



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 04:16 PM UTC

PDB ID : 8RJC / pdb_00008rjc
EMDB ID : EMD-19197
Title : Structure of the rabbit 80S ribosome stalled on a 2-TMD rhodopsin intermediate in complex with Sec61-TRAP, open conformation 1
Authors : Lewis, A.J.O.; Hegde, R.S.
Deposited on : 2023-12-20
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

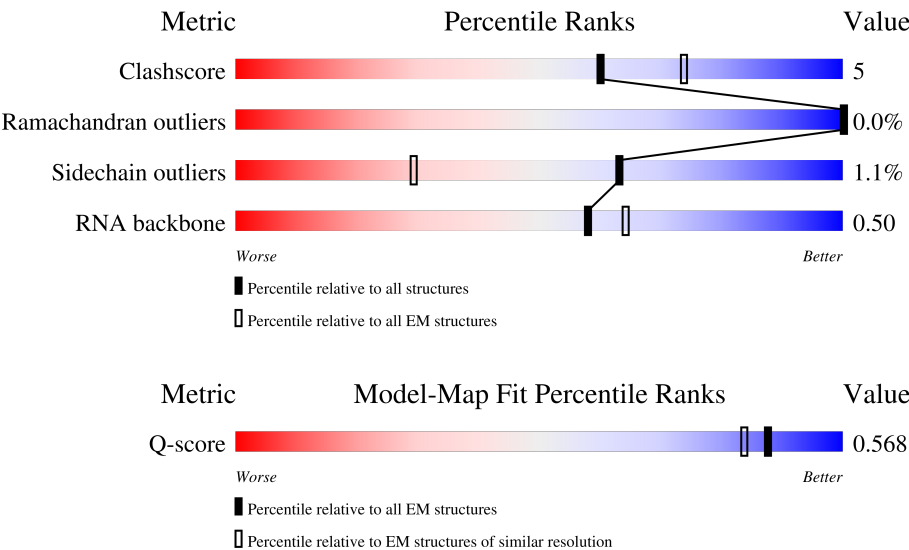
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.90 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	12906 (2.41 - 3.40)

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	1	476	17% 80% 17%
2	2	96	24% 8% 67%
3	3	68	74% 24%

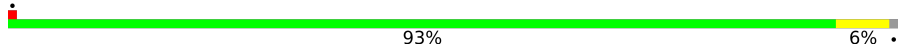
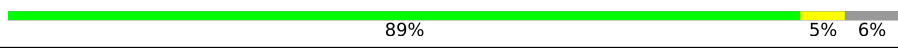
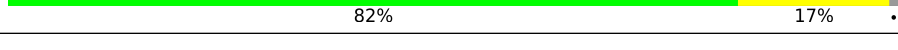
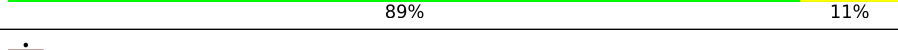
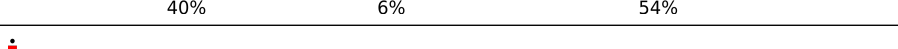
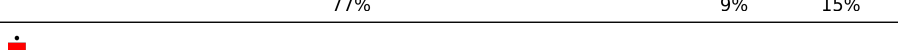
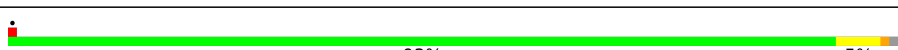
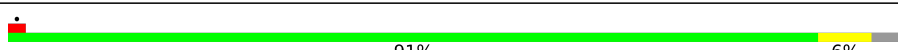
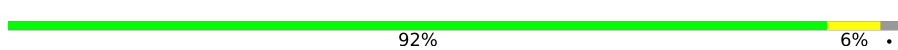
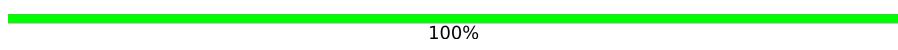
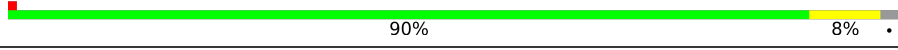
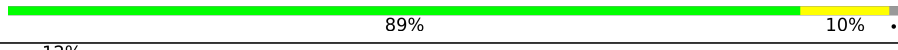
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	4	66	
5	5	286	
6	6	183	
7	7	185	
8	8	173	
9	9	593	
10	A	257	
11	B	229	
12	C	425	
13	D	297	
14	E	291	
15	F	247	
16	G	319	
17	H	192	
18	I	214	
19	J	178	
20	K	3543	
21	L	211	
22	M	218	
23	N	204	
24	O	203	
25	P	184	
26	Q	187	
27	R	196	
28	S	176	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	T	160	
30	U	128	
31	V	140	
32	W	157	
33	X	156	
34	Y	145	
35	Z	136	
36	a	148	
37	b	226	
38	c	115	
39	d	125	
40	e	135	
41	f	110	
42	g	116	
43	h	123	
44	i	105	
45	j	97	
46	k	70	
47	l	51	
48	m	102	
49	n	25	
50	o	106	
51	p	92	
52	q	76	
53	r	137	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	u	120	79% 20%
55	v	156	66% 26% 8%
56	w	403	86% 12%

2 Entry composition [i](#)

There are 58 unique types of molecules in this entry. The entry contains 255550 atoms, of which 108756 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 Protein transport protein Sec61 subunit alpha isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	1	461	Total	C	H	N	O	S	0	0
			7275	2347	3700	576	629	23		

- Molecule 2 is a protein called Protein transport protein Sec61 subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	2	32	Total	C	H	N	O	S	0	0
			524	171	273	40	38	2		

- Molecule 3 is a protein called Protein transport protein Sec61 subunit gamma.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	3	66	Total	C	H	N	O	S	0	0
			1105	351	571	92	86	5		

- Molecule 4 is a protein called Stress-associated endoplasmic reticulum protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	4	31	Total	C	H	N	O	S	0	0
			504	145	260	55	43	1		

- Molecule 5 is a protein called Translocon-associated protein subunit alpha.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	5	178	Total	C	H	N	O	S	0	0
			2813	919	1390	231	269	4		

- Molecule 6 is a protein called Translocon-associated protein subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	6	162	Total	C	H	N	O	S	0	0
			2507	813	1244	212	236	2		

- Molecule 7 is a protein called Translocon-associated protein subunit gamma.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	7	179	Total	C	H	N	O	S	0	0
			2942	947	1490	239	263	3		

- Molecule 8 is a protein called Translocon-associated protein subunit delta.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	8	150	Total	C	H	N	O	S	0	0
			2335	755	1149	199	229	3		

- Molecule 9 is a protein called Calnexin.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	9	38	Total	C	H	N	O	S	0	0
			610	206	309	43	50	2		

- Molecule 10 is a protein called Ribosomal protein L8.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	A	248	Total	C	H	N	O	S	0	0
			3892	1189	1994	389	314	6		

- Molecule 11 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	B	59	Total	C	H	N	O	S	0	0
			856	283	424	67	80	2		

- Molecule 12 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	C	362	Total	C	H	N	O	S	0	0
			5937	1812	3054	577	480	14		

- Molecule 13 is a protein called Ribosomal_L18_c domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	D	293	Total	C	H	N	O	S	0	0
			4816	1512	2425	438	427	14		

- Molecule 14 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	E	223	Total	C	H	N	O	S	0	0
			3754	1154	1963	341	293	3		

- Molecule 15 is a protein called Ribosomal Protein uL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	F	225	Total	C	H	N	O	S	0	0
			3872	1205	1997	358	303	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	61	ARG	GLY	conflict	UNP G1TUB1
F	93	ARG	GLY	conflict	UNP G1TUB1
F	131	MET	VAL	conflict	UNP G1TUB1
F	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 16 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	G	233	Total	C	H	N	O	S	0	0
			3908	1199	2029	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 17 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	H	190	Total	C	H	N	O	S	0	0
			3114	954	1598	284	272	6		

- Molecule 18 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	I	205	Total	C	H	N	O	S	0	0
			3380	1056	1716	321	274	13		

- Molecule 19 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	J	170	Total	C	H	N	O	S	0	0
			2763	861	1401	254	241	6		

- Molecule 20 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	K	3543	Total	C	H	N	O	P	0	0
			114335	33833	38363	13910	24686	3543		

- Molecule 21 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	L	210	Total	C	H	N	O	S	0	0
			3525	1065	1823	354	279	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	74	ARG	HIS	conflict	UNP G1TKB3
L	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 22 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	M	138	Total	C	H	N	O	S	0	0
			2349	727	1212	221	182	7		

- Molecule 23 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	N	203	Total	C	H	N	O	S	0	0
			3454	1072	1753	359	266	4		

- Molecule 24 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	O	199	Total	C	H	N	O	S	0	0
			3410	1051	1780	319	255	5		

- Molecule 25 is a protein called uL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	P	181	Total	C	H	N	O	S	0	0
			3012	924	1542	282	254	10		

- Molecule 26 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	Q	187	Total	C	H	N	O	S	0	0
			3153	946	1638	315	250	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	4	ASP	ASN	conflict	UNP G1TFE0
Q	14	ARG	TRP	conflict	UNP G1TFE0
Q	53	MET	LEU	conflict	UNP G1TFE0
Q	58	ARG	TRP	conflict	UNP G1TFE0
Q	75	ARG	GLN	conflict	UNP G1TFE0
Q	80	ALA	PRO	conflict	UNP G1TFE0
Q	86	VAL	ILE	conflict	UNP G1TFE0
Q	104	ARG	HIS	conflict	UNP G1TFE0
Q	110	ARG	CYS	conflict	UNP G1TFE0
Q	137	VAL	GLY	conflict	UNP G1TFE0
Q	157	GLY	ARG	conflict	UNP G1TFE0
Q	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 27 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	R	155	Total	C	H	N	O	S	0	0
			2730	808	1436	278	199	9		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	CYS	conflict	UNP G1TJR3
R	64	ARG	GLN	conflict	UNP G1TJR3
R	94	THR	LYS	conflict	UNP G1TJR3

