
10:H:85:ALA:HB3	10:H:151:GLN:HB3	2.01	0.42
11:I:31:LEU:HB3	11:I:36:LEU:HD12	2.01	0.42
11:I:40:ARG:NH1	34:A:1201:G:H4'	2.34	0.42
12:J:98:LYS:CE	12:J:140:THR:HG22	2.49	0.42
18:P:55:LEU:HD23	18:P:55:LEU:HA	1.72	0.42
18:P:83:ARG:HD3	18:P:83:ARG:O	2.20	0.42
29:b:37:ARG:HA	29:b:37:ARG:HD2	1.66	0.42
34:A:446:G:OP2	34:A:446:G:H8	2.01	0.42
34:A:948:G:H2'	34:A:949:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:1001:C:H3'	34:A:1002:C:O4'	2.19	0.42
34:A:1202:A:H2'	34:A:1203:A:C4	2.54	0.42
34:A:1721:U:H2'	34:A:1722:C:C6	2.55	0.42
34:A:1733:C:H2'	34:A:1734:C:H6	1.84	0.42
34:A:2364:C:H2'	34:A:2365:A:C8	2.50	0.42
34:A:2713:G:O2'	34:A:2714:G:H5'	2.19	0.42
3:4:193:GLY:HA2	3:4:207:LYS:CE	2.49	0.42
3:4:200:THR:HG23	3:4:200:THR:O	2.19	0.42
3:4:293:ARG:HA	3:4:438:HIS:NE2	2.34	0.42
4:B:30:G:H21	4:B:58:A:N6	2.16	0.42
5:C:78:LYS:HB2	5:C:78:LYS:HE2	1.82	0.42
5:C:273:ARG:CZ	5:C:274:THR:H	2.32	0.42
8:F:14:ARG:HB2	8:F:18:GLU:OE1	2.20	0.42
8:F:105:GLU:O	8:F:109:ARG:HG2	2.20	0.42
8:F:122:ARG:HH11	8:F:122:ARG:HA	1.83	0.42
9:G:37:VAL:HG23	9:G:69:SER:HB3	2.00	0.42
11:I:28:TYR:HB2	11:I:31:LEU:HD12	2.00	0.42
14:L:19:ILE:HB	14:L:41:ALA:HB1	2.01	0.42
15:M:6:LEU:HD23	15:M:6:LEU:HA	1.81	0.42
15:M:118:LEU:HD12	15:M:119:THR:N	2.35	0.42
18:P:85:GLY:O	18:P:88:ILE:HG22	2.19	0.42
22:T:7:PHE:HB3	22:T:116:SER:O	2.20	0.42
31:d:13:ARG:HH12	34:A:886:G:P	2.42	0.42
34:A:331:U:H2'	34:A:332:C:C6	2.54	0.42
34:A:387:U:H2'	34:A:388:U:C6	2.55	0.42
34:A:689:U:H2'	34:A:690:G:H8	1.84	0.42
34:A:1005:A:H2'	34:A:1006:G:O4'	2.19	0.42
34:A:1197:C:C2	34:A:1198:C:C5	3.08	0.42
34:A:1733:C:H2'	34:A:1734:C:C6	2.54	0.42
34:A:2761:U:H2'	34:A:2762:C:H6	1.84	0.42
34:A:3074:C:H2'	34:A:3075:C:H6	1.83	0.42
6:D:54:TYR:CG	6:D:55:GLY:N	2.87	0.42
6:D:100:GLU:OE2	6:D:100:GLU:HA	2.20	0.42
7:E:30:ASN:O	7:E:34:MET:HG3	2.18	0.42
7:E:48:GLY:O	7:E:95:PRO:HA	2.19	0.42
8:F:9:PRO:HG2	8:F:104:TRP:HB3	2.01	0.42
8:F:24:GLN:HA	8:F:27:PHE:CE2	2.54	0.42
8:F:128:GLN:HA	34:A:2528:G:OP1	2.19	0.42
12:J:89:LYS:HE3	12:J:89:LYS:HB3	1.94	0.42
13:K:36:LEU:HD11	13:K:122:LEU:HD13	2.02	0.42
15:M:91:GLY:HA2	15:M:122:VAL:HG12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:56:GLU:HB3	19:Q:75:VAL:HB	2.01	0.42
21:S:17:ALA:N	21:S:20:ASP:OD1	2.52	0.42
21:S:64:VAL:HG22	21:S:97:LEU:HD21	2.01	0.42
23:U:31:PHE:CE2	23:U:96:PHE:CZ	3.07	0.42
23:U:42:ILE:O	23:U:46:ILE:HG12	2.20	0.42
24:V:39:ASN:ND2	24:V:66:ILE:HB	2.35	0.42
34:A:307:G:H2'	34:A:308:U:C6	2.53	0.42
34:A:502:C:N4	34:A:503:A:H62	2.18	0.42
34:A:772:U:H2'	34:A:773:G:C8	2.54	0.42
34:A:847:C:H2'	34:A:848:G:O4'	2.19	0.42
34:A:1289:A:H2'	34:A:1290:C:O4'	2.20	0.42
34:A:1935:C:H2'	34:A:1936:G:H8	1.85	0.42
1:2:38:GLU:OE1	1:2:40:ASN:ND2	2.53	0.42
3:4:14:GLU:C	3:4:16:ALA:H	2.27	0.42
3:4:21:ALA:HB1	3:4:88:ARG:HB2	1.90	0.42
8:F:136:THR:OG1	34:A:2527:G:N2	2.53	0.42
12:J:129:ILE:HG12	34:A:1198:C:O2	2.19	0.42
13:K:117:GLN:O	13:K:120:LYS:HG2	2.20	0.42
20:R:31:LEU:HD13	34:A:672:C:H4'	2.01	0.42
20:R:101:SER:OG	20:R:102:ASP:N	2.53	0.42
22:T:14:ALA:HB2	22:T:57:VAL:HG22	2.01	0.42
34:A:578:G:OP2	34:A:578:G:H8	2.02	0.42
34:A:947:U:H2'	34:A:948:G:C8	2.55	0.42
34:A:1434:G:O2'	34:A:1435:C:H5'	2.19	0.42
34:A:1533:U:O2	34:A:1533:U:H2'	2.19	0.42
34:A:1854:U:O2'	34:A:1977:C:O2'	2.21	0.42
34:A:2324:A:N6	34:A:2413:G:C5	2.88	0.42
34:A:2588:C:H2'	34:A:2589:G:O4'	2.20	0.42
5:C:54:LYS:HE2	34:A:2040:G:OP1	2.19	0.42
8:F:25:GLN:C	8:F:27:PHE:H	2.27	0.42
8:F:68:THR:HG21	8:F:96:VAL:HG11	2.02	0.42
16:N:76:LYS:HD3	16:N:91:GLU:HG2	2.02	0.42
19:Q:88:ARG:HB2	19:Q:112:LYS:HB2	2.02	0.42
34:A:74:C:H2'	34:A:75:U:H6	1.83	0.42
34:A:1418:G:O6	34:A:1419:A:N6	2.53	0.42
34:A:1951:G:H2'	34:A:1952:C:C6	2.55	0.42
34:A:2321:U:H2'	34:A:2322:C:C6	2.55	0.42
34:A:2870:C:H2'	34:A:2871:U:O4'	2.20	0.42
3:4:136:VAL:HG13	3:4:138:VAL:HB	2.02	0.42
6:D:151:ILE:HG23	6:D:160:VAL:HG13	2.02	0.42
7:E:53:LYS:HE2	34:A:539:C:H4'	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:128:THR:O	7:E:129:GLU:C	2.63	0.42
9:G:152:LEU:HD23	9:G:152:LEU:HA	1.91	0.42
11:I:46:SER:HA	11:I:83:LYS:HB2	2.01	0.42
12:J:42:LYS:HA	12:J:42:LYS:HD3	1.64	0.42
15:M:57:ILE:HD13	15:M:60:ARG:HH21	1.84	0.42
34:A:1002:C:O2'	34:A:1003:A:OP1	2.26	0.42
34:A:1301:G:H2'	34:A:1302:G:O4'	2.20	0.42
34:A:1542:A:H8	34:A:1543:A:N7	2.18	0.42
34:A:3013:C:H5'	34:A:3014:A:C5'	2.50	0.42
3:4:20:ARG:HB3	3:4:88:ARG:HH12	1.85	0.42
3:4:177:ARG:HD2	3:4:177:ARG:HA	1.86	0.42
3:4:443:GLU:H	3:4:450:ARG:HG3	1.85	0.42
6:D:150:SER:O	34:A:2736:C:H1'	2.19	0.42
17:O:16:HIS:CE1	17:O:20:LEU:HD12	2.55	0.42
22:T:99:ARG:HH12	34:A:862:U:H4'	1.85	0.42
34:A:504:C:H2'	34:A:505:C:C6	2.55	0.42
34:A:1278:C:N3	34:A:1279:G:N7	2.68	0.42
34:A:1869:G:H2'	34:A:1870:U:O4'	2.20	0.42
34:A:2127:G:O2'	34:A:2151:A:H4'	2.20	0.42
34:A:2366:C:H3'	34:A:2367:G:C8	2.55	0.42
34:A:2777:G:N2	34:A:2779:U:OP1	2.53	0.42
34:A:2869:C:H4'	34:A:2956:G:O2'	2.20	0.42
34:A:3014:A:N6	34:A:3112:A:H2'	2.35	0.42
34:A:3074:C:H2'	34:A:3075:C:C6	2.55	0.42
3:4:22:SER:HB3	3:4:23:LEU:H	1.59	0.41
4:B:50:C:H2'	4:B:51:G:H8	1.85	0.41
6:D:86:LEU:HD22	6:D:95:TYR:HE2	1.85	0.41
6:D:173:ASP:OD1	6:D:173:ASP:N	2.53	0.41
8:F:178:ARG:HA	8:F:182:PHE:HD2	1.85	0.41
11:I:110:MET:HE2	11:I:122:LYS:NZ	2.35	0.41
12:J:102:VAL:HG12	12:J:103:THR:H	1.85	0.41
15:M:31:LYS:HB3	15:M:32:THR:H	1.61	0.41
18:P:82:VAL:HG23	18:P:119:ALA:HB2	2.02	0.41
20:R:91:ASP:OD1	20:R:93:LYS:HB3	2.20	0.41
34:A:24:G:C2	34:A:599:G:N3	2.88	0.41
34:A:183:G:H2'	34:A:184:C:H6	1.85	0.41
34:A:339:U:H2'	34:A:340:A:N7	2.34	0.41
34:A:966:U:H2'	34:A:967:G:H8	1.85	0.41
34:A:1001:C:C6	34:A:1002:C:H1'	2.55	0.41
34:A:1652:A:H2'	34:A:1653:G:C8	2.55	0.41
34:A:1833:C:H2'	34:A:1835:C:C5	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:2134:G:O2'	34:A:2146:A:N6	2.51	0.41
34:A:2396:A:C6	34:A:2397:C:C4	3.09	0.41
4:B:95:G:O2'	34:A:1033:A:H5''	2.20	0.41
8:F:34:GLN:HB3	18:P:3:HIS:HD2	1.84	0.41
8:F:158:GLY:HA3	34:A:2529:A:C6	2.55	0.41
12:J:57:PRO:CB	12:J:73:LYS:HB2	2.50	0.41
13:K:120:LYS:HE2	13:K:120:LYS:HB3	1.75	0.41
15:M:77:VAL:HG11	34:A:730:G:H1	1.85	0.41
23:U:12:LEU:HB2	23:U:32:VAL:HG13	2.03	0.41
30:c:10:LYS:HE2	34:A:2644:C:H5''	2.02	0.41
34:A:446:G:N2	34:A:447:A:H1'	2.35	0.41
34:A:949:C:C2	34:A:950:A:C8	3.08	0.41
34:A:996:G:C5	34:A:997:G:N7	2.88	0.41
34:A:998:G:H8	34:A:998:G:OP2	2.03	0.41
34:A:1934:G:H2'	34:A:1935:C:H6	1.85	0.41
34:A:2420:U:O2'	34:A:2421:A:H2'	2.20	0.41
34:A:2971:G:H2'	34:A:2972:A:C8	2.55	0.41
3:4:383:ARG:NE	3:4:383:ARG:HA	2.36	0.41
3:4:454:ARG:H	3:4:454:ARG:HG2	1.60	0.41
5:C:162:SER:HB3	5:C:195:GLU:HB2	2.03	0.41
6:D:78:ARG:HA	6:D:78:ARG:HD2	1.95	0.41
10:H:78:VAL:HG13	10:H:146:LEU:HD12	2.01	0.41
10:H:80:LEU:HD13	10:H:103:ALA:HB2	2.02	0.41
13:K:88:THR:OG1	13:K:91:GLU:HG3	2.20	0.41
15:M:86:ALA:O	15:M:88:PRO:HD3	2.21	0.41
18:P:70:VAL:HG22	18:P:83:ARG:HG3	2.01	0.41
19:Q:61:ARG:NH1	19:Q:70:GLU:OE1	2.41	0.41
24:V:41:ILE:HG13	24:V:64:ALA:HB2	2.03	0.41
26:X:29:GLN:HE21	26:X:29:GLN:HB3	1.76	0.41
34:A:334:G:C6	34:A:348:G:C5	3.08	0.41
34:A:441:G:H2'	34:A:442:U:H6	1.84	0.41
34:A:479:A:H1'	34:A:499:G:O4'	2.20	0.41
34:A:980:C:HO2'	34:A:981:U:P	2.42	0.41
34:A:1006:G:H2'	34:A:1007:G:O4'	2.21	0.41
34:A:1175:A:N6	34:A:1205:G:OP1	2.53	0.41
34:A:2125:A:N3	34:A:2126:C:N4	2.68	0.41
34:A:2623:A:H2'	34:A:2624:C:H6	1.86	0.41
3:4:230:LYS:HE3	3:4:316:ARG:NH2	2.35	0.41
8:F:174:ARG:HD3	8:F:178:ARG:HH21	1.86	0.41
11:I:41:ARG:HH22	34:A:1200:U:H4'	1.86	0.41
15:M:61:LEU:HD13	32:e:24:ARG:HD2	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:124:VAL:HG21	15:M:137:ILE:HD13	2.03	0.41
17:O:2:PRO:HG2	34:A:2914:A:C2	2.55	0.41
23:U:30:THR:HA	23:U:82:ALA:O	2.20	0.41
34:A:9:U:O2	34:A:2850:C:O2'	2.34	0.41
34:A:279:U:H2'	34:A:280:G:C8	2.51	0.41
34:A:680:U:H2'	34:A:681:C:C6	2.55	0.41
34:A:1383:A:H2'	34:A:1384:G:O4'	2.19	0.41
34:A:1931:A:H61	34:A:1962:A:H61	1.67	0.41
34:A:2366:C:H2'	34:A:2367:G:O4'	2.20	0.41
34:A:2389:U:H3'	34:A:2390:U:C5	2.54	0.41
34:A:2482:U:O2'	34:A:2651:C:OP2	2.32	0.41
34:A:3033:G:H2'	34:A:3034:C:H6	1.84	0.41
3:4:221:LYS:HD3	34:A:2686:U:OP1	2.21	0.41
5:C:212:MET:HE2	5:C:217:LYS:HD2	2.02	0.41
9:G:6:LYS:HD3	9:G:6:LYS:HA	1.83	0.41
9:G:116:ILE:HD11	9:G:152:LEU:HD11	2.02	0.41
10:H:113:ASP:O	10:H:116:THR:OG1	2.27	0.41
15:M:133:ALA:O	15:M:137:ILE:HG13	2.20	0.41
20:R:46:ALA:O	20:R:50:ARG:HB2	2.21	0.41
24:V:15:LYS:HZ3	34:A:411:G:H1	1.69	0.41
34:A:1091:A:H5'	34:A:1303:U:H1'	2.01	0.41
34:A:1250:U:H2'	34:A:1251:A:C8	2.55	0.41
34:A:1387:A:OP1	34:A:1387:A:H4'	2.20	0.41
34:A:1621:C:H2'	34:A:1622:G:H5'	2.01	0.41
34:A:1622:G:H2'	34:A:1623:U:H5'	2.01	0.41
34:A:2027:A:H2'	34:A:2028:G:O4'	2.21	0.41
34:A:2740:G:H2'	34:A:2741:C:C6	2.55	0.41
34:A:2998:C:H2'	34:A:2999:A:O4'	2.21	0.41
3:4:118:VAL:O	3:4:140:VAL:HA	2.20	0.41
3:4:151:PHE:CE2	3:4:311:LEU:HD13	2.55	0.41
3:4:204:GLY:C	3:4:207:LYS:H	2.29	0.41
10:H:80:LEU:HD23	10:H:95:VAL:HG22	2.02	0.41
12:J:19:GLN:H	12:J:19:GLN:CD	2.27	0.41
12:J:95:HIS:NE2	12:J:135:ARG:HG2	2.36	0.41
14:L:23:ARG:NH2	34:A:2771:U:O2	2.47	0.41
15:M:84:ASN:HB2	15:M:118:LEU:HD13	2.02	0.41
15:M:98:LEU:HD23	15:M:98:LEU:HA	1.86	0.41
17:O:45:ARG:HB3	17:O:46:PRO:HD3	2.03	0.41
17:O:64:ARG:NH1	34:A:3072:A:O3'	2.54	0.41
17:O:87:TYR:CD2	17:O:90:ARG:HD3	2.56	0.41
18:P:119:ALA:O	18:P:122:GLU:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:26:ARG:HE	22:T:26:ARG:HB3	1.63	0.41