- Molecule 28 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	S	176	Total	C	H	N	O	S	0	0
			2972	930	1510	285	236	11		

- Molecule 29 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	T	159	Total	C	H	N	O	S	0	0
			2667	823	1369	252	217	6		

- Molecule 30 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	U	102	Total	C	H	N	O	S	0	0
			1693	534	859	146	152	2		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	18	LEU	VAL	conflict	UNP G1TSG1
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1
U	54	GLY	ARG	conflict	UNP G1TSG1
U	60	VAL	ALA	conflict	UNP G1TSG1
U	62	SER	THR	conflict	UNP G1TSG1
U	63	LEU	ILE	conflict	UNP G1TSG1
U	97	ARG	HIS	conflict	UNP G1TSG1
U	106	THR	SER	conflict	UNP G1TSG1
U	126	GLU	ASP	conflict	UNP G1TSG1

- Molecule 31 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	V	131	Total	C	H	N	O	S	0	0
			2019	618	1040	184	172	5		

- Molecule 32 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	W	63	Total	C	H	N	O	S	0	0
			1070	337	542	103	85	3		

- Molecule 33 is a protein called Ribosomal_L23eN domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	X	118	Total	C	H	N	O	S	0	0
			2008	618	1041	181	167	1		

- Molecule 34 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	Y	134	Total	C	H	N	O	S	0	0
			2320	700	1205	226	186	3		

- Molecule 35 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	Z	135	Total	C	H	N	O	S	0	0
			2292	714	1185	208	182	3		

- Molecule 36 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	a	147	Total	C	H	N	O	S	0	0
			2372	734	1210	239	185	4		

- Molecule 37 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	b	104	Total	C	H	N	O	S	0	0
			1771	527	923	189	129	3		

- Molecule 38 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	c	98	Total	C	H	N	O	S	0	0
			1557	481	796	134	140	6		

- Molecule 39 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	d	107	Total	C	H	N	O	S	0	0
			1820	560	932	171	155	2		

- Molecule 40 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	e	128	Total	C	H	N	O	S	0	0
			2203	667	1150	216	165	5		

- Molecule 41 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	f	109	Total	C	H	N	O	S	0	0
			1789	555	913	174	143	4		

- Molecule 42 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	g	114	Total	C	H	N	O	S	0	0
			1910	566	1004	187	147	6		

- Molecule 43 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	h	122	Total	C	H	N	O	S	0	0
			2161	640	1148	204	168	1		

- Molecule 44 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	i	102	Total	C	H	N	O	S	0	0
			1747	520	917	176	129	5		

- Molecule 45 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	j	86	Total	C	H	N	O	S	0	0
			1448	434	743	155	111	5		

- Molecule 46 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	k	69	Total	C	H	N	O	S	0	0
			1206	366	637	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	24	LYS	ASN	conflict	UNP G1U001

- Molecule 47 is a protein called 60S ribosomal protein L39-like.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	l	50	Total	C	H	N	O	S	0	0
			928	286	481	96	64	1		

- Molecule 48 is a protein called eL40.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	m	52	Total	C	H	N	O	S	0	0
			899	266	470	90	67	6		

- Molecule 49 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	n	25	Total	C	H	N	O	S	0	0
			529	145	289	64	28	3		

- Molecule 50 is a protein called 60S ribosomal protein L36a-like.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	o	104	Total	C	H	N	O	S	0	0
			1778	533	927	174	138	6		

- Molecule 51 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	p	91	Total	C	H	N	O	S	0	0
			1470	445	762	136	120	7		

- Molecule 52 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	q	76	Total	C	H	N	O	P	0	0
			2439	723	823	291	527	75		

- Molecule 53 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	r	124	Total	C	H	N	O	S	0	0
			2046	616	1052	205	167	6		

- Molecule 54 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	u	120	Total	C	H	N	O	P	0	0
			3854	1141	1296	456	842	119		

- Molecule 55 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	v	156	Total	C	H	N	O	P	0	0
			4997	1480	1683	585	1094	155		

- Molecule 56 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	w	394	Total	C	H	N	O	S	0	0
			6487	2020	3315	597	542	13		

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	I	1	Total	Mg	0
			1	1	
57	K	201	Total	Mg	0
			201	201	
57	V	1	Total	Mg	0
			1	1	
57	a	1	Total	Mg	0
			1	1	
57	g	1	Total	Mg	0
			1	1	
57	j	1	Total	Mg	0
			1	1	
57	u	7	Total	Mg	0
			7	7	
57	v	4	Total	Mg	0
			4	4	
57	w	1	Total	Mg	0
			1	1	

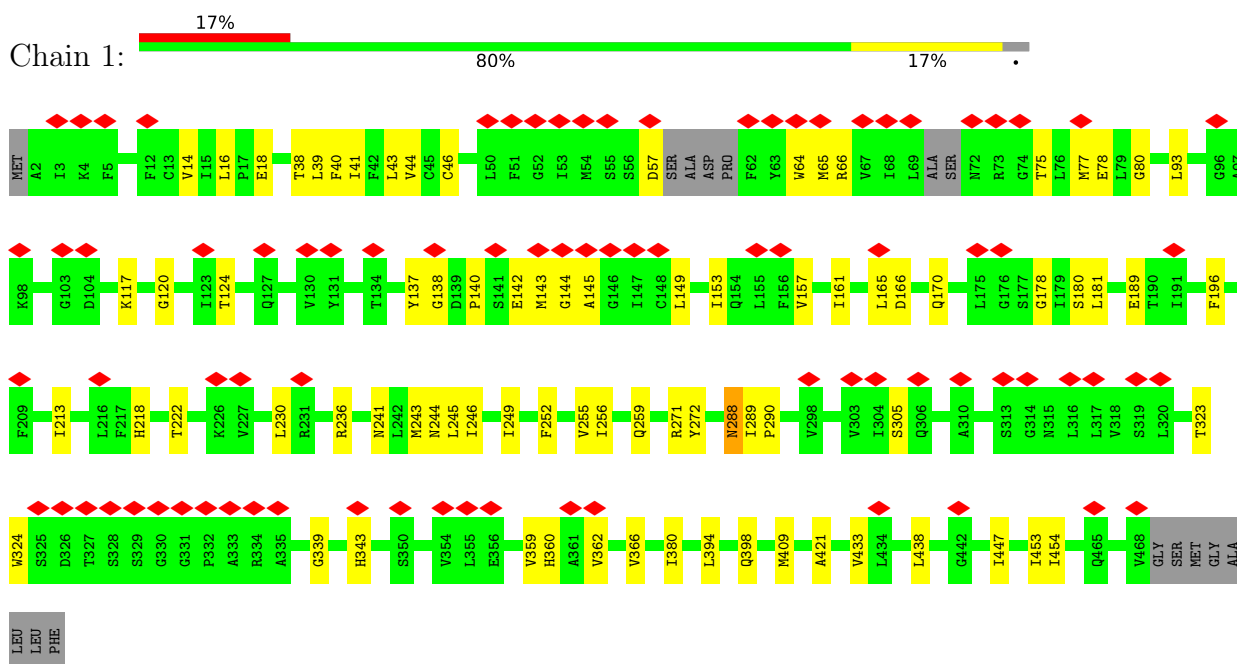
- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
58	g	1	Total 1	Zn 1	0
58	j	1	Total 1	Zn 1	0
58	m	1	Total 1	Zn 1	0
58	o	1	Total 1	Zn 1	0
58	p	1	Total 1	Zn 1	0

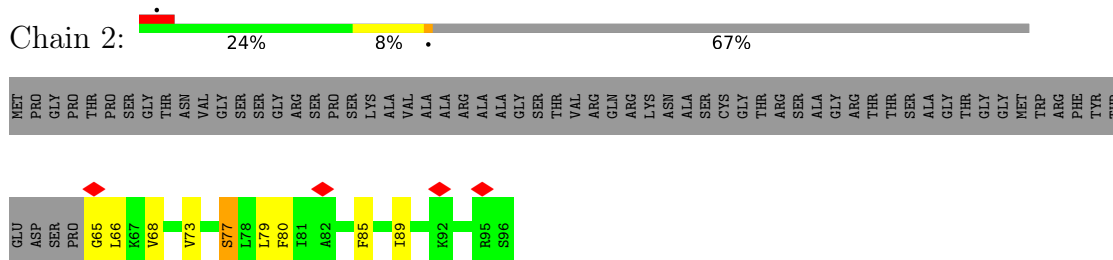
3 Residue-property plots

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

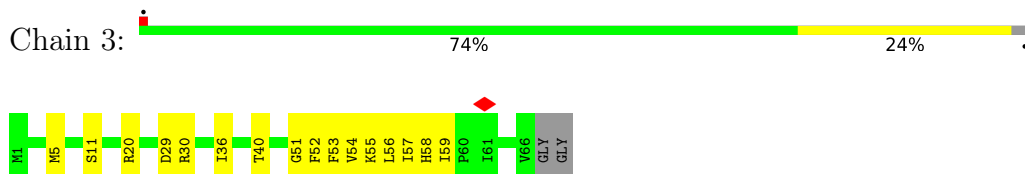
- Molecule 1: Protein transport protein Sec61 subunit alpha isoform 1