23:U:93:ILE:H	23:U:93:ILE:HG13	1.72	0.41
25:W:16:ARG:HG2	25:W:48:GLU:HB3	2.02	0.41
34:A:287:A:H1'	34:A:300:G:C6	2.55	0.41
34:A:322:A:H2'	34:A:323:C:O4'	2.20	0.41
34:A:376:G:H2'	34:A:377:C:C6	2.55	0.41
34:A:449:G:C6	34:A:450:G:C5	3.09	0.41
34:A:813:C:O2'	34:A:849:A:N6	2.47	0.41
34:A:819:G:O2'	34:A:841:G:N2	2.39	0.41
34:A:1002:C:H2'	34:A:1003:A:H5''	2.03	0.41
34:A:1314:C:H2'	34:A:1315:C:H6	1.84	0.41
3:4:434:HIS:CE1	3:4:439:VAL:HG11	2.55	0.41
8:F:106:PHE:HA	8:F:109:ARG:HG2	2.02	0.41
9:G:90:ILE:HB	9:G:130:THR:HA	2.02	0.41
11:I:49:TYR:HE1	11:I:78:ALA:HB1	1.85	0.41
33:f:5:PRO:HG2	34:A:2689:C:H4'	2.03	0.41
34:A:48:G:H1'	34:A:115:A:N6	2.36	0.41
34:A:630:U:H2'	34:A:631:C:C6	2.55	0.41
34:A:2350:G:H4'	34:A:2351:A:OP1	2.20	0.41
34:A:2537:C:H2'	34:A:2538:A:C8	2.56	0.41
34:A:3013:C:H5'	34:A:3014:A:H5'	2.02	0.41
6:D:43:GLU:OE2	6:D:43:GLU:N	2.31	0.41
7:E:182:GLN:HB3	34:A:708:G:H22	1.86	0.41
9:G:19:ILE:HA	9:G:19:ILE:HD13	1.71	0.41
11:I:100:ASN:C	11:I:102:ALA:H	2.28	0.41
17:O:82:GLU:HG3	17:O:83:ILE:HG13	2.02	0.41
19:Q:4:LEU:HD23	19:Q:6:PHE:HE1	1.84	0.41
19:Q:26:ASN:HB2	19:Q:84:ASP:OD1	2.20	0.41
22:T:16:TYR:H	22:T:109:HIS:CE1	2.39	0.41
34:A:337:U:H2'	34:A:344:G:C6	2.56	0.41
34:A:490:A:C2'	34:A:491:U:H5'	2.51	0.41
34:A:862:U:OP2	34:A:2835:U:O2'	2.37	0.41
34:A:1007:G:C6	34:A:1008:G:C6	3.09	0.41
34:A:1177:G:N1	34:A:1198:C:N3	2.68	0.41
34:A:1226:U:C4	34:A:1227:C:C4	3.09	0.41
34:A:2523:A:H2'	34:A:2524:C:C6	2.55	0.41
34:A:2603:G:H2'	34:A:2604:U:C6	2.56	0.41
34:A:2755:A:C6	34:A:2756:G:C5	3.09	0.41
34:A:3026:G:H2'	34:A:3027:G:O4'	2.21	0.41
1:2:32:ARG:NH1	34:A:1116:C:O2	2.46	0.41
3:4:24:ARG:H	3:4:87:GLN:NE2	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:64:G:H2'	4:B:65:C:C6	2.56	0.41
6:D:43:GLU:H	6:D:43:GLU:CD	2.24	0.41
8:F:23:LEU:HA	8:F:23:LEU:HD12	1.76	0.41
8:F:85:LYS:O	8:F:90:MET:HE1	2.20	0.41
8:F:113:ILE:HG22	8:F:146:HIS:CE1	2.55	0.41
8:F:170:ASP:O	8:F:174:ARG:HB2	2.20	0.41
11:I:39:LEU:HD21	11:I:96:PHE:CG	2.56	0.41
11:I:83:LYS:HB2	11:I:83:LYS:HE3	1.89	0.41
13:K:55:ILE:HA	13:K:123:LYS:O	2.20	0.41
19:Q:2:ASN:HB3	19:Q:5:ASP:OD2	2.20	0.41
23:U:8:ARG:HG2	28:Z:30:PHE:HB2	2.03	0.41
24:V:58:GLY:N	34:A:571:A:N3	2.60	0.41
27:Y:36:VAL:HG11	27:Y:61:VAL:HG11	2.02	0.41
32:e:40:ARG:HG3	32:e:43:ARG:NH2	2.36	0.41
34:A:139:U:H2'	34:A:140:G:O4'	2.21	0.41
34:A:494:G:H2'	34:A:495:C:O4'	2.21	0.41
34:A:940:A:H2'	34:A:941:U:O4'	2.21	0.41
34:A:1105:C:O2'	34:A:1118:A:N3	2.44	0.41
34:A:1139:A:H2'	34:A:1141:U:H5'	2.02	0.41
34:A:1314:C:H2'	34:A:1315:C:C6	2.56	0.41
34:A:1752:C:H2'	34:A:1753:C:O4'	2.21	0.41
34:A:2329:G:H1	34:A:2406:U:H3	1.69	0.41
34:A:2346:G:C2	34:A:2399:A:N7	2.89	0.41
34:A:2469:U:O2'	34:A:2660:G:OP2	2.25	0.41
34:A:2481:U:O2'	34:A:2482:U:H5'	2.21	0.41
3:4:432:ARG:NH2	3:4:459:LEU:HG	2.36	0.41
5:C:182:ILE:HD13	5:C:270:ARG:NH1	2.36	0.41
6:D:174:ARG:NH1	34:A:2997:C:OP1	2.54	0.41
16:N:29:PHE:HZ	34:A:1020:A:H2	1.69	0.41
16:N:45:ARG:H	16:N:45:ARG:HG3	1.64	0.41
16:N:58:ILE:O	16:N:59:LYS:HG2	2.21	0.41
23:U:15:VAL:HB	23:U:30:THR:HG23	2.03	0.41
26:X:8:SER:O	34:A:2479:G:N2	2.41	0.41
34:A:1003:A:OP1	34:A:1003:A:H2'	2.20	0.41
34:A:1195:A:N1	34:A:1206:A:H2'	2.36	0.41
34:A:1295:U:H2'	34:A:1296:G:C8	2.54	0.41
34:A:1337:G:N2	34:A:1340:A:OP2	2.47	0.41
34:A:1417:A:H5'	34:A:1826:A:OP2	2.21	0.41
34:A:1443:G:H2'	34:A:1445:C:C5	2.55	0.41
34:A:1649:C:C5	34:A:1789:A:H5''	2.56	0.41
34:A:1755:A:C2	34:A:1759:A:H1'	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:1806:A:H2'	34:A:1807:C:C6	2.56	0.41
34:A:1934:G:H2'	34:A:1935:C:C6	2.55	0.41
34:A:2133:G:C8	34:A:2134:G:C8	3.09	0.41
34:A:2335:G:N1	34:A:2390:U:O3'	2.51	0.41
34:A:2408:G:H2'	34:A:2409:U:O4'	2.21	0.41
34:A:2885:G:H2'	34:A:2886:A:C8	2.55	0.41
1:2:3:GLU:HA	1:2:3:GLU:OE1	2.20	0.40
3:4:193:GLY:HA2	3:4:207:LYS:HE2	2.01	0.40
3:4:424:TYR:CE2	3:4:447:ALA:HA	2.56	0.40
9:G:164:ARG:HE	9:G:164:ARG:HB2	1.62	0.40
10:H:80:LEU:HD21	10:H:95:VAL:HG13	2.03	0.40
11:I:41:ARG:NH2	34:A:1200:U:H4'	2.35	0.40
12:J:19:GLN:NE2	12:J:52:ARG:NH1	2.69	0.40
13:K:45:THR:HG23	13:K:48:VAL:HB	2.03	0.40
19:Q:110:LYS:CD	19:Q:113:ARG:HH22	2.33	0.40
32:e:56:SER:O	32:e:60:LYS:HG2	2.20	0.40
34:A:6:G:N2	34:A:7:U:O4	2.54	0.40
34:A:155:G:H2'	34:A:156:C:H6	1.84	0.40
34:A:155:G:H2'	34:A:156:C:C6	2.55	0.40
34:A:220:A:H2	34:A:266:U:H4'	1.87	0.40
34:A:1406:U:H2'	34:A:1407:G:H8	1.86	0.40
34:A:2125:A:N3	34:A:2125:A:C2'	2.83	0.40
34:A:2248:C:H2'	34:A:2249:G:H8	1.85	0.40
34:A:2358:A:C2	34:A:2359:G:H1'	2.56	0.40
34:A:2522:A:H2'	34:A:2523:A:O4'	2.21	0.40
34:A:2543:U:H1'	34:A:2544:U:C5	2.55	0.40
7:E:182:GLN:HB3	34:A:708:G:N2	2.36	0.40
9:G:17:VAL:HB	9:G:45:ARG:CZ	2.51	0.40
10:H:25:TYR:CD1	34:A:2317:G:H5'	2.56	0.40
12:J:40:PHE:CE1	12:J:60:ILE:HD13	2.57	0.40
12:J:101:LYS:HE2	12:J:140:THR:OG1	2.21	0.40
16:N:1:MET:HE1	16:N:45:ARG:HG2	2.03	0.40
24:V:37:GLY:HA2	24:V:40:ARG:HH22	1.86	0.40
28:Z:21:LYS:HE2	28:Z:21:LYS:HB2	1.77	0.40
28:Z:54:ILE:HA	28:Z:54:ILE:HD13	1.80	0.40
33:f:5:PRO:HD2	34:A:2689:C:O3'	2.21	0.40
34:A:183:G:H2'	34:A:184:C:C6	2.56	0.40
34:A:468:G:O2'	34:A:469:G:H5'	2.22	0.40
34:A:489:A:H2'	34:A:490:A:H8	1.86	0.40
34:A:545:A:N1	34:A:558:A:H5''	2.36	0.40
34:A:1073:G:O6	34:A:1075:U:O2'	2.38	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:1109:U:H3	34:A:1282:G:H1	1.69	0.40
34:A:1194:C:H2'	34:A:1195:A:O4'	2.21	0.40
34:A:1205:G:C6	34:A:1207:G:C2	3.09	0.40
34:A:1227:C:H2'	34:A:1228:A:C4	2.56	0.40
34:A:1647:G:OP2	34:A:1648:A:O2'	2.37	0.40
35:4:501:GCP:O2B	35:4:501:GCP:O3G	2.39	0.40
10:H:109:GLY:N	10:H:110:PRO:HD2	2.37	0.40
11:I:94:LYS:HZ2	11:I:121:GLU:HA	1.86	0.40
14:L:29:SER:HB2	34:A:2899:A:H4'	2.03	0.40
15:M:86:ALA:C	15:M:87:PHE:HD1	2.30	0.40
17:O:63:ARG:HA	17:O:80:PHE:CZ	2.57	0.40
23:U:10:ILE:H	23:U:10:ILE:HD12	1.86	0.40
34:A:229:U:H3'	34:A:230:G:C5'	2.51	0.40
34:A:503:A:H2'	34:A:504:C:H6	1.85	0.40
34:A:722:G:H2'	34:A:723:C:C6	2.56	0.40
34:A:931:C:H2'	34:A:932:C:C6	2.57	0.40
34:A:1117:U:O2	34:A:1118:A:C8	2.74	0.40
34:A:1127:A:N3	34:A:1272:C:O2'	2.51	0.40
34:A:2053:C:OP2	34:A:2134:G:N2	2.54	0.40
34:A:2054:C:C6	34:A:2133:G:O6	2.75	0.40
34:A:2054:C:H5''	34:A:2133:G:C6	2.56	0.40
34:A:2059:G:H2'	34:A:2060:C:C6	2.55	0.40
34:A:2359:G:H3'	34:A:2360:C:H5''	2.02	0.40
34:A:2414:G:H2'	34:A:2415:G:C8	2.55	0.40
34:A:3055:G:H1'	34:A:3104:A:N6	2.36	0.40
7:E:126:ALA:HA	7:E:196:PHE:O	2.22	0.40
9:G:138:ASP:O	9:G:142:VAL:HG23	2.21	0.40
12:J:94:PRO:O	12:J:95:HIS:HB2	2.20	0.40
14:L:87:ILE:HA	14:L:93:PRO:HA	2.04	0.40
16:N:15:PRO:O	16:N:41:TYR:OH	2.32	0.40
34:A:565:A:H2'	34:A:566:A:C8	2.55	0.40
34:A:1010:U:H2'	34:A:1012:C:C6	2.56	0.40
34:A:1405:U:H2'	34:A:1406:U:H6	1.86	0.40
34:A:2307:C:H2'	34:A:2308:U:O4'	2.21	0.40
34:A:3040:G:H2'	34:A:3042:A:N7	2.36	0.40
34:A:3116:C:H2'	34:A:3117:U:H6	1.87	0.40
4:B:32:C:C2'	4:B:54:A:H61	2.34	0.40
5:C:100:GLY:O	34:A:1720:G:O2'	2.35	0.40
17:O:10:LEU:HB3	17:O:17:GLN:HG3	2.04	0.40
19:Q:1:MET:N	34:A:3064:G:N3	2.69	0.40
21:S:12:LYS:HE3	34:A:1112:C:O2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:S:14:TYR:CE2	21:S:24:VAL:HG23	2.56	0.40
21:S:21:VAL:HG12	21:S:98:LYS:HB2	2.04	0.40
26:X:18:ALA:HB1	34:A:2495:G:OP1	2.21	0.40
34:A:94:G:H2'	34:A:95:C:C6	2.57	0.40
34:A:248:G:N3	34:A:2655:U:H4'	2.36	0.40
34:A:609:G:H2'	34:A:610:C:C6	2.57	0.40
34:A:694:C:H2'	34:A:695:G:O4'	2.22	0.40
34:A:819:G:H1'	34:A:842:A:N6	2.35	0.40
34:A:1162:G:H1'	34:A:1166:A:H1'	2.03	0.40
34:A:1369:A:H5''	34:A:1370:U:H5''	2.04	0.40
34:A:1804:G:H2'	34:A:1805:G:C8	2.56	0.40
34:A:2466:G:H2'	34:A:2467:U:O4'	2.22	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	2	57/61 (93%)	54 (95%)	3 (5%)	0	100	100
2	3	21/24 (88%)	21 (100%)	0	0	100	100
3	4	464/470 (99%)	396 (85%)	67 (14%)	1 (0%)	43	66
5	C	273/278 (98%)	256 (94%)	17 (6%)	0	100	100
6	D	212/217 (98%)	197 (93%)	15 (7%)	0	100	100
7	E	207/215 (96%)	192 (93%)	15 (7%)	0	100	100
8	F	180/187 (96%)	162 (90%)	18 (10%)	0	100	100
9	G	174/179 (97%)	153 (88%)	21 (12%)	0	100	100
10	H	149/151 (99%)	117 (78%)	32 (22%)	0	100	100
11	I	124/175 (71%)	103 (83%)	21 (17%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	J	130/142 (92%)	113 (87%)	16 (12%)	1 (1%)	16	37
13	K	144/147 (98%)	133 (92%)	11 (8%)	0	100	100
14	L	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
15	M	143/147 (97%)	128 (90%)	15 (10%)	0	100	100
16	N	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
17	O	116/199 (58%)	111 (96%)	5 (4%)	0	100	100
18	P	124/127 (98%)	112 (90%)	12 (10%)	0	100	100
19	Q	111/113 (98%)	97 (87%)	14 (13%)	0	100	100
20	R	122/129 (95%)	119 (98%)	3 (2%)	0	100	100
21	S	98/103 (95%)	90 (92%)	8 (8%)	0	100	100
22	T	112/153 (73%)	101 (90%)	11 (10%)	0	100	100
23	U	95/100 (95%)	88 (93%)	7 (7%)	0	100	100
24	V	93/105 (89%)	80 (86%)	13 (14%)	0	100	100
25	W	93/215 (43%)	85 (91%)	8 (9%)	0	100	100
26	X	77/88 (88%)	75 (97%)	2 (3%)	0	100	100
27	Y	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
28	Z	62/77 (80%)	60 (97%)	2 (3%)	0	100	100
29	b	52/57 (91%)	49 (94%)	3 (6%)	0	100	100
30	c	47/55 (86%)	45 (96%)	2 (4%)	0	100	100
31	d	44/47 (94%)	39 (89%)	5 (11%)	0	100	100
32	e	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
33	f	35/37 (95%)	35 (100%)	0	0	100	100
All	All	3935/4386 (90%)	3566 (91%)	367 (9%)	2 (0%)	49	72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	J	75	PRO
3	4	22	SER