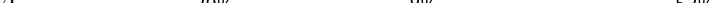


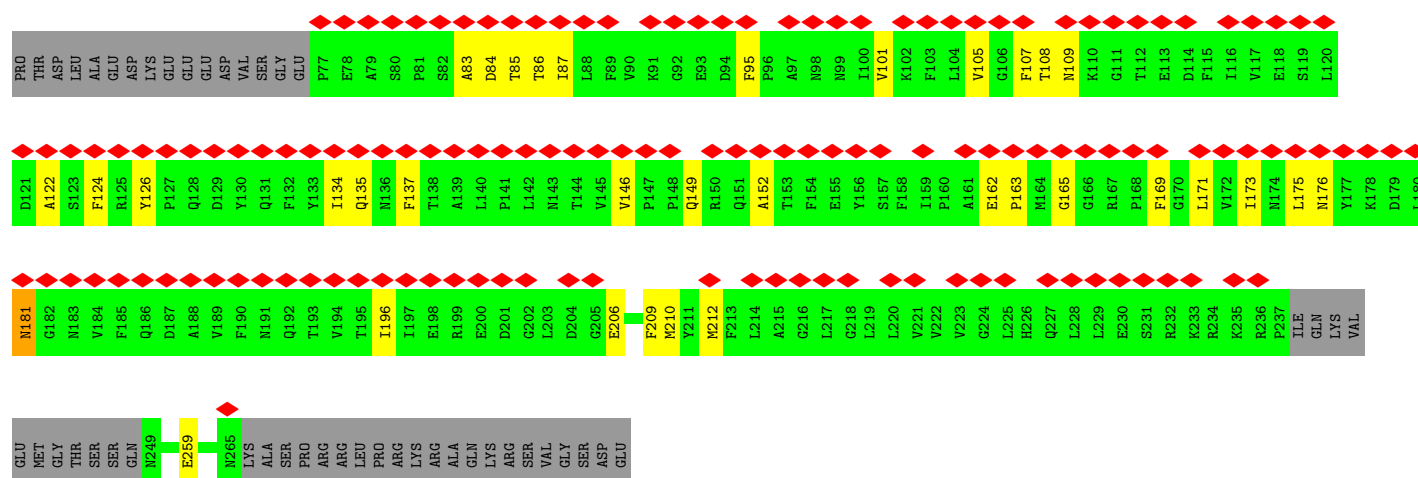
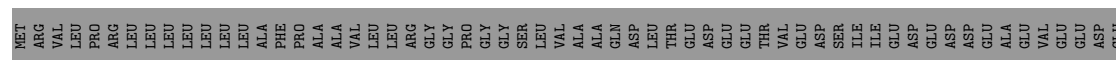
- Molecule 2: Protein transport protein Sec61 subunit beta

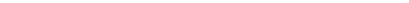


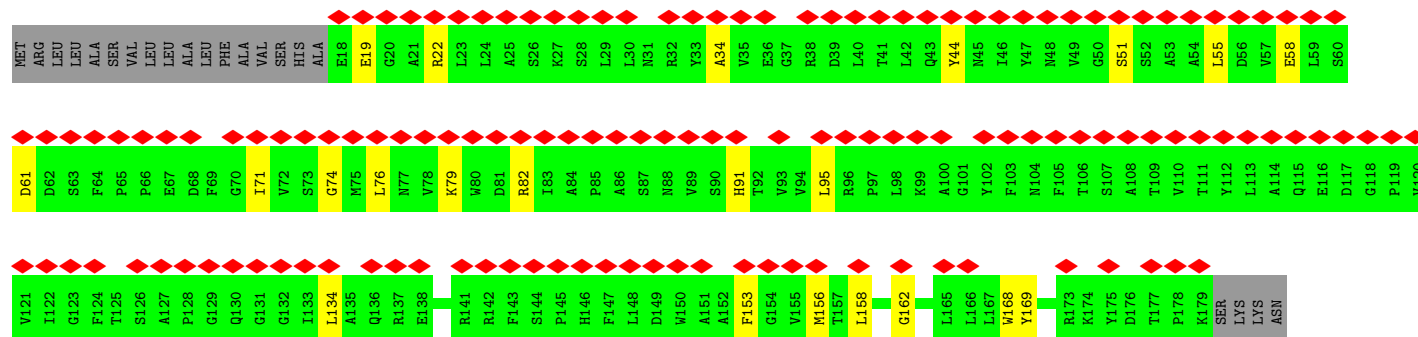
- Molecule 3: Protein transport protein Sec61 subunit gamma

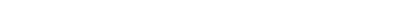


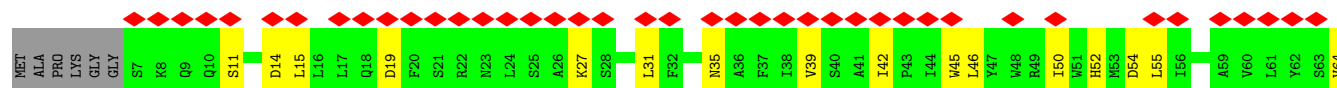
- Chain 4: 



- Chain 6:  75% 77% 12% 11%



- Chain 7:  42% 77% 20%



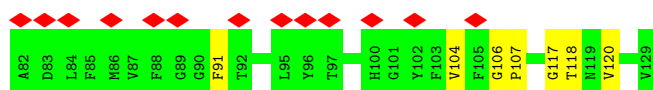
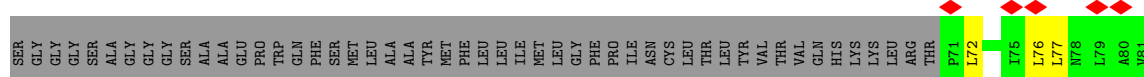
- Molecule 10: Ribosomal protein L8

Chain A:  88% 9%



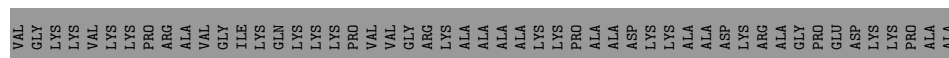
- Molecule 11: Nascent chain

Chain B:  8% 21% 74%



- Molecule 12: Large ribosomal subunit protein uL4

Chain C:  80% 15%



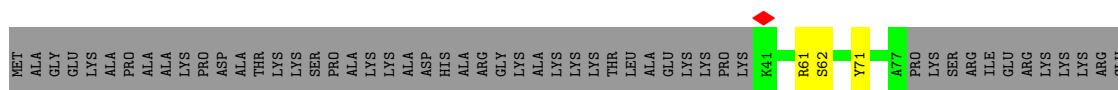
- Molecule 13: Ribosomal_L18_c domain-containing protein

Chain D:  88% 10%



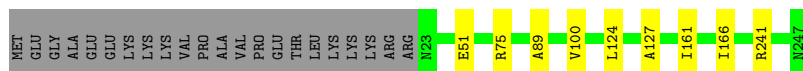
- Molecule 14: 60S ribosomal protein L6

Chain E:  72% 23%



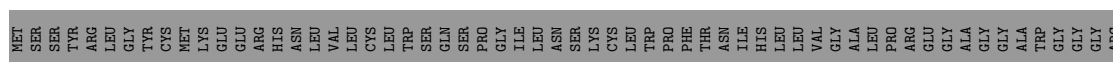
• Molecule 15: Ribosomal Protein uL30

Chain F: 87% 9%



• Molecule 16: 60S ribosomal protein L7a

Chain G: 70% 27%



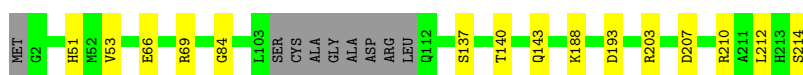
• Molecule 17: 60S ribosomal protein L9

Chain H: 88% 11%



• Molecule 18: 60S ribosomal protein L10

Chain I: 89% 7%

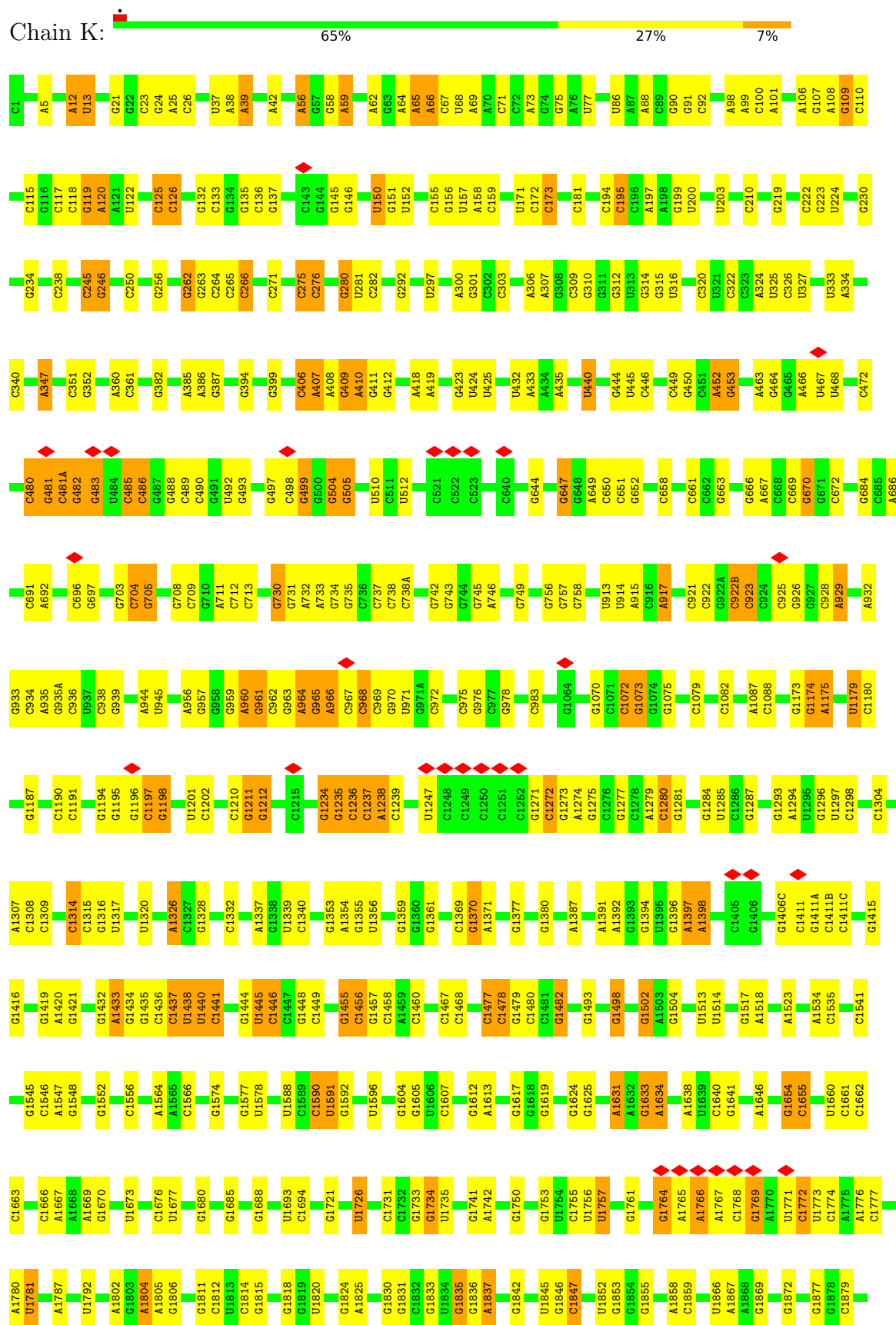


• Molecule 19: 60S ribosomal protein L11

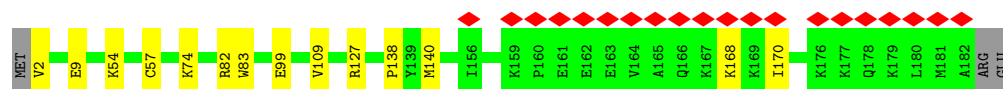
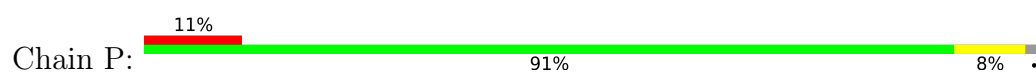
Chain J: 87% 7%



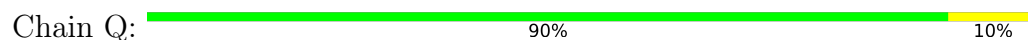
• Molecule 20: 28S rRNA



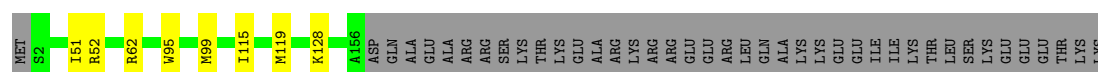
A4348	A4349	C4284	C4112	G3889	G3765	A3653	C2814	G2705	U2554	U2440	A2332	G2089	U1986	U1882
C4349	C4350	U4260	C4119	A3890	A3766	C3654	A2815	G2706	G2562	C2441	G2332	U2090	C1987	A1891
U4351	U4120	C4261	U4120	G3897	U3770	C3655	G2816	U2707	C2563	G2448	G2333	U2091	G1988	A1892
U4354	G4121	C4121	G3771	G3900	C3772	A3656	G2822	C2709	C2564	A2449	C2338	G2092	G1989	C1893
G4355	G4122	A4122	U3772	A3901	U3773	C3658	U2826	G2711	A2565	G2450	C2338	G2093	A1990	A1897
G4371	A4127	A4267	A3774	G3904	A3775	G3659	G2827	C2719	G2566	G2457	A2341	A2095	A1991	G1910
U4372	C4148	G4268	G3776	A3905	U3775	A3662	U2828	A2725	U2580	C2458	G2342	G2096	U1992	C1915
G4373	A4162	A4271	G3777	A3906	G3777	G3671	G2829	G2726	A2861	C2465	C2346	A2097	C1994	C1915
A4376	A4163	A4274	A3784	G3907	A3785	G3672	A2830	C2729	C2582	C2466	A2347	G2098	G1995	U1918
G4377	A4170	G4275	A3786	A3908	U3786	C3673	A2840	U2730	A2587	U2467	G2348	G2100	C1996	U1919
A4378	G4169	G4276	U3786	C3909	U3786	G3673	G2842	G2731	C2588	U2468	A2349	A2101	U1997	G1919
A4379	A4170	G4277	G3811	C3910	U3786	U3688	G2842	C2730	C2588	C2469	U2350	G2102	A1998	C1920
C4387	A4171	A4280	G3811	U3912	G3811	U3688	G2842	G2731	C2588	C2469	U2350	A2103	A1999	C1921
A4389	A4172	A4281	U3814	U3915	U3814	A3692	G2844	G2735	A2801	G2475	G2358	A2104	G2000	G1922
G4391	G4173	A4282	G3815	G3916	G3815	U3693	A2844	U2740	G2620	G2476	U2359	A2105	G2001	G1922
G4392	G4173	A4282	G3816	G3916	G3816	U3694	A2844	U2740	G2620	G2476	U2359	G2106	A2002	U1927
G4393	G4173	A4282	G3817	G3916	G3817	U3695	A2844	U2740	G2620	G2476	U2359	G2106	A2002	U1927
G4394	G4183	C4287	U3818	C3931	U3818	C3696	G2848	A2743	C2627	G2483	U2362	A2107	G2003	C1928
A4394	G4184	C4288	G3819	C3931	U3819	C3696	G2848	A2744	U2630	U2485	A2368	A2109	U2004	C1929
U4395	U4188	G4291	U3822	G3938	U3822	C3706	G2855	G2750	U2638	G2488	A2376	G2258	U2006	A1932
C4398	U4189	A4292	G3823	G3939	G3823	C3707	G2856	G2751	U2639	C2489	C2377	G2259	U2008	C1896
G4401	G4190	A4293	G3823	A3943	G3823	C3708	G2857	G2752	G2640	U2490	C2378	G2261	A2009	C1937
C4412	G4191	A4298	A3828	G3944	A3828	C3709	G2858	G2753	G2640	U2490	C2378	G2261	A2010	U1930
C4413	G4195	A4302	U3837	G3945	U3837	A3711	G2859	G2753	A2647	C2491	G2380	A2263	C2011	G1940
A4414	A4203	U4303	U3838	G3946	U3838	A3712	G2878	G2758	G2652	G2492	A2395	C2266	A2012	A1941
A4415	C4303	A4304	G3839	G3946	U3839	U3713	A2879	G2759	G2653	A2502	A2396	U2267	U2015	G1948
G4416	U4208	A4304	U3840	G3946	U3840	U3715	G2882	G2760	C2654	G2503	G2399	A2268	U2019	U1949
C4417	U4070	A4305	A3856	G3946	A3856	C3716	G2883	G2762	G2658	G2504	G2402	C2269	C2018	G1952
G4418	A4212	U4306	A3856	G3946	A3856	C3717	G2883	G2763	A2659	G2505	G2403	G2270	U2020	U1957
U4419	A4213	U4306	A3856	G3946	A3856	C3718	G2883	G2764	A2659	G2505	G2403	A2276	G2021	A1958
A4422	A4214	C4314	G3859	G3946	A3856	C3719	G2883	G2765	G2662	A2512	A2404	C2277	G2022	C2022
U4423	A4219	A4317	A3860	G3946	A3860	U3720	G2883	G2766	G2662	A2513	G2407	C2278	A2025	G1961
A4424	A4220	A4318	A3861	G3946	A3861	A3727	G2883	U2769	C2669	A2513	U2408	C2279	A2026	A1962
C4429	C4221	C4319	A3862	G3946	A3862	A3728	G2883	G2770	G2673	U2519	U2409	C2280	A2026	G1963
C4434	G4225	C4320	A3863	G3946	A3863	A3733	G2883	A2783	A2676	U2519	U2409	C2280	A2026	A1964
C4443	G4228	A4322	G3864	G3946	A3864	U3734	G2883	A2787	A2676	A2529	A2412	C2289	U2044	G1965
U4445	U4229	A4323	C3865	G3946	A3865	U3735	G2883	U2788	C2683	A2530	U2413	C2292	G2045	C1966
U4446	C4230	A4324	C3870	G3946	A3866	A3736	G2883	U2790	C2684	C2531	G2414	C2293	G2046	U1970
C4447	G4231	A4325	G3873	G3946	A3867	A3737	G2883	G2794	C2685	A2537	G2415	U2293	U2048	G1971
G4448	U4232	A4326	G3874	G3946	A3868	U3740	G2883	C2794	C2686	U2538	A2416	C2299	G2052	G1972
A4449	U4233	A4327	A3875	G3946	A3869	A3748	G2883	A2798	U2687	U2538	A2418	C2300	C2053	G1976
U4450	A4234	C4330	A3877	G3946	A3870	A3748	G2883	A2798	U2687	A2543	C2419	G2301	U2054	C1977
G4451	G4237	G4331	G3878	G3946	A3871	U3751	G2883	A2806	G2694	G2544	C2422	C2306	G2056	C1978
U4452	C4237	C4332	G3879	G3946	A3872	C3752	G2883	A2806	A2696	U2545	C2422	C2306	G2056	A1979
U4453	U4242	A4339	G3880	G3946	A3873	C3753	G2883	G2809	G2700	G2546	U2425	A2307	C2062	U1980
U4454	C4243	C4345	G3881	G3946	A3874	G3753	G2883	U2810	G2701	G2547	U2428	A2308	G2063	G1981
U4455	U4243	C4345	G3882	G3946	A3875	A3759	G2883	G2811	G2702	G2552	U2436	A2313	G2064	G1982
U4456	C4251	C4345	G3883	G3946	A3876	A3760	G2883	G2812	G2703	A2553	U2436	A2313	G2064	A1984
U4457	U4251	C4345	G3884	G3946	A3877	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
C4458	U4251	C4345	G3885	G3946	A3878	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4459	U4251	C4345	G3886	G3946	A3879	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4460	U4251	C4345	G3887	G3946	A3880	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4461	U4251	C4345	G3888	G3946	A3881	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4462	U4251	C4345	G3889	G3946	A3882	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4463	U4251	C4345	G3890	G3946	A3883	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4464	U4251	C4345	G3891	G3946	A3884	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4465	U4251	C4345	G3892	G3946	A3885	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4466	U4251	C4345	G3893	G3946	A3886	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4467	U4251	C4345	G3894	G3946	A3887	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4468	U4251	C4345	G3895	G3946	A3888	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4469	U4251	C4345	G3896	G3946	A3889	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4470	U4251	C4345	G3897	G3946	A3890	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4471	U4251	C4345	G3898	G3946	A3891	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4472	U4251	C4345	G3899	G3946	A3892	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4473	U4251	C4345	G3900	G3946	A3893	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4474	U4251	C4345	G3901	G3946	A3894	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4475	U4251	C4345	G3902	G3946	A3895	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4476	U4251	C4345	G3903	G3946	A3896	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4477	U4251	C4345	G3904	G3946	A3897	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4478	U4251	C4345	G3905	G3946	A3898	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4479	U4251	C4345	G3906	G3946	A3899	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4480	U4251	C4345	G3907	G3946	A3900	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4481	U4251	C4345	G3908	G3946	A3901	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4482	U4251	C4345	G3909	G3946	A3902	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4483	U4251	C4345	G3910	G3946	A3903	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4484	U4251	C4345	G3911	G3946	A3904	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4485	U4251	C4345	G3912	G3946	A3905	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4486	U4251	C4345	G3913	G3946	A3906	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4487	U4251	C4345	G3914	G3946	A3907	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4488	U4251	C4345	G3915	G3946	A3908	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4489	U4251	C4345	G3916	G3946	A3909	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4490	U4251	C4345	G3917	G3946	A3910	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4491	U4251	C4345	G3918	G3946	A3911	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4492	U4251	C4345	G3919	G3946	A3912	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4493	U4251	C4345	G3920	G3946	A3913	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4494	U4251	C4345	G3921	G3946	A3914	U3764	G2883	G2813	G2704	A2553	U2436	A2313	G2064	A1985
U4495														