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	2	52/54 (96%)	52 (100%)	0	100	100
2	3	18/19 (95%)	18 (100%)	0	100	100
3	4	367/372 (99%)	365 (100%)	2 (0%)	81	90
5	C	215/218 (99%)	215 (100%)	0	100	100
6	D	160/163 (98%)	160 (100%)	0	100	100
7	E	169/173 (98%)	167 (99%)	2 (1%)	63	79
8	F	151/156 (97%)	148 (98%)	3 (2%)	48	71
9	G	148/150 (99%)	145 (98%)	3 (2%)	48	71
10	H	90/116 (78%)	90 (100%)	0	100	100
11	I	89/120 (74%)	88 (99%)	1 (1%)	65	80
12	J	93/108 (86%)	93 (100%)	0	100	100
13	K	119/120 (99%)	118 (99%)	1 (1%)	73	85
14	L	100/100 (100%)	100 (100%)	0	100	100
15	M	112/114 (98%)	112 (100%)	0	100	100
16	N	114/116 (98%)	114 (100%)	0	100	100
17	O	97/158 (61%)	96 (99%)	1 (1%)	68	82
18	P	93/94 (99%)	92 (99%)	1 (1%)	65	80
19	Q	100/100 (100%)	98 (98%)	2 (2%)	48	71
20	R	97/99 (98%)	96 (99%)	1 (1%)	68	82
21	S	81/83 (98%)	81 (100%)	0	100	100
22	T	90/117 (77%)	89 (99%)	1 (1%)	65	80
23	U	83/85 (98%)	83 (100%)	0	100	100
24	V	81/86 (94%)	79 (98%)	2 (2%)	42	66
25	W	77/168 (46%)	75 (97%)	2 (3%)	40	65
26	X	58/63 (92%)	58 (100%)	0	100	100
27	Y	50/51 (98%)	49 (98%)	1 (2%)	48	71
28	Z	58/66 (88%)	58 (100%)	0	100	100
29	b	43/46 (94%)	42 (98%)	1 (2%)	44	67
30	c	47/52 (90%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	d	35/36 (97%)	35 (100%)	0	100	100
32	e	53/54 (98%)	53 (100%)	0	100	100
33	f	35/35 (100%)	34 (97%)	1 (3%)	37	61
All	All	3175/3492 (91%)	3150 (99%)	25 (1%)	70	85

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	4	33	LEU
3	4	296	VAL
7	E	6	ASP
7	E	186	TYR
8	F	165	THR
8	F	169	ASN
8	F	182	PHE
9	G	18	THR
9	G	20	ASN
9	G	51	ILE
11	I	35	ASN
13	K	129	ASP
17	O	78	THR
18	P	47	ILE
19	Q	8	ASP
19	Q	20	SER
20	R	36	LYS
22	T	92	ILE
24	V	61	THR
24	V	97	ILE
25	W	47	LEU
25	W	66	ILE
27	Y	19	SER
29	b	29	THR
33	f	17	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
2	3	23	ASN
3	4	338	ASN
3	4	444	HIS

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Mol	Chain	Res	Type
5	C	87	ASN
5	C	227	ASN
6	D	21	ASN
6	D	130	HIS
7	E	202	ASN
8	F	31	ASN
8	F	44	ASN
8	F	134	ASN
8	F	142	GLN
11	I	100	ASN
12	J	106	GLN
15	M	69	ASN
15	M	89	GLN
17	O	77	HIS
18	P	3	HIS
18	P	50	GLN
19	Q	79	ASN
20	R	94	ASN
21	S	13	GLN
25	W	76	GLN
28	Z	43	ASN
30	c	31	ASN
30	c	44	ASN
33	f	4	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	A	2946/3120 (94%)	662 (22%)	23 (0%)
4	B	117/118 (99%)	29 (24%)	0
All	All	3063/3238 (94%)	691 (22%)	23 (0%)

All (691) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	B	4	A
4	B	5	C
4	B	6	G
4	B	8	C
4	B	9	G
4	B	10	G

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Mol	Chain	Res	Type
4	B	12	C
4	B	13	C
4	B	20	G
4	B	23	G
4	B	26	A
4	B	30	G
4	B	35	G
4	B	36	U
4	B	38	C
4	B	42	C
4	B	43	C
4	B	54	A
4	B	57	U
4	B	58	A
4	B	67	A
4	B	88	C
4	B	89	C
4	B	103	G
4	B	105	A
4	B	106	C
4	B	107	A
4	B	109	C
4	B	116	C
34	A	3	A
34	A	7	U
34	A	9	U
34	A	10	A
34	A	12	G
34	A	20	G
34	A	23	G
34	A	31	U
34	A	41	A
34	A	42	G
34	A	48	G
34	A	60	A
34	A	66	C
34	A	68	A
34	A	69	U
34	A	71	A
34	A	72	G
34	A	91	C
34	A	94	G

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Mol	Chain	Res	Type
34	A	96	G
34	A	97	U
34	A	98	U
34	A	99	G
34	A	115	A
34	A	116	A
34	A	117	U
34	A	122	A
34	A	125	C
34	A	128	G
34	A	143	G
34	A	144	U
34	A	145	G
34	A	151	A
34	A	162	A
34	A	164	A
34	A	174	G
34	A	175	G
34	A	180	A
34	A	195	A
34	A	198	A
34	A	212	A
34	A	214	G
34	A	215	A
34	A	218	A
34	A	221	A
34	A	227	A
34	A	229	U
34	A	230	G
34	A	233	A
34	A	246	U
34	A	248	G
34	A	263	G
34	A	264	G
34	A	265	A
34	A	268	G
34	A	274	C
34	A	275	C
34	A	276	G
34	A	278	A
34	A	283	U
34	A	285	U

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Mol	Chain	Res	Type
34	A	286	G
34	A	287	A
34	A	288	U
34	A	289	A
34	A	290	C
34	A	291	C
34	A	292	G
34	A	301	U
34	A	302	U
34	A	303	G
34	A	304	U
34	A	307	G
34	A	315	U
34	A	316	U
34	A	318	U
34	A	319	G
34	A	324	C
34	A	325	U
34	A	326	A
34	A	327	U
34	A	330	U
34	A	331	U
34	A	334	G
34	A	335	G
34	A	336	C
34	A	337	U
34	A	338	C
34	A	340	A
34	A	342	C
34	A	343	U
34	A	349	G
34	A	350	A
34	A	351	G
34	A	353	G
34	A	356	G
34	A	357	U
34	A	363	A
34	A	364	A
34	A	366	G
34	A	367	U
34	A	370	U
34	A	371	G

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Mol	Chain	Res	Type
34	A	384	G
34	A	385	G
34	A	386	C
34	A	387	U
34	A	392	A
34	A	393	U
34	A	411	G
34	A	412	A
34	A	413	G
34	A	434	G
34	A	439	C
34	A	445	U
34	A	446	G
34	A	450	G
34	A	451	U
34	A	452	G
34	A	453	U
34	A	454	U
34	A	455	C
34	A	460	G
34	A	469	G
34	A	474	G
34	A	482	U
34	A	484	C
34	A	489	A
34	A	490	A
34	A	491	U
34	A	494	G
34	A	500	A
34	A	505	C
34	A	512	G
34	A	516	G
34	A	517	A
34	A	519	U
34	A	524	C
34	A	527	A
34	A	528	G
34	A	531	A
34	A	543	U
34	A	545	A
34	A	555	G
34	A	569	G

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Mol	Chain	Res	Type
34	A	578	G
34	A	591	G
34	A	592	A
34	A	594	U
34	A	595	A
34	A	596	C
34	A	597	C
34	A	600	A
34	A	605	G
34	A	614	C
34	A	617	U
34	A	618	C
34	A	619	C
34	A	620	G
34	A	635	G
34	A	636	U
34	A	637	G
34	A	638	U
34	A	642	G
34	A	655	G
34	A	658	U
34	A	665	G
34	A	667	A
34	A	679	G
34	A	684	G
34	A	691	U
34	A	692	C
34	A	696	A
34	A	697	G
34	A	704	C
34	A	706	G
34	A	707	G
34	A	709	U
34	A	721	A
34	A	724	G
34	A	725	A
34	A	731	A
34	A	737	A
34	A	739	U
34	A	741	G
34	A	743	G
34	A	747	A

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Mol	Chain	Res	Type
34	A	755	A
34	A	756	A
34	A	758	A
34	A	759	G
34	A	760	U
34	A	761	G
34	A	762	U
34	A	764	U
34	A	765	G
34	A	766	G
34	A	770	A
34	A	801	U
34	A	826	G
34	A	828	G
34	A	830	A
34	A	836	G
34	A	838	G
34	A	839	U
34	A	840	G
34	A	841	G
34	A	845	C
34	A	862	U
34	A	872	G
34	A	879	A
34	A	890	G
34	A	891	G
34	A	897	A
34	A	899	G
34	A	900	G
34	A	904	A
34	A	907	A
34	A	920	G
34	A	927	C
34	A	942	U
34	A	944	A
34	A	963	U
34	A	972	A
34	A	974	G
34	A	981	U
34	A	982	A
34	A	993	G
34	A	994	A

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Mol	Chain	Res	Type
34	A	998	G
34	A	999	C
34	A	1002	C
34	A	1003	A
34	A	1004	C
34	A	1008	G
34	A	1009	U
34	A	1010	U
34	A	1012	C
34	A	1017	G
34	A	1024	A
34	A	1025	A
34	A	1029	C
34	A	1030	C
34	A	1042	A
34	A	1048	A
34	A	1049	G
34	A	1063	G
34	A	1075	U
34	A	1076	A
34	A	1078	G
34	A	1085	G
34	A	1092	G
34	A	1098	A
34	A	1101	A
34	A	1102	G
34	A	1114	G
34	A	1115	G
34	A	1117	U
34	A	1130	C
34	A	1131	G
34	A	1135	G
34	A	1140	G
34	A	1141	U
34	A	1144	A
34	A	1151	U
34	A	1152	G
34	A	1158	U
34	A	1176	G
34	A	1177	G
34	A	1184	U
34	A	1187	A

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Mol	Chain	Res	Type
34	A	1188	A
34	A	1189	G
34	A	1191	A
34	A	1196	C
34	A	1201	G
34	A	1203	A
34	A	1205	G
34	A	1206	A
34	A	1207	G
34	A	1208	U
34	A	1212	U
34	A	1213	A
34	A	1214	A
34	A	1215	U
34	A	1225	G
34	A	1228	A
34	A	1229	A
34	A	1230	G
34	A	1235	U
34	A	1237	U
34	A	1250	U
34	A	1251	A
34	A	1253	C
34	A	1254	G
34	A	1260	C
34	A	1261	A
34	A	1285	G
34	A	1292	U
34	A	1293	G
34	A	1317	G
34	A	1326	G
34	A	1335	G
34	A	1343	G
34	A	1344	A
34	A	1347	G
34	A	1351	G
34	A	1352	A
34	A	1353	G
34	A	1365	G
34	A	1368	A
34	A	1371	G
34	A	1380	A

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Mol	Chain	Res	Type
34	A	1386	G
34	A	1387	A
34	A	1399	A
34	A	1405	U
34	A	1409	C
34	A	1415	A
34	A	1416	A
34	A	1436	C
34	A	1444	U
34	A	1456	G
34	A	1465	C
34	A	1467	U
34	A	1475	G
34	A	1477	C
34	A	1480	A
34	A	1493	A
34	A	1494	U
34	A	1499	A
34	A	1501	C
34	A	1502	G
34	A	1509	U
34	A	1512	U
34	A	1528	G
34	A	1529	U
34	A	1531	C
34	A	1533	U
34	A	1534	C
34	A	1535	C
34	A	1538	G
34	A	1542	A
34	A	1543	A
34	A	1545	C
34	A	1622	G
34	A	1623	U
34	A	1624	U
34	A	1629	G
34	A	1632	G
34	A	1636	A
34	A	1640	A
34	A	1641	U
34	A	1645	G
34	A	1648	A

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Mol	Chain	Res	Type
34	A	1649	C
34	A	1673	A
34	A	1674	G
34	A	1676	G
34	A	1680	A
34	A	1681	U
34	A	1703	G
34	A	1709	U
34	A	1710	A
34	A	1711	G
34	A	1714	A
34	A	1716	A
34	A	1717	U
34	A	1727	A
34	A	1728	U
34	A	1729	A
34	A	1730	U
34	A	1731	A
34	A	1737	A
34	A	1746	G
34	A	1754	G
34	A	1755	A
34	A	1756	G
34	A	1758	G
34	A	1759	A
34	A	1760	G
34	A	1762	C
34	A	1767	U
34	A	1768	C
34	A	1769	G
34	A	1778	A
34	A	1780	G
34	A	1786	G
34	A	1788	G
34	A	1789	A
34	A	1798	U
34	A	1810	A
34	A	1825	C
34	A	1826	A
34	A	1828	A
34	A	1832	A
34	A	1852	A

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Mol	Chain	Res	Type
34	A	1853	A
34	A	1864	U
34	A	1866	C
34	A	1871	G
34	A	1872	A
34	A	1883	A
34	A	1885	G
34	A	1892	G
34	A	1904	C
34	A	1911	U
34	A	1933	G
34	A	1938	G
34	A	1946	U
34	A	1947	U
34	A	1959	G
34	A	1981	U
34	A	1985	A
34	A	1990	A
34	A	1999	U
34	A	2016	G
34	A	2017	C
34	A	2018	G
34	A	2019	A
34	A	2025	C
34	A	2033	U
34	A	2038	A
34	A	2046	A
34	A	2051	U
34	A	2052	G
34	A	2053	C
34	A	2054	C
34	A	2055	C
34	A	2056	G
34	A	2057	G
34	A	2058	U
34	A	2062	G
34	A	2063	G
34	A	2120	A
34	A	2122	U
34	A	2123	A
34	A	2124	A
34	A	2125	A

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Mol	Chain	Res	Type
34	A	2126	C
34	A	2127	G
34	A	2128	G
34	A	2129	C
34	A	2130	G
34	A	2131	G
34	A	2133	G
34	A	2134	G
34	A	2135	U
34	A	2146	A
34	A	2147	U
34	A	2149	C
34	A	2150	U
34	A	2151	A
34	A	2154	G
34	A	2156	A
34	A	2157	G
34	A	2158	C
34	A	2159	G
34	A	2160	A
34	A	2162	A
34	A	2163	U
34	A	2193	A
34	A	2194	A
34	A	2195	U
34	A	2196	G
34	A	2199	G
34	A	2215	U
34	A	2217	U
34	A	2220	C
34	A	2244	A
34	A	2245	C
34	A	2247	A
34	A	2255	A
34	A	2256	G
34	A	2257	A
34	A	2267	C
34	A	2277	G
34	A	2279	C
34	A	2280	G
34	A	2282	A
34	A	2284	A

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Mol	Chain	Res	Type
34	A	2285	G
34	A	2286	A
34	A	2310	G
34	A	2315	U
34	A	2316	G
34	A	2319	G
34	A	2320	C
34	A	2327	C
34	A	2330	U
34	A	2333	G
34	A	2336	U
34	A	2337	A
34	A	2338	G
34	A	2339	G
34	A	2340	A
34	A	2341	U
34	A	2342	A
34	A	2345	U
34	A	2346	G
34	A	2347	G
34	A	2348	G
34	A	2349	A
34	A	2351	A
34	A	2352	C
34	A	2353	U
34	A	2354	G
34	A	2355	U
34	A	2357	A
34	A	2358	A
34	A	2360	C
34	A	2361	U
34	A	2368	C
34	A	2369	C
34	A	2370	A
34	A	2371	G
34	A	2373	G
34	A	2378	U
34	A	2379	G
34	A	2380	G
34	A	2381	A
34	A	2382	G
34	A	2384	C