- Molecule 26: Ribosomal protein L18



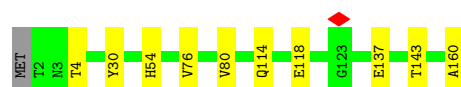
- Molecule 27: Ribosomal protein L19



- Molecule 28: 60S ribosomal protein L18a



- Molecule 29: 60S ribosomal protein L21

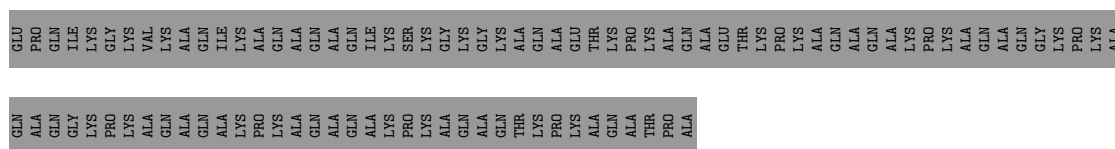


- Molecule 30: Ribosomal protein L22

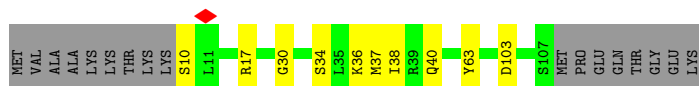
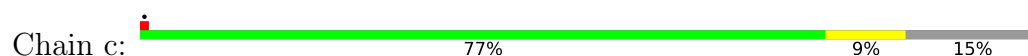


- Molecule 31: Ribosomal protein L23





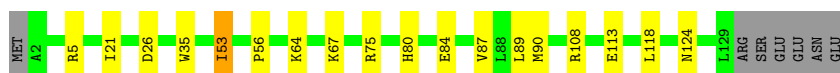
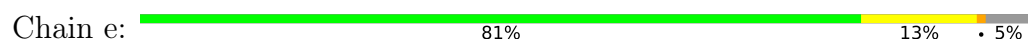
- Molecule 38: 60S ribosomal protein L30



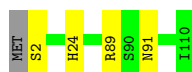
- Molecule 39: 60S ribosomal protein L31



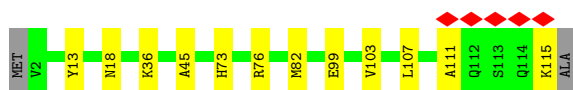
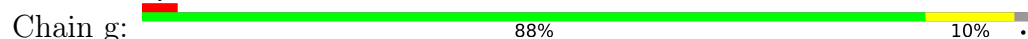
- Molecule 40: Ribosomal protein L32



- Molecule 41: 60S ribosomal protein L35a



- Molecule 42: 60S ribosomal protein L34



- Molecule 43: 60S ribosomal protein L35



- Molecule 44: 60S ribosomal protein L36

Chain i:  91% 6%



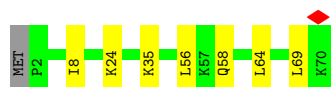
- Molecule 45: Ribosomal protein L37

Chain j:  81% 7% 11%

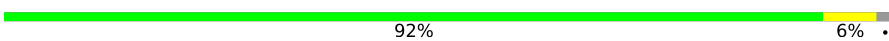


- Molecule 46: 60S ribosomal protein L38

Chain k:  89% 10%



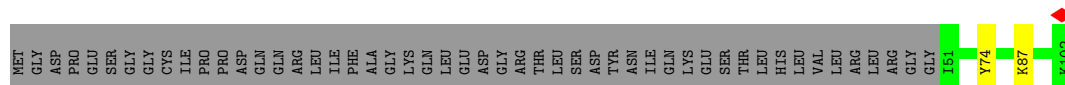
- Molecule 47: 60S ribosomal protein L39-like

Chain l:  92% 6%

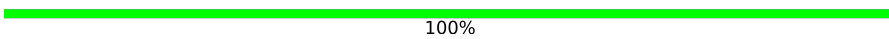


- Molecule 48: eL40

Chain m:  49% 49%



- Molecule 49: 60S ribosomal protein L41

Chain n:  100%

There are no outlier residues recorded for this chain.

- Molecule 50: 60S ribosomal protein L36a-like

Chain o:  90% 8%



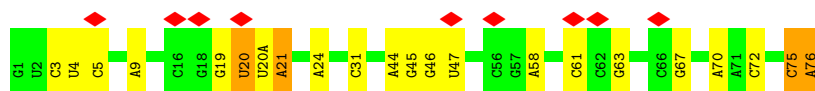
- Molecule 51: 60S ribosomal protein L37a

Chain p:  89% 10%



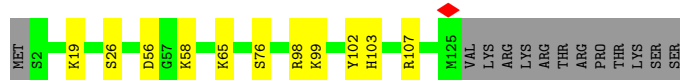
• Molecule 52: P-site tRNA

Chain q:  12% 71% 24% 5%



• Molecule 53: 60S ribosomal protein L28

Chain r:  82% 8% 9%



• Molecule 54: 5S rRNA

Chain u:  79% 20%



• Molecule 55: 5.8S rRNA

Chain v:  66% 26% 8%



• Molecule 56: Ribosomal protein L3

Chain w:  86% 12%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	28770	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	1900	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.200	Depositor
Minimum map value	-0.063	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0231	Depositor
Map size ($\text{\AA}$)	562.7185, 562.7185, 562.7185	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.339806, 1.339806, 1.339806	Depositor

5 Model quality

5.1 Standard geometry

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

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	1	0.15	0/3651	0.32	1/4947 (0.0%)
2	2	0.22	0/258	0.42	0/348
3	3	0.16	0/544	0.35	0/728
4	4	0.17	0/245	0.28	0/325
5	5	0.14	0/1457	0.32	0/1980
6	6	0.13	0/1296	0.30	0/1764
7	7	0.12	0/1482	0.27	0/2001
8	8	0.12	0/1215	0.29	0/1656
9	9	0.12	0/311	0.32	0/427
10	A	0.27	0/1936	0.36	1/2596 (0.0%)
11	B	0.21	0/446	0.43	0/610
12	C	0.26	0/2937	0.28	0/3946
13	D	0.22	0/2437	0.27	0/3264
14	E	0.22	0/1825	0.29	0/2445
15	F	0.26	0/1911	0.30	0/2549
16	G	0.23	0/1910	0.29	0/2569
17	H	0.24	0/1535	0.30	0/2063
18	I	0.24	0/1702	0.28	0/2272
19	J	0.19	0/1385	0.28	0/1852
20	K	0.31	0/84980	0.33	0/132536
21	L	0.23	0/1733	0.33	1/2316 (0.0%)
22	M	0.24	0/1158	0.34	2/1547 (0.1%)
23	N	0.29	0/1746	0.34	1/2338 (0.0%)
24	O	0.27	0/1662	0.28	0/2222
25	P	0.25	0/1498	0.35	0/2003
26	Q	0.27	0/1539	0.30	0/2054
27	R	0.25	0/1310	0.26	0/1734
28	S	0.27	0/1501	0.28	0/2012
29	T	0.25	0/1326	0.36	1/1770 (0.1%)
30	U	0.19	0/848	0.31	0/1138
31	V	0.25	0/993	0.27	0/1332
32	W	0.26	0/541	0.28	0/720

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	X	0.24	0/984	0.27	0/1323
34	Y	0.24	0/1132	0.31	0/1504
35	Z	0.24	0/1130	0.29	0/1507
36	a	0.27	0/1191	0.33	0/1590
37	b	0.22	0/861	0.30	0/1138
38	c	0.23	0/771	0.28	0/1034
39	d	0.26	0/903	0.31	0/1216
40	e	0.28	0/1071	0.30	0/1429
41	f	0.27	0/895	0.30	0/1198
42	g	0.26	0/916	0.30	0/1220
43	h	0.24	0/1021	0.29	0/1348
44	i	0.22	0/841	0.29	0/1112
45	j	0.30	0/720	0.32	0/952
46	k	0.22	0/575	0.28	0/761
47	l	0.27	0/459	0.30	0/608
48	m	0.24	0/435	0.29	0/575
49	n	0.19	0/241	0.28	0/305
50	o	0.24	0/864	0.28	0/1140
51	p	0.25	0/718	0.41	1/953 (0.1%)
52	q	0.13	0/1805	0.28	0/2809
53	r	0.25	0/1010	0.28	0/1354
54	u	0.31	0/2858	0.28	0/4455
55	v	0.30	0/3701	0.30	0/5766
56	w	0.27	0/3240	0.33	2/4339 (0.0%)
All	All	0.28	0/157660	0.32	10/231700 (0.0%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	w	371	THR	OG1-CB-CG2	5.76	120.82	109.30
29	T	143	THR	OG1-CB-CG2	5.69	120.68	109.30
21	L	63	THR	OG1-CB-CG2	5.67	120.63	109.30
23	N	148	THR	OG1-CB-CG2	5.62	120.54	109.30
22	M	105	THR	OG1-CB-CG2	5.60	120.50	109.30
51	p	73	THR	OG1-CB-CG2	5.49	120.28	109.30
10	A	135	THR	OG1-CB-CG2	5.37	120.04	109.30
22	M	105	THR	CA-CB-CG2	5.22	119.37	110.50
1	l	137	TYR	N-CA-C	-5.05	107.78	114.04
56	w	371	THR	CA-CB-CG2	5.02	119.03	110.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	3575	3700	3697	52	0
2	2	251	273	272	6	0
3	3	534	571	571	12	0
4	4	244	260	259	3	0
5	5	1423	1390	1389	25	0
6	6	1263	1244	1243	14	0
7	7	1452	1490	1489	29	0
8	8	1186	1149	1148	13	0
9	9	301	309	308	9	0
10	A	1898	1994	1993	14	0
11	B	432	424	423	9	0
12	C	2883	3054	3053	13	0
13	D	2391	2425	2424	24	0
14	E	1791	1963	1956	11	0
15	F	1875	1997	1995	5	0
16	G	1879	2029	2027	7	0
17	H	1516	1598	1597	19	0
18	I	1664	1716	1712	10	0
19	J	1362	1401	1399	10	0
20	K	75972	38363	38383	693	0
21	L	1702	1823	1820	4	0
22	M	1137	1212	1211	12	0
23	N	1701	1753	1749	10	0
24	O	1630	1780	1778	16	0
25	P	1470	1542	1541	12	0
26	Q	1515	1638	1634	14	0
27	R	1294	1436	1434	5	0
28	S	1462	1510	1508	9	0
29	T	1298	1369	1366	8	0
30	U	834	859	858	19	0
31	V	979	1040	1039	4	0
32	W	528	542	541	2	0
33	X	967	1041	1040	6	0
34	Y	1115	1205	1205	10	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	Z	1107	1185	1182	18	0
36	a	1162	1210	1209	14	0
37	b	848	923	920	10	0
38	c	761	796	794	6	0
39	d	888	932	930	10	0
40	e	1053	1150	1147	14	0
41	f	876	913	912	2	0
42	g	906	1004	998	8	0
43	h	1013	1148	1147	9	0
44	i	830	917	916	4	0
45	j	705	743	737	7	0
46	k	569	637	637	3	0
47	l	447	481	480	4	0
48	m	429	470	465	1	0
49	n	240	289	289	0	0
50	o	851	927	920	7	0
51	p	708	762	756	7	0
52	q	1616	823	824	8	0
53	r	994	1052	1051	6	0
54	u	2558	1296	1296	14	0
55	v	3314	1683	1683	37	0
56	w	3172	3315	3310	32	0
57	I	1	0	0	0	0
57	K	201	0	0	0	0
57	V	1	0	0	0	0
57	a	1	0	0	0	0
57	g	1	0	0	0	0
57	j	1	0	0	0	0
57	u	7	0	0	0	0
57	v	4	0	0	0	0
57	w	1	0	0	0	0
58	g	1	0	0	0	0
58	j	1	0	0	0	0
58	m	1	0	0	0	0
58	o	1	0	0	0	0
58	p	1	0	0	0	0
All	All	146794	108756	108665	1135	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 5.