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Mol	Chain	Res	Type
34	A	2385	G
34	A	2386	U
34	A	2387	U
34	A	2388	G
34	A	2389	U
34	A	2390	U
34	A	2392	A
34	A	2394	A
34	A	2396	A
34	A	2399	A
34	A	2400	C
34	A	2402	C
34	A	2404	G
34	A	2405	A
34	A	2406	U
34	A	2407	C
34	A	2409	U
34	A	2411	U
34	A	2413	G
34	A	2418	U
34	A	2421	A
34	A	2427	G
34	A	2436	A
34	A	2447	G
34	A	2449	A
34	A	2462	G
34	A	2463	G
34	A	2467	U
34	A	2503	G
34	A	2507	C
34	A	2511	A
34	A	2512	A
34	A	2527	G
34	A	2528	G
34	A	2529	A
34	A	2531	G
34	A	2532	G
34	A	2533	C
34	A	2534	A
34	A	2541	U
34	A	2542	G
34	A	2543	U

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Mol	Chain	Res	Type
34	A	2547	G
34	A	2549	G
34	A	2557	A
34	A	2558	C
34	A	2559	A
34	A	2560	A
34	A	2571	C
34	A	2574	C
34	A	2585	U
34	A	2587	U
34	A	2607	G
34	A	2609	A
34	A	2615	G
34	A	2627	C
34	A	2628	U
34	A	2630	A
34	A	2649	A
34	A	2650	A
34	A	2653	G
34	A	2654	A
34	A	2656	A
34	A	2659	A
34	A	2665	C
34	A	2672	A
34	A	2693	A
34	A	2694	G
34	A	2698	C
34	A	2700	A
34	A	2715	U
34	A	2726	G
34	A	2729	G
34	A	2742	A
34	A	2744	C
34	A	2753	G
34	A	2759	G
34	A	2776	U
34	A	2777	G
34	A	2778	U
34	A	2779	U
34	A	2788	A
34	A	2790	A
34	A	2791	G

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Mol	Chain	Res	Type
34	A	2797	C
34	A	2809	U
34	A	2810	U
34	A	2826	A
34	A	2827	G
34	A	2833	U
34	A	2834	C
34	A	2837	U
34	A	2838	A
34	A	2839	U
34	A	2847	G
34	A	2848	C
34	A	2854	A
34	A	2865	G
34	A	2883	G
34	A	2913	U
34	A	2915	C
34	A	2926	A
34	A	2936	C
34	A	2950	C
34	A	2957	A
34	A	2968	G
34	A	2969	C
34	A	2972	A
34	A	2975	G
34	A	2976	C
34	A	2981	A
34	A	2985	G
34	A	2989	A
34	A	3002	A
34	A	3003	C
34	A	3014	A
34	A	3015	C
34	A	3020	U
34	A	3021	A
34	A	3022	G
34	A	3023	G
34	A	3025	G
34	A	3027	G
34	A	3029	U
34	A	3041	C
34	A	3042	A

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Mol	Chain	Res	Type
34	A	3052	A
34	A	3053	U
34	A	3055	G
34	A	3070	G
34	A	3080	A
34	A	3082	U
34	A	3088	C
34	A	3093	A
34	A	3101	C
34	A	3104	A
34	A	3112	A
34	A	3114	A
34	A	3115	A

All (23) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	A	97	U
34	A	161	U
34	A	325	U
34	A	326	A
34	A	980	C
34	A	981	U
34	A	1002	C
34	A	1151	U
34	A	1207	G
34	A	1234	U
34	A	1758	G
34	A	2053	C
34	A	2054	C
34	A	2121	G
34	A	2122	U
34	A	2123	A
34	A	2124	A
34	A	2125	A
34	A	2336	U
34	A	2350	G
34	A	2975	G
34	A	2980	U
34	A	3113	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](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
35	GCP	4	501	-	32,34,34	1.37	5 (15%)	49,54,54	1.85	6 (12%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	GCP	4	501	-	-	7/19/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	4	501	GCP	C5-C4	3.01	1.47	1.38
35	4	501	GCP	PG-O2G	2.82	1.61	1.55
35	4	501	GCP	PG-O3G	2.75	1.61	1.55
35	4	501	GCP	C6-N1	-2.59	1.34	1.38
35	4	501	GCP	C5-N7	-2.18	1.34	1.39

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	4	501	GCP	C5-C4-N3	-5.98	118.87	128.39
35	4	501	GCP	PB-O3A-PA	-5.08	115.78	132.37
35	4	501	GCP	C2-N3-C4	4.91	120.76	112.30
35	4	501	GCP	N9-C4-N3	4.30	134.54	125.95
35	4	501	GCP	C6-C5-N7	3.45	136.56	130.29
35	4	501	GCP	C4-C5-N7	-2.76	106.30	110.67

There are no chirality outliers.

All (7) torsion outliers are listed below:

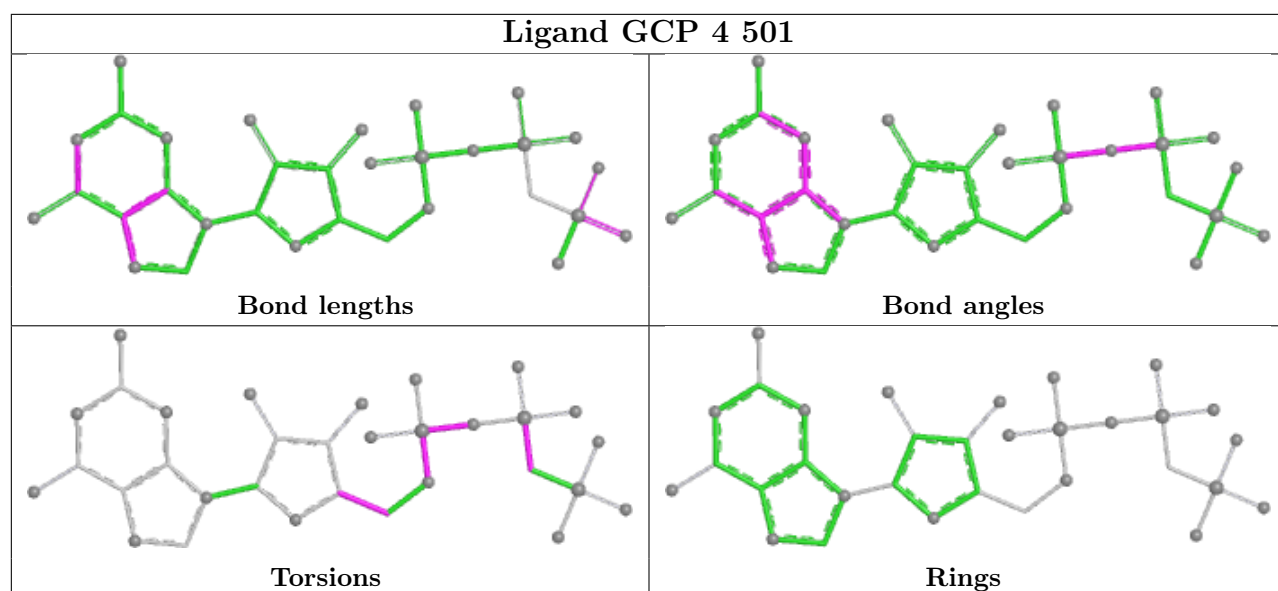
Mol	Chain	Res	Type	Atoms
35	4	501	GCP	C5'-O5'-PA-O3A
35	4	501	GCP	C5'-O5'-PA-O1A
35	4	501	GCP	C5'-O5'-PA-O2A
35	4	501	GCP	O4'-C4'-C5'-O5'
35	4	501	GCP	C3'-C4'-C5'-O5'
35	4	501	GCP	PG-C3B-PB-O1B
35	4	501	GCP	PB-O3A-PA-O1A

There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	4	501	GCP	11	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

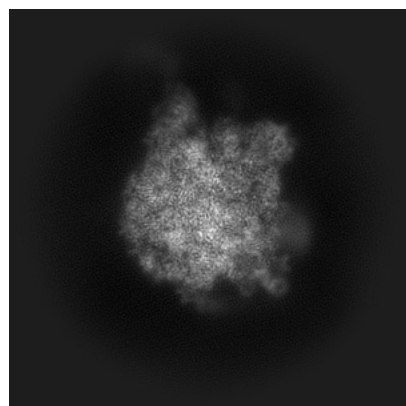
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43317. These allow visual inspection of the internal detail of the map and identification of artifacts.

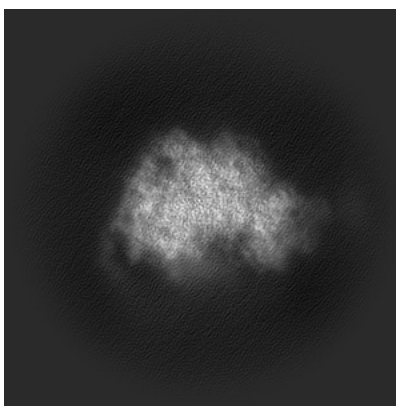
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

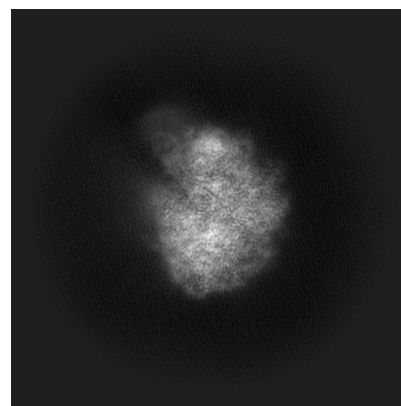
6.1.1 Primary map



X

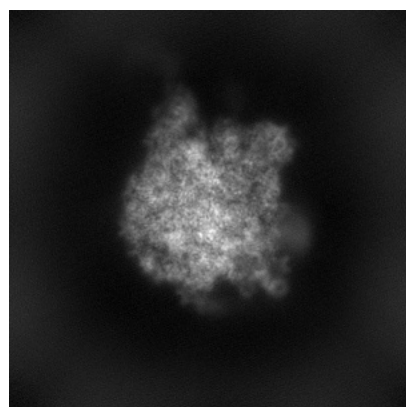


Y

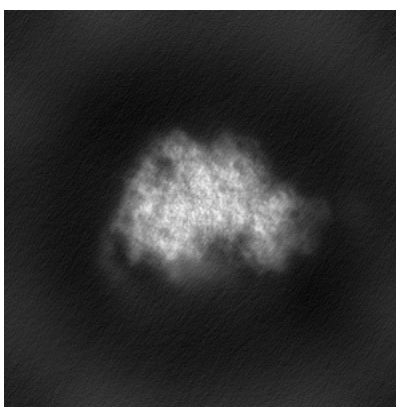


Z

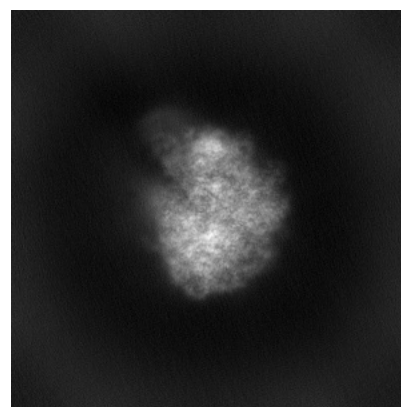
6.1.2 Raw map



X



Y

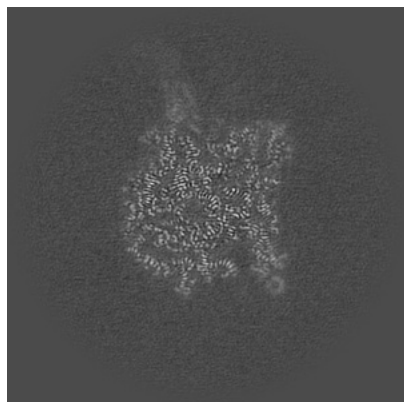


Z

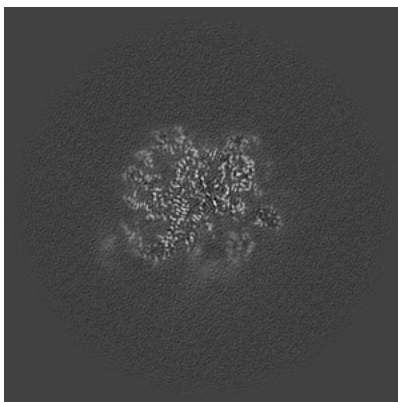
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