All (1135) 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)
20:K:2104:A:O2'	20:K:2105:A:O5'	1.77	1.02
20:K:2440:U:O2'	20:K:2441:C:OP1	1.79	1.00
20:K:3603:G:O2'	20:K:3604:A:O5'	1.83	0.96
55:v:110:U:O2'	55:v:111:U:OP1	1.86	0.92
20:K:1764:G:O2'	20:K:1766:A:N6	2.03	0.91
20:K:3765:G:O2'	20:K:3766:A:N7	2.05	0.89
20:K:1437:C:O2'	20:K:1438:U:O5'	1.92	0.88
5:5:259:GLU:N	5:5:259:GLU:OE2	2.08	0.86
2:2:73:VAL:O	2:2:77:SER:OG	1.92	0.86
20:K:1646:A:O2'	45:j:49:TRP:O	1.93	0.86
20:K:1369:C:OP2	20:K:1370:G:O2'	1.92	0.85
20:K:1757:U:OP1	20:K:1768:C:N4	2.10	0.85
1:1:236:ARG:N	1:1:241:ASN:OD1	2.10	0.84
20:K:245:C:O2'	20:K:246:G:OP2	1.95	0.84
20:K:3717:A:OP2	20:K:3735:G:N2	2.09	0.84
20:K:2544:G:N3	20:K:2546:G:O2'	2.09	0.84
20:K:2552:G:OP2	20:K:2553:A:O2'	1.95	0.84
20:K:4472:G:O2'	48:m:74:TYR:O	1.95	0.83
13:D:286:SER:OG	20:K:1179:U:O2	1.95	0.83
13:D:186:GLU:N	13:D:186:GLU:OE1	2.12	0.83
20:K:3904:G:O2'	20:K:3905:A:OP1	1.97	0.82
19:J:151:ILE:O	54:u:55:A:O2'	1.98	0.82
3:3:20:ARG:NH2	33:X:148:ASP:OD2	2.12	0.82
20:K:4907:G:H2'	20:K:4913:G:H22	1.46	0.81
20:K:1293:G:OP2	20:K:1293:G:N2	2.10	0.81
20:K:490:C:O2	20:K:663:G:N2	2.11	0.81
7:7:110:ARG:NH1	20:K:2763:U:OP2	2.14	0.80
20:K:264:C:O2	20:K:266:C:N4	2.12	0.80
20:K:1970:A:N6	20:K:2015:U:OP2	2.14	0.80
18:I:203:ARG:NH1	54:u:105:C:OP2	2.15	0.80
20:K:1986:U:N3	20:K:2006:U:O4	2.15	0.80
20:K:5047:C:O2'	20:K:5050:C:OP2	1.99	0.80
20:K:1075:G:H22	20:K:1235:G:H22	1.30	0.79
20:K:1480:C:O2'	20:K:1482:G:OP2	2.00	0.79
51:p:88:GLU:O	51:p:92:GLN:N	2.14	0.79
20:K:3692:A:H62	20:K:3823:G:H21	1.30	0.79
20:K:1818:G:O2'	20:K:1820:U:OP2	1.99	0.79
17:H:64:ARG:NH2	20:K:4693:C:OP1	2.17	0.78
20:K:1075:G:H22	20:K:1235:G:N2	1.81	0.78
20:K:4771:C:O2	20:K:4773:C:N4	2.15	0.78
20:K:4119:C:O2'	20:K:4120:U:O2	2.00	0.78
12:C:321:ASN:OD1	20:K:1280:C:O2'	2.00	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:3888:G:O2'	20:K:3889:G:OP1	2.02	0.77
25:P:9:GLU:OE1	25:P:9:GLU:N	2.17	0.77
13:D:196:ARG:NH2	13:D:237:GLU:OE2	2.18	0.77
20:K:1234:G:O2'	20:K:1235:G:OP2	2.03	0.77
20:K:1353:G:N7	26:Q:104:ARG:NH2	2.32	0.77
20:K:1235:G:O2'	20:K:1236:C:OP2	2.03	0.75
20:K:1397:A:HO2'	20:K:1467:C:HO2'	1.30	0.75
20:K:3770:U:OP1	52:q:24:A:O2'	2.03	0.75
54:u:23:A:N3	54:u:118:C:O2'	2.19	0.75
20:K:2588:C:OP1	20:K:2768:C:O2'	2.05	0.75
20:K:922(B):C:O2'	20:K:923:C:OP1	2.05	0.74
20:K:1961:G:O2'	20:K:2025:A:N6	2.20	0.74
16:G:253:THR:OG1	20:K:150:U:OP2	2.04	0.74
1:1:380:ILE:HD12	1:1:421:ALA:HB2	1.69	0.74
13:D:234:ASP:OD2	13:D:235:MET:N	2.21	0.74
15:F:51:GLU:OE2	20:K:1237:C:O2'	2.04	0.74
20:K:1477:C:O2'	20:K:1478:C:OP1	2.04	0.74
20:K:1398:A:OP1	36:a:136:LYS:NZ	2.20	0.74
20:K:2848:G:O2'	20:K:3838:U:O4	2.05	0.74
6:6:19:GLU:O	6:6:51:SER:OG	2.06	0.73
20:K:2759:G:O2'	20:K:2760:G:O4'	2.05	0.73
20:K:3860:A:H61	20:K:4560:C:H5	1.37	0.73
20:K:2326:G:OP1	40:e:108:ARG:NH2	2.22	0.73
20:K:1998:A:O2'	20:K:2019:C:O2'	2.06	0.72
1:1:18:GLU:O	2:2:68:VAL:N	2.22	0.72
17:H:14:GLU:OE2	17:H:14:GLU:N	2.19	0.72
20:K:1326:A:OP2	20:K:4445:U:O2'	2.06	0.72
20:K:1802:A:O2'	20:K:1837:A:OP1	2.07	0.72
20:K:1872:G:O2'	20:K:4219:A:N3	2.22	0.72
7:7:19:ASP:OD2	7:7:85:LYS:NZ	2.22	0.72
20:K:108:A:N1	20:K:333:U:O2'	2.22	0.72
20:K:1406(C):G:N2	20:K:1411:C:N3	2.37	0.72
20:K:3692:A:H62	20:K:3823:G:N2	1.88	0.71
20:K:181:C:O2	20:K:256:G:N2	2.24	0.71
20:K:4580:U:O2'	56:w:182:GLU:OE2	2.09	0.71
22:M:55:MET:O	28:S:157:ARG:NH2	2.24	0.71
20:K:394:G:OP1	25:P:168:LYS:NZ	2.18	0.70
20:K:1271:G:OP2	37:b:114:ARG:NH1	2.25	0.70
20:K:2368:A:N6	20:K:2827:G:O2'	2.23	0.70
20:K:1445:U:O2'	20:K:1446:C:OP1	2.06	0.70
20:K:3604:A:O2'	20:K:3605:C:O4'	2.07	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:2583:C:OP2	42:g:76:ARG:NH1	2.24	0.70
20:K:238:C:OP2	34:Y:45:ARG:NH2	2.24	0.69
6:6:34:ALA:O	6:6:134:LEU:N	2.25	0.69
32:W:14:TYR:OH	56:w:384:GLU:OE2	2.06	0.69
20:K:314:G:O2'	20:K:4355:G:OP1	2.09	0.69
20:K:2669:C:OP2	27:R:128:LYS:NZ	2.20	0.69
5:5:206:GLU:OE2	5:5:206:GLU:N	2.23	0.69
20:K:266:C:O2	43:h:112:ARG:NH1	2.24	0.69
20:K:2487:G:OP2	20:K:2489:C:N4	2.22	0.69
20:K:4354:U:O2'	20:K:4355:G:OP2	2.10	0.69
20:K:4672:A:OP1	31:V:15:ARG:NH2	2.26	0.69
20:K:5013:C:N4	20:K:5029:C:OP1	2.25	0.69
3:3:53:PHE:O	3:3:57:ILE:HG23	1.91	0.69
18:I:188:LYS:NZ	18:I:212:LEU:O	2.23	0.69
8:8:69:ASP:OD2	8:8:105:ARG:NH2	2.25	0.68
52:q:21:A:N6	52:q:46:G:O2'	2.26	0.68
13:D:260:GLU:O	54:u:120:U:N3	2.26	0.68
19:J:80:GLU:N	19:J:80:GLU:OE1	2.26	0.68
24:O:27:VAL:O	24:O:101:ARG:NH1	2.27	0.68
20:K:1174:G:O2'	20:K:1175:A:OP1	2.11	0.68
2:2:79:LEU:HD12	2:2:80:PHE:N	2.09	0.68
20:K:1456:C:O2'	26:Q:73:PRO:O	2.12	0.68
7:7:110:ARG:NH2	20:K:2764:A:OP2	2.25	0.68
20:K:275:C:O2'	20:K:276:C:O5'	2.07	0.68
3:3:5:MET:N	3:3:5:MET:SD	2.67	0.67
20:K:978:G:O6	20:K:1277:G:O6	2.12	0.67
20:K:407:A:O2'	20:K:410:A:OP1	2.13	0.67
20:K:1197:C:O2'	20:K:1198:G:O5'	2.12	0.67
20:K:4926:C:O2'	20:K:4927:G:O5'	2.08	0.67
12:C:307:LYS:NZ	20:K:2090:U:OP2	2.28	0.67
20:K:4371:G:O2'	20:K:4372:U:OP2	2.12	0.67
35:Z:88:ASP:O	35:Z:121:ARG:NH2	2.28	0.67
40:e:67:LYS:O	40:e:75:ARG:NH2	2.27	0.67
1:1:166:ASP:OD1	1:1:178:GLY:N	2.28	0.66
20:K:3642:A:HO2'	45:j:2:THR:N	1.93	0.66
20:K:3716:C:N4	20:K:3735:G:O2'	2.25	0.66
20:K:347:A:OP2	34:Y:8:THR:OG1	2.07	0.66
20:K:1075:G:N2	20:K:1235:G:H22	1.92	0.66
26:Q:133:GLY:O	26:Q:136:THR:OG1	2.09	0.66
3:3:29:ASP:OD1	3:3:30:ARG:N	2.28	0.66
20:K:1741:G:O2'	20:K:1781:U:OP2	2.12	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:w:218:ASP:OD2	56:w:348:ARG:NH2	2.27	0.66
56:w:283:LYS:NZ	56:w:359:ALA:O	2.29	0.66
20:K:2395:A:O2'	20:K:2806:A:H1'	1.96	0.66
20:K:1320:U:O2'	20:K:1891:A:N1	2.24	0.66
20:K:2647:A:H62	20:K:2686:G:H8	1.41	0.66
20:K:968:C:O2'	20:K:969:C:O5'	2.08	0.66
20:K:3603:G:HO2'	20:K:3604:A:P	2.16	0.65
53:r:65:LYS:O	53:r:102:TYR:OH	2.13	0.65
20:K:4648:A:OP1	27:R:62:ARG:NH2	2.30	0.65
39:d:123:ASP:OD1	39:d:123:ASP:N	2.26	0.65
20:K:4982:A:OP1	25:P:74:LYS:NZ	2.28	0.65
20:K:4620:U:OP2	20:K:4670:C:N4	2.20	0.65
7:7:64:VAL:O	7:7:68:VAL:HG23	1.96	0.65
20:K:1397:A:O2'	20:K:1467:C:O2'	2.05	0.65