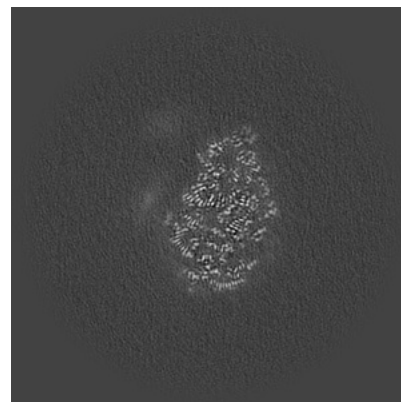
6.2.1 Primary map



X Index: 200

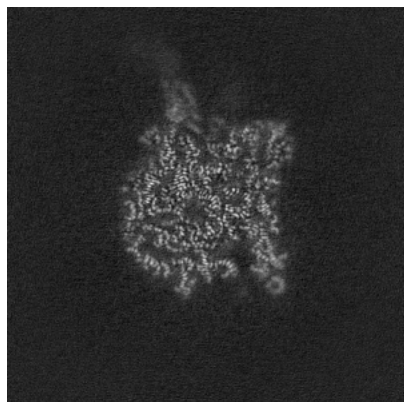


Y Index: 200

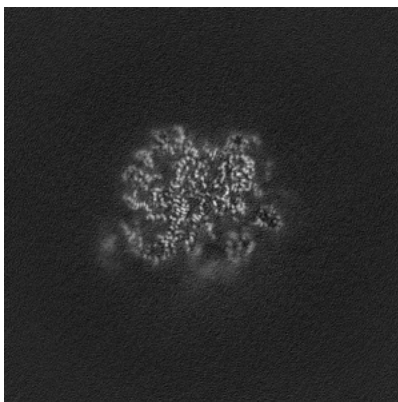


Z Index: 200

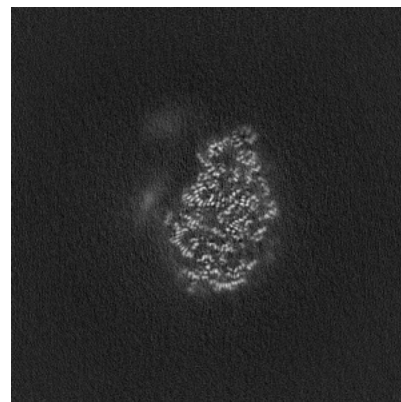
6.2.2 Raw map



X Index: 200



Y Index: 200

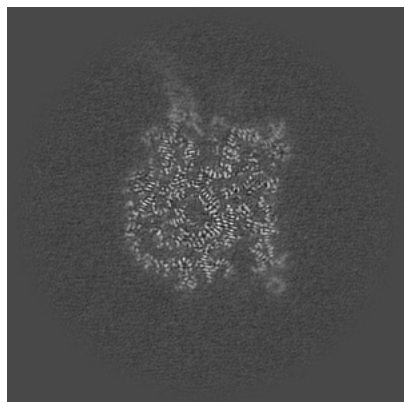


Z Index: 200

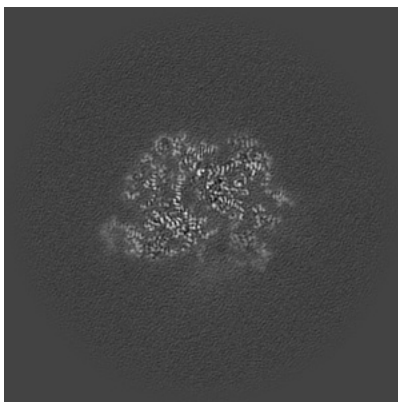
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

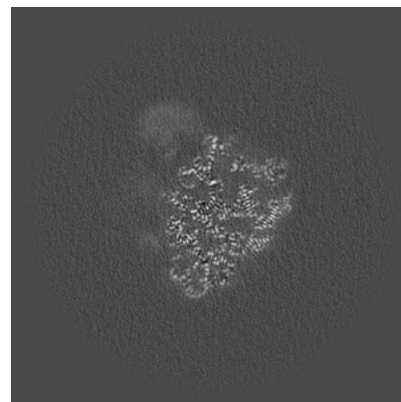
6.3.1 Primary map



X Index: 202

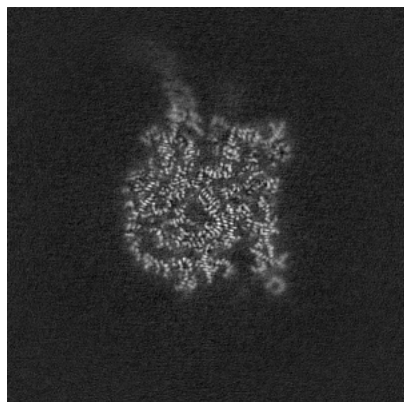


Y Index: 192

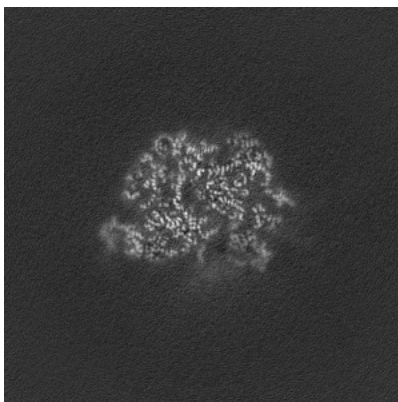


Z Index: 176

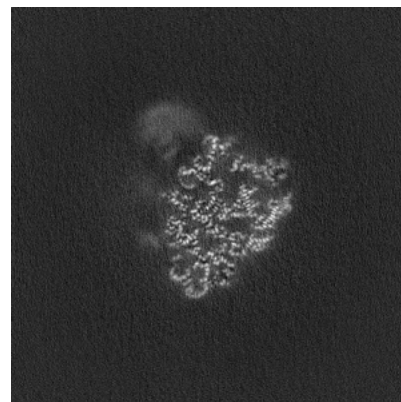
6.3.2 Raw map



X Index: 202



Y Index: 192

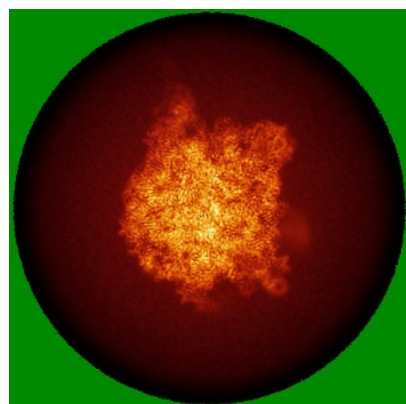


Z Index: 176

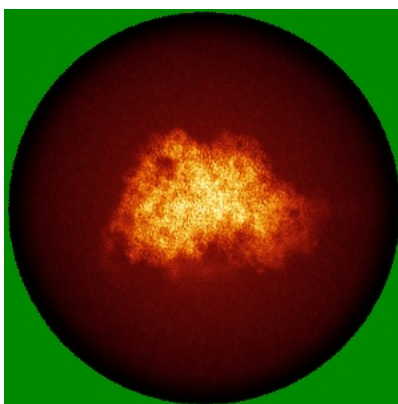
The images above show the largest variance slices of the map in three orthogonal directions.

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

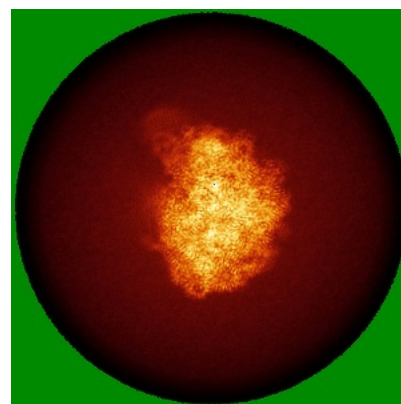
6.4.1 Primary map



X

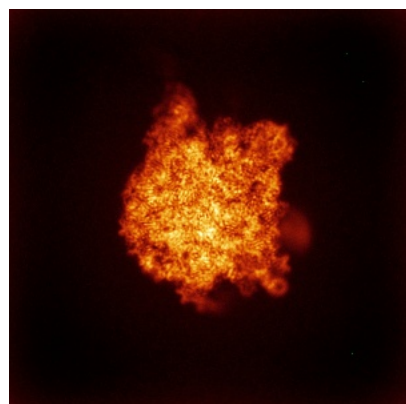


Y

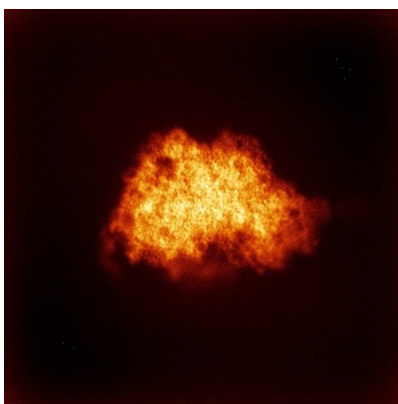


Z

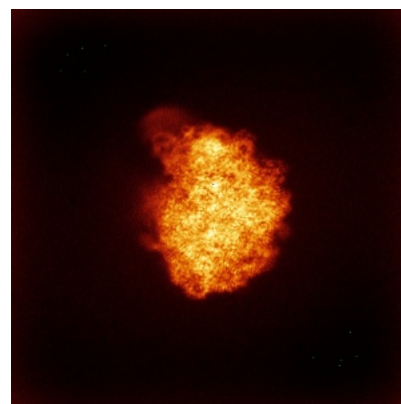
6.4.2 Raw map



X



Y



Z

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

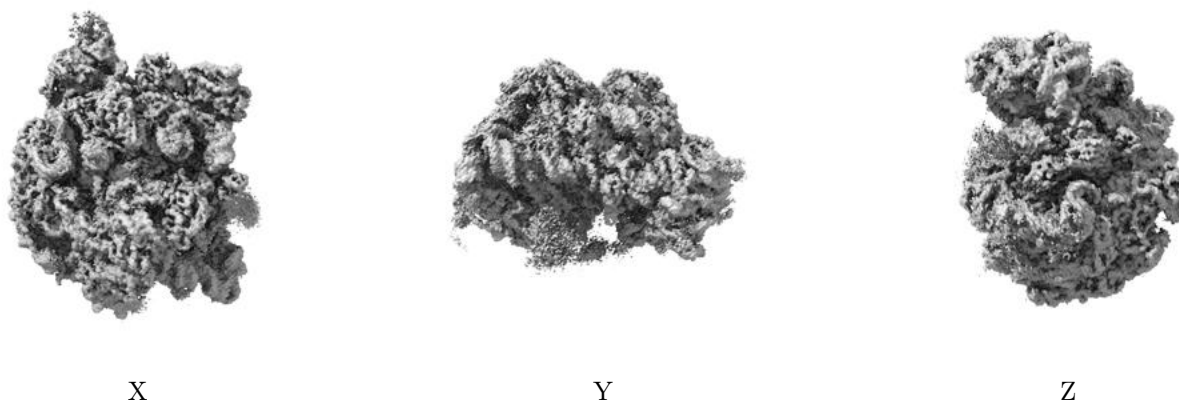
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.35. 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.

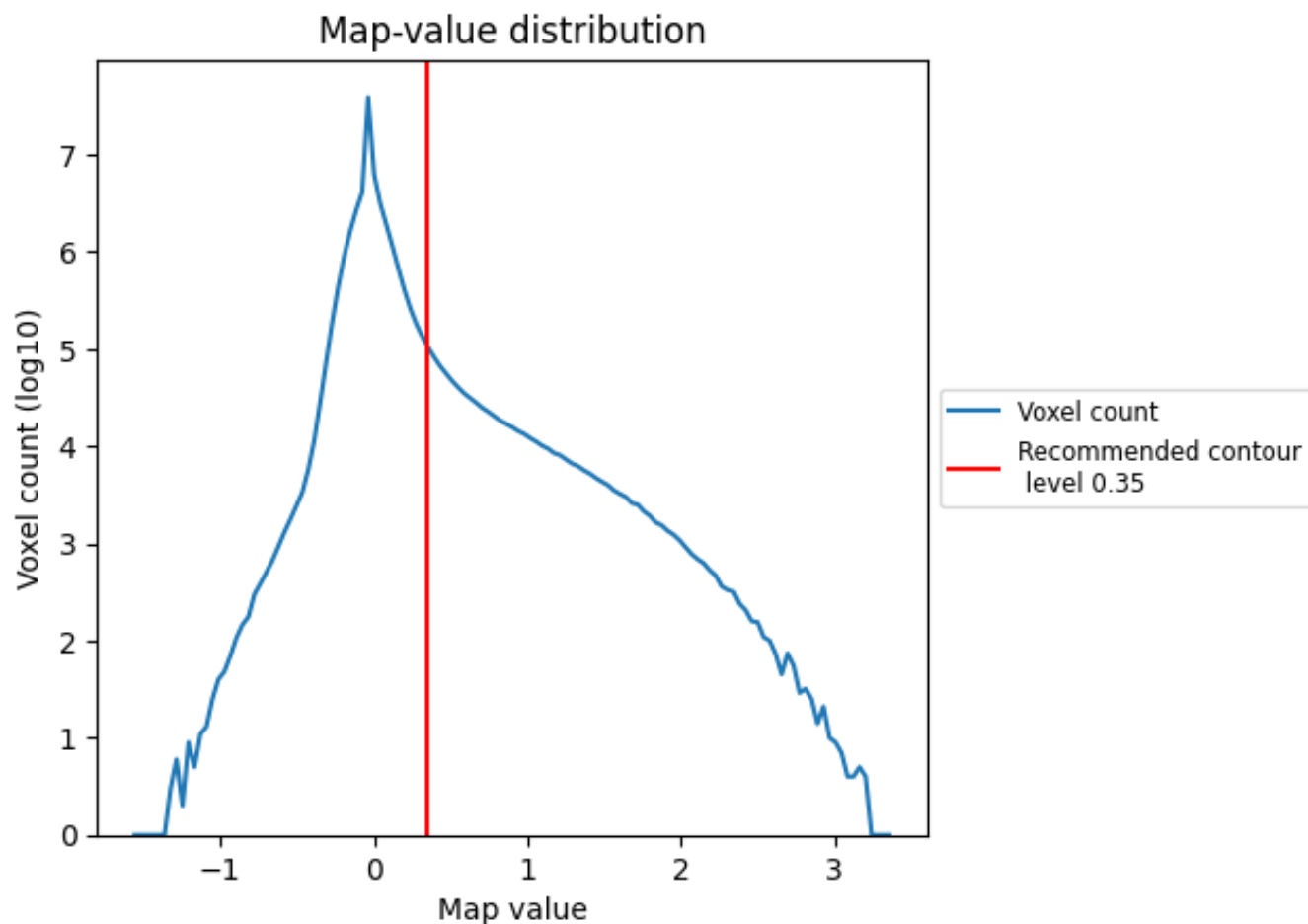
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

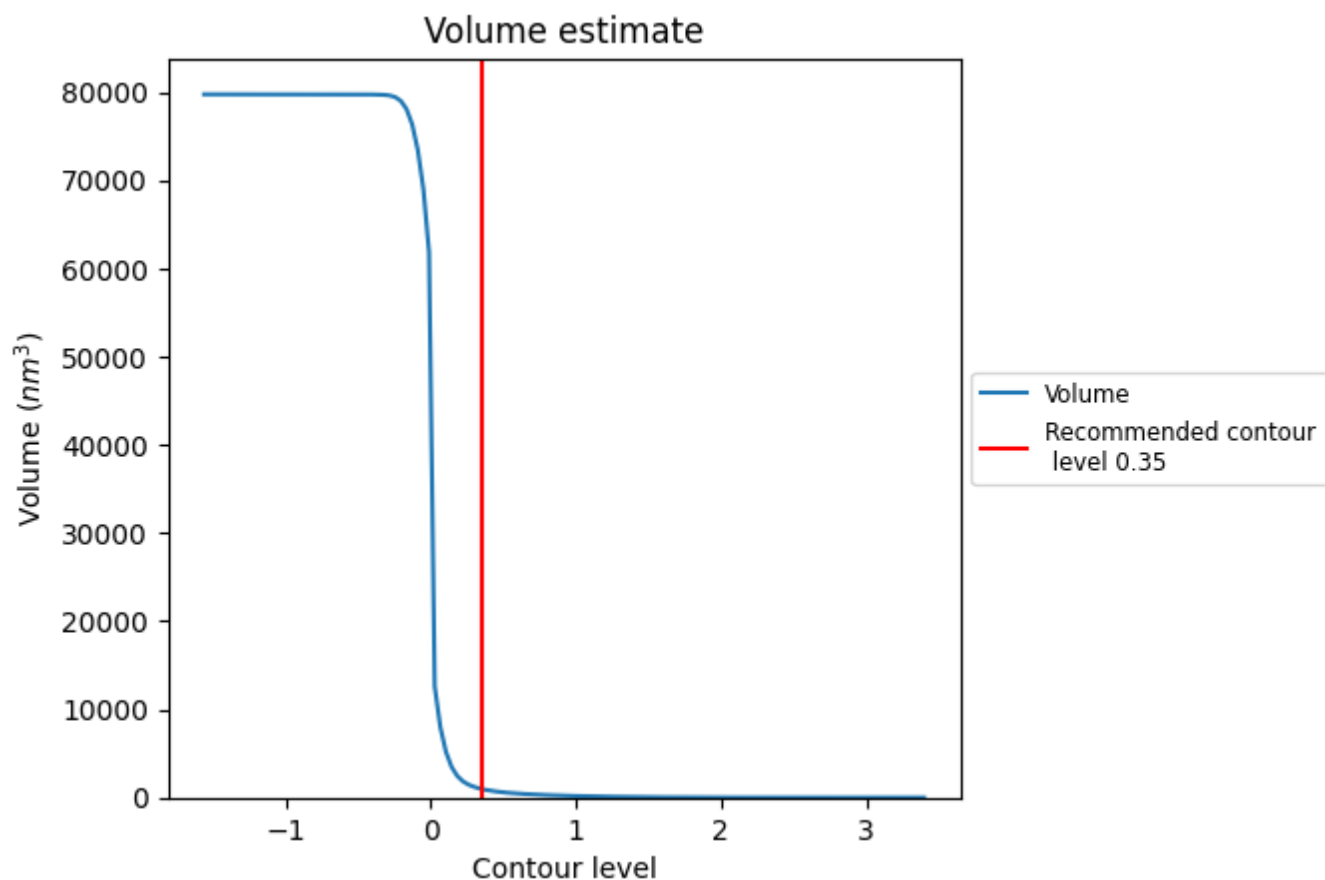
This section contains the results of statistical analysis of the map.

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.

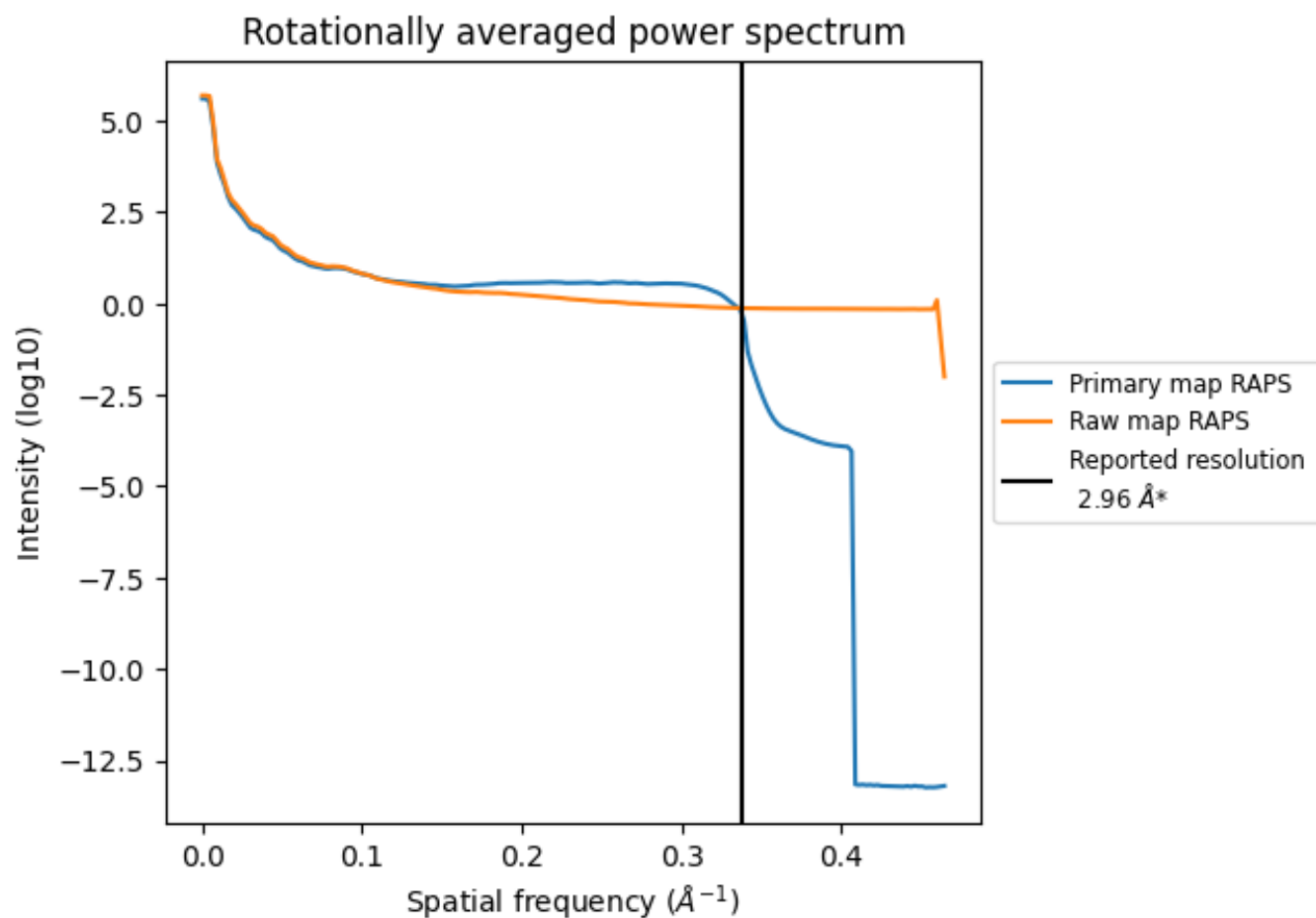
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 982 nm³; this corresponds to an approximate mass of 887 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 ⓘ

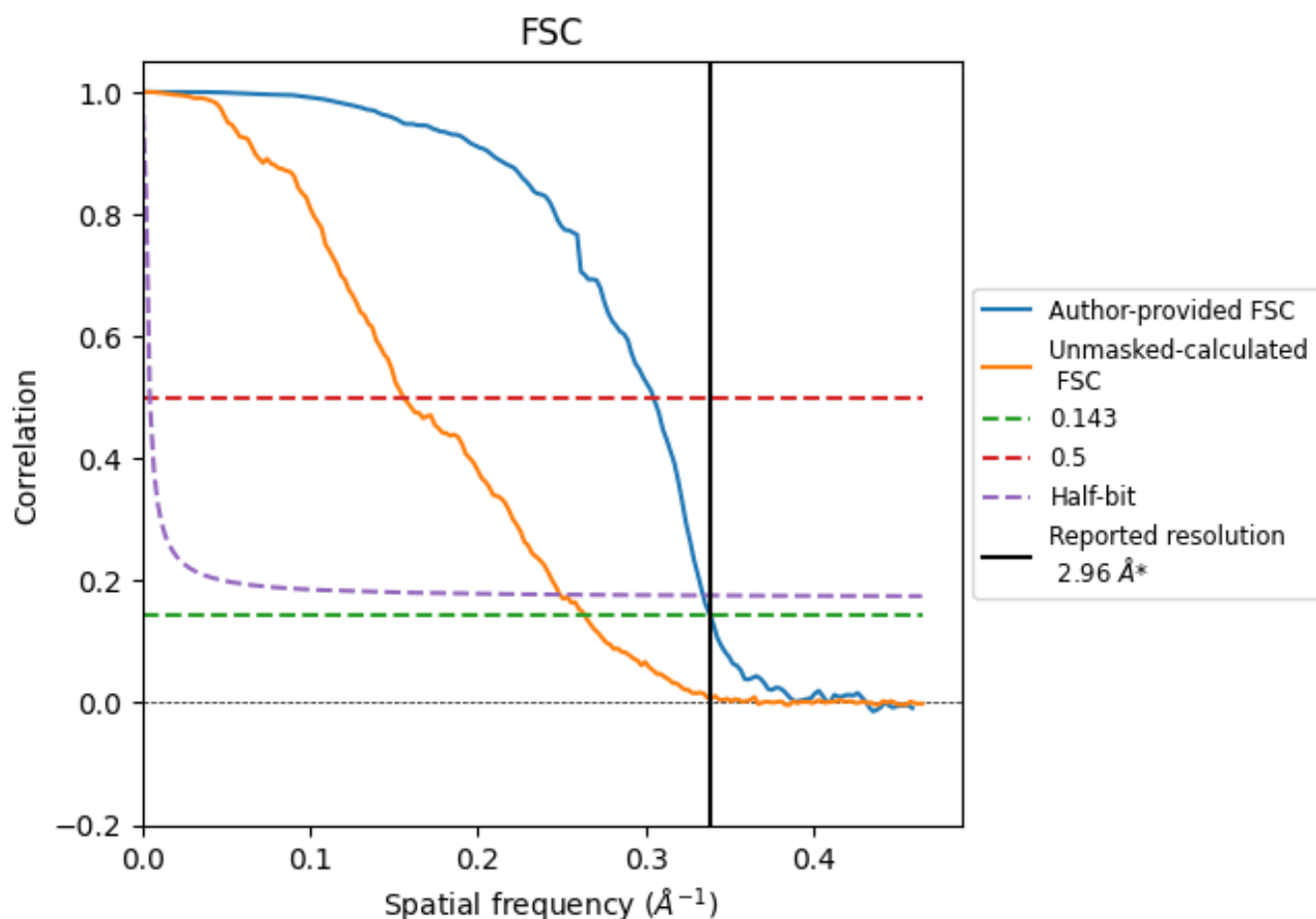


*Reported resolution corresponds to spatial frequency of 0.338 Å⁻¹

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 0.338 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

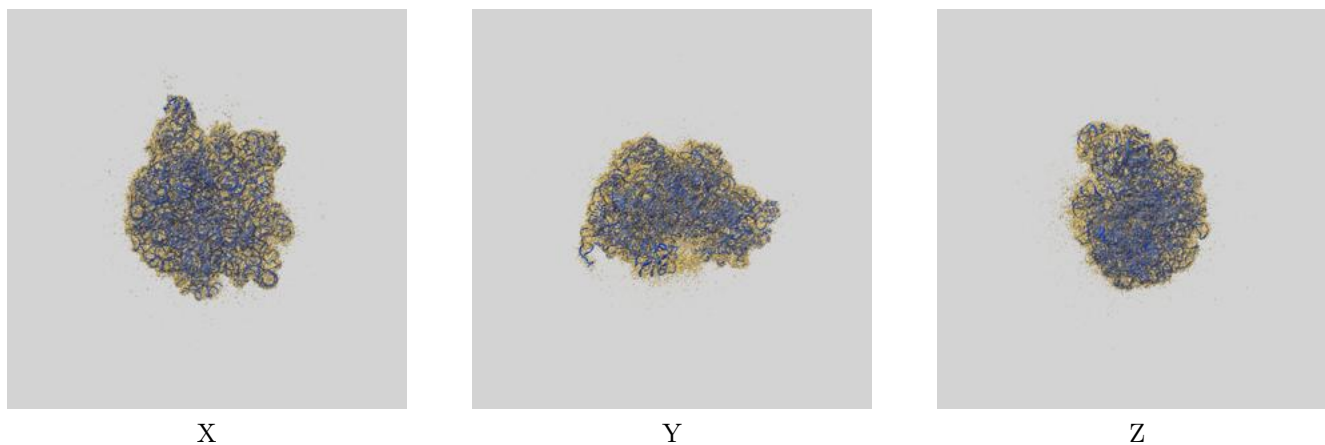
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.96	-	-
Author-provided FSC curve	2.96	3.28	2.99
Unmasked-calculated*	3.79	6.43	4.02

*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 3.79 differs from the reported value 2.96 by more than 10 %

9 Map-model fit [i](#)

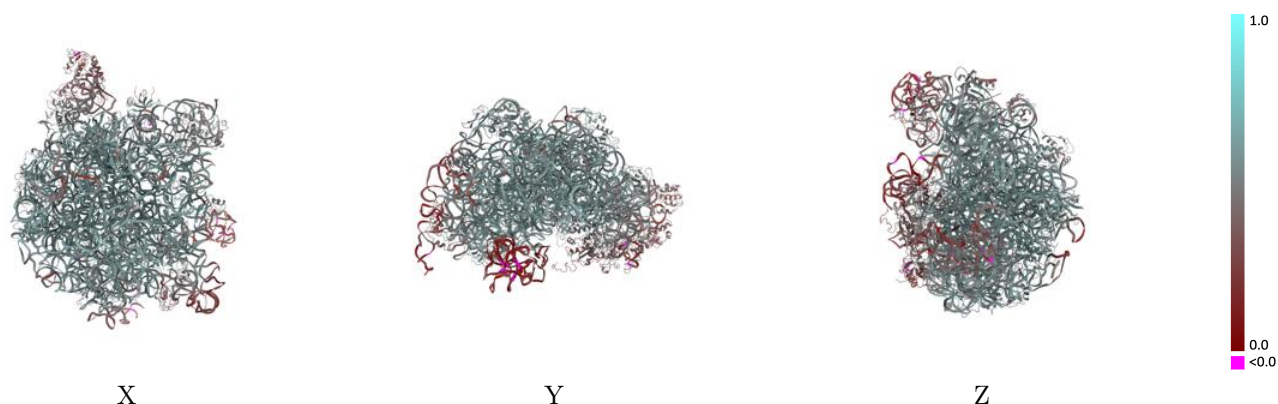
This section contains information regarding the fit between EMDB map EMD-43317 and PDB model 8VKI. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



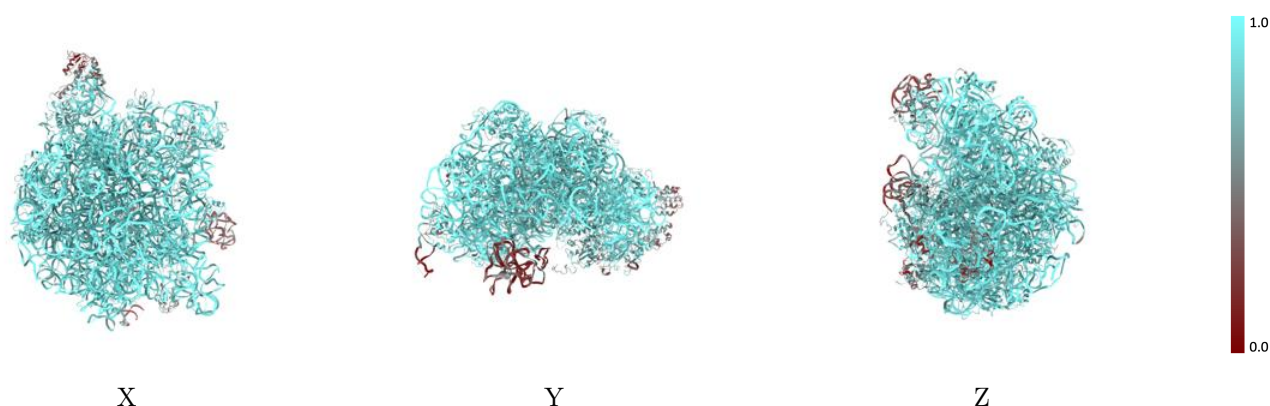
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



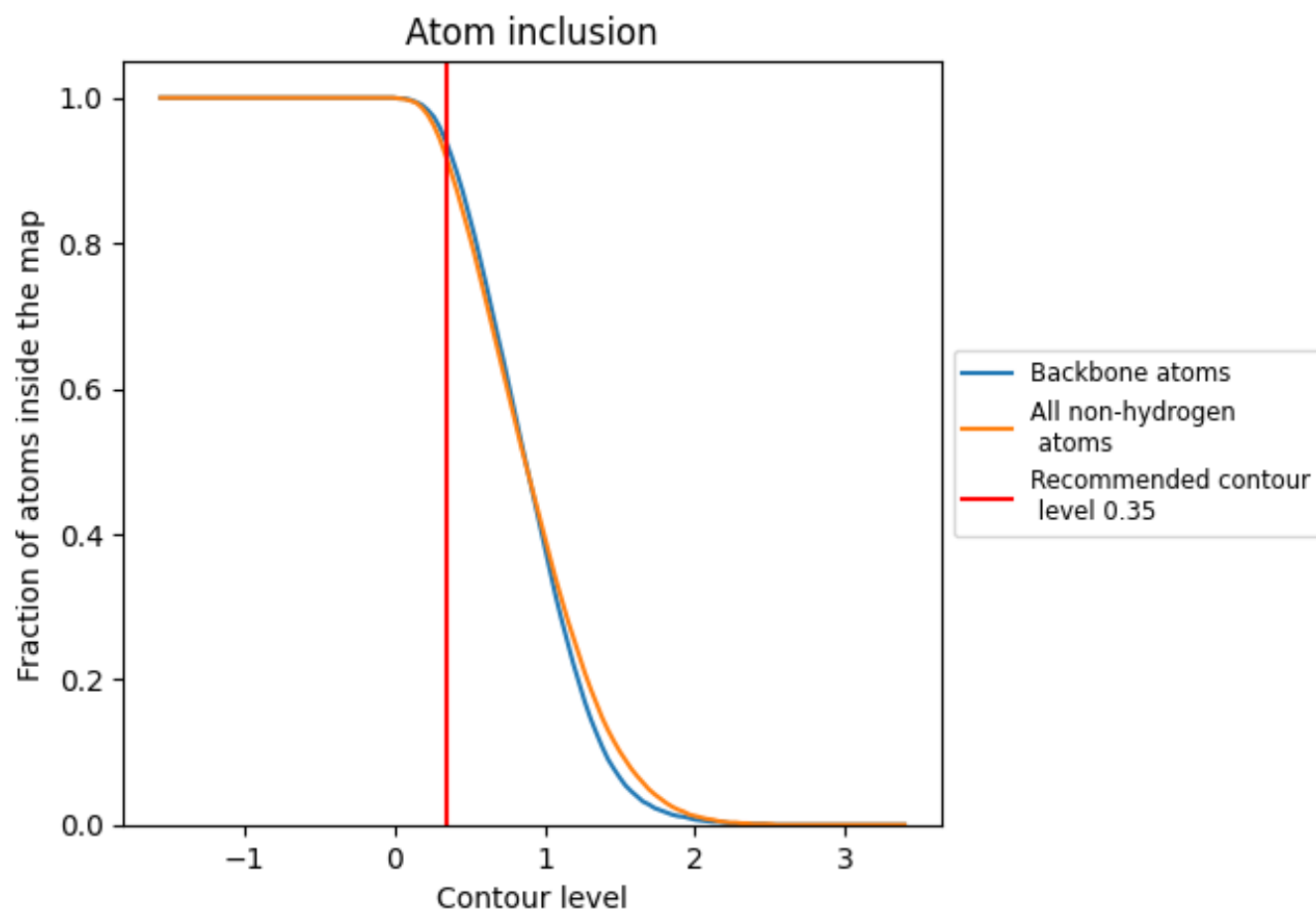
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.35).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9150	 0.5200
2	 0.9350	 0.5680
3	 0.9550	 0.6090
4	 0.7710	 0.4150
A	 0.9370	 0.5250
B	 0.9700	 0.5110
C	 0.9330	 0.5660
D	 0.9530	 0.5670
E	 0.9240	 0.5470
F	 0.7600	 0.3950
G	 0.8260	 0.4740
H	 0.7230	 0.4480
I	 0.4020	 0.3090
J	 0.4590	 0.3130
K	 0.9520	 0.5700
L	 0.9310	 0.5560
M	 0.9350	 0.5590
N	 0.9280	 0.5670
O	 0.9500	 0.5720
P	 0.9050	 0.4960
Q	 0.8870	 0.5250
R	 0.9570	 0.5700
S	 0.9100	 0.5550
T	 0.9490	 0.5720
U	 0.9430	 0.5490
V	 0.8940	 0.5020
W	 0.8450	 0.5210
X	 0.9400	 0.5810
Y	 0.9690	 0.5700
Z	 0.9250	 0.5290
b	 0.9680	 0.5820
c	 0.9570	 0.5620
d	 0.9600	 0.5930
e	 0.9750	 0.5890
f	 0.9650	 0.5780