20:K:1669:A:N3	20:K:1852:U:O2'	2.28	0.65
20:K:2811:G:N1	20:K:2814:C:OP2	2.28	0.65
20:K:2580:U:O2'	35:Z:79:HIS:ND1	2.30	0.65
20:K:4587:G:OP1	24:O:61:ARG:NH1	2.29	0.64
7:7:27:LYS:NZ	9:9:509:GLN:OE1	2.30	0.64
13:D:9:ASN:OD1	13:D:11:ALA:N	2.28	0.64
56:w:80:GLU:OE1	56:w:323:TYR:OH	2.12	0.64
17:H:113:GLU:OE2	17:H:115:ARG:NH2	2.29	0.64
19:J:125:ILE:O	19:J:125:ILE:HD12	1.98	0.64
20:K:3877:A:N3	20:K:4401:G:O2'	2.22	0.64
30:U:65:ARG:NH1	30:U:66:SER:O	2.31	0.63
30:U:106:THR:OG1	30:U:107:LYS:N	2.31	0.63
14:E:289:LEU:HD11	14:E:291:PHE:CZ	2.34	0.63
20:K:4393:G:O2'	20:K:4446:U:OP2	2.11	0.63
20:K:2378:G:O2'	20:K:2380:G:N7	2.30	0.63
13:D:292:GLU:OE1	13:D:293:ARG:NH1	2.32	0.63
20:K:1211:G:O2'	20:K:1212:G:OP1	2.16	0.63
20:K:4322:G:O2'	20:K:4324:A:N7	2.27	0.63
19:J:163:MET:HG2	19:J:174:ILE:HD13	1.81	0.63
20:K:152:U:OP2	23:N:49:ARG:NH2	2.31	0.63
14:E:227:LYS:HD2	14:E:227:LYS:C	2.24	0.62
20:K:4288:C:O2'	20:K:4321:U:OP1	2.15	0.62
10:A:117:GLU:O	10:A:162:ASN:ND2	2.32	0.62
20:K:1957:U:O2'	20:K:1958:A:O5'	2.18	0.62
20:K:3751:G:H21	20:K:3775:A:H8	1.46	0.62
20:K:2404:A:H61	20:K:2787:A:N6	1.97	0.62
5:5:107:PHE:CD1	5:5:175:LEU:HD21	2.35	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:2046:G:O2'	20:K:2047:A:OP2	2.11	0.62
20:K:2263:A:OP1	53:r:107:ARG:NH2	2.33	0.62
20:K:975:C:H3'	20:K:976:G:H21	1.63	0.62
20:K:1072:C:H42	20:K:1239:C:H42	1.46	0.62
20:K:1965:G:N7	20:K:1966:C:N4	2.47	0.62
20:K:4947:U:O2'	20:K:4948:C:OP1	2.17	0.62
20:K:2502:A:O2'	20:K:2503:G:O5'	2.13	0.61
20:K:2695:A:OP1	46:k:35:LYS:NZ	2.24	0.61
20:K:1734:G:N2	20:K:1735:U:O4	2.29	0.61
37:b:99:ILE:O	37:b:109:ARG:NH1	2.34	0.61
20:K:194:C:O2	34:Y:121:ARG:NH2	2.33	0.61
10:A:215:ASN:ND2	20:K:4546:A:N7	2.48	0.60
1:1:57:ASP:OD1	1:1:66:ARG:NE	2.29	0.60
1:1:166:ASP:OD2	1:1:170:GLN:NE2	2.32	0.60
20:K:1879:C:O2'	20:K:1891:A:N3	2.34	0.60
35:Z:29:ILE:HD12	35:Z:40:HIS:CD2	2.36	0.60
20:K:1814:C:O2'	37:b:42:ASN:OD1	2.16	0.60
20:K:2262:G:OP2	53:r:98:ARG:NH1	2.34	0.60
20:K:2758:G:O2'	20:K:2765:A:N3	2.29	0.60
38:c:30:GLY:O	38:c:34:SER:OG	2.14	0.60
7:7:91:LYS:NZ	8:8:171:ILE:O	2.26	0.59
20:K:4392:G:N2	20:K:4395:U:O2	2.33	0.59
30:U:61:VAL:HG22	30:U:74:SER:HB2	1.83	0.59
56:w:215:GLU:OE2	56:w:349:LYS:NZ	2.21	0.59
20:K:481(A):C:O2'	20:K:483:G:O2'	2.20	0.59
20:K:1397:A:N1	20:K:1498:G:O2'	2.35	0.59
20:K:3765:G:H4'	20:K:3766:A:OP1	2.02	0.59
20:K:115:C:O2'	20:K:276:C:OP1	2.21	0.59
20:K:1437:C:HO2'	20:K:1438:U:P	2.23	0.59
20:K:1445:U:HO2'	20:K:1446:C:P	2.24	0.59
20:K:2639:U:O2'	20:K:2640:G:O5'	2.20	0.59
20:K:1766:A:O2'	20:K:1767:A:O4'	2.19	0.59
20:K:3888:G:HO2'	20:K:3889:G:P	2.24	0.59
56:w:383:GLU:OE1	56:w:383:GLU:N	2.33	0.59
34:Y:50:ARG:NH2	55:v:84:A:N1	2.51	0.59
20:K:151:G:OP2	23:N:4:TYR:OH	2.16	0.59
20:K:4924:C:O2	20:K:4926:C:N4	2.36	0.58
1:1:380:ILE:CD1	1:1:421:ALA:HB2	2.32	0.58
20:K:3879:G:O2'	20:K:3881:G:OP2	2.20	0.58
15:F:75:ARG:NE	20:K:730:G:OP2	2.36	0.58
1:1:14:VAL:O	2:2:65:GLY:N	2.36	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:1845:U:OP1	37:b:25:ARG:NE	2.36	0.58
20:K:4882:U:OP1	22:M:117:LYS:NZ	2.25	0.58
13:D:185:SER:OG	13:D:186:GLU:OE1	2.17	0.58
20:K:3696:C:O2'	20:K:3816:A:N1	2.36	0.57
20:K:3938:G:N2	20:K:4171:C:OP2	2.37	0.57
45:j:20:ARG:NH1	55:v:102:G:OP1	2.36	0.57
5:5:83:ALA:HB1	5:5:107:PHE:CE2	2.40	0.57
20:K:1556:C:O2'	20:K:2669:C:OP1	2.13	0.57
6:6:44:TYR:N	6:6:91:HIS:O	2.28	0.57
17:H:145:VAL:HG12	17:H:147:GLU:OE1	2.04	0.57
13:D:226:TYR:OH	54:u:48:G:OP1	2.19	0.57
17:H:112:VAL:HG21	17:H:128:MET:HE3	1.87	0.57
13:D:116:ASP:OD1	13:D:116:ASP:N	2.35	0.56
40:e:21:ILE:HD11	40:e:53:ILE:HD11	1.87	0.56
52:q:3:C:H42	52:q:70:A:H61	1.52	0.56
5:5:95:PHE:CE2	5:5:101:VAL:HG11	2.39	0.56
20:K:125:C:O2'	20:K:126:C:O5'	2.22	0.56
20:K:1548:G:O2'	20:K:2812:A:N3	2.38	0.56
5:5:124:PHE:N	5:5:135:GLN:O	2.34	0.56
20:K:3765:G:O2'	20:K:3766:A:C8	2.58	0.56
8:8:48:VAL:HG22	8:8:91:SER:HB3	1.88	0.56
26:Q:88:ASP:OD1	26:Q:89:ASP:N	2.39	0.56
20:K:86:U:OP1	26:Q:169:SER:OG	2.20	0.56
20:K:3692:A:N6	20:K:3823:G:H21	2.02	0.56
10:A:118:GLU:OE1	20:K:3662:A:O2'	2.17	0.56
6:6:74:GLY:N	8:8:52:GLU:OE2	2.33	0.56
27:R:115:ILE:HG22	27:R:119:MET:HE3	1.87	0.56
29:T:80:VAL:HG23	29:T:80:VAL:O	2.06	0.56
1:1:323:THR:OG1	1:1:339:GLY:N	2.39	0.55
13:D:93:THR:O	13:D:158:LYS:NZ	2.24	0.55
14:E:61:ARG:NH2	20:K:978:G:OP2	2.36	0.55
20:K:4413:C:H5	20:K:4429:C:H42	1.53	0.55
5:5:84:ASP:OD1	5:5:85:THR:N	2.39	0.55
20:K:409:G:O2'	20:K:410:A:OP1	2.21	0.55
20:K:4354:U:O2'	20:K:4355:G:P	2.64	0.55
6:6:168:TRP:NE1	7:7:132:GLU:OE1	2.39	0.55
20:K:504:G:O2'	20:K:505:G:O5'	2.23	0.55
35:Z:121:ARG:NH1	35:Z:127:ASN:OD1	2.39	0.55
14:E:164:ARG:NH1	14:E:276:SER:OG	2.40	0.55
20:K:709:C:OP1	41:f:89:ARG:NH2	2.40	0.55
54:u:35:U:O2	54:u:45:U:O2'	2.25	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:D:28:THR:O	20:K:4280:A:N6	2.35	0.55
20:K:4322:G:N2	20:K:4325:A:OP2	2.37	0.55
20:K:1361:G:OP2	21:L:28:GLN:NE2	2.39	0.54
20:K:1502:G:H22	36:a:77:LYS:HE2	1.72	0.54
20:K:1339:U:OP1	36:a:8:THR:OG1	2.19	0.54
20:K:2260:C:O2	53:r:99:LYS:NZ	2.39	0.54
28:S:93:MET:SD	28:S:95:ARG:NH1	2.80	0.54
7:7:130:ASP:O	7:7:134:THR:OG1	2.24	0.54
28:S:24:THR:O	28:S:24:THR:HG22	2.07	0.54
45:j:18:LEU:HD11	47:l:51:LEU:CD1	2.37	0.54
16:G:284:ASP:OD1	16:G:284:ASP:N	2.40	0.54
5:5:95:PHE:O	5:5:196:ILE:HG23	2.08	0.54
13:D:33:ARG:NH1	54:u:7:G:OP1	2.39	0.54
30:U:33:ILE:HG22	30:U:96:LEU:HD21	1.90	0.54
7:7:119:GLU:CD	9:9:515:TYR:HH	2.16	0.54
20:K:452:A:H4'	20:K:453:G:H5''	1.90	0.54
20:K:1518:A:OP1	36:a:27:LYS:NZ	2.27	0.54
20:K:737:C:OP2	22:M:71:LYS:NZ	2.30	0.54
20:K:4524:G:N3	56:w:252:ALA:HB1	2.22	0.54
39:d:18:ASN:N	39:d:18:ASN:HD22	2.06	0.54
1:1:93:LEU:HD11	11:B:77:LEU:HD11	1.89	0.54
20:K:386:A:O2'	34:Y:87:ARG:NH2	2.41	0.54
20:K:3773:U:H2'	20:K:3775:A:H2	1.72	0.54
1:1:18:GLU:N	2:2:66:LEU:O	2.38	0.54
20:K:1328:G:O2'	20:K:2349:A:OP1	2.24	0.54
20:K:2104:A:HO2'	20:K:2105:A:C5'	2.21	0.53
20:K:2639:U:HO2'	20:K:2640:G:P	2.31	0.53
55:v:84:A:OP1	55:v:86:U:O2'	2.26	0.53
20:K:2809:G:O2'	20:K:4644:G:OP1	2.21	0.53
30:U:44:GLN:C	30:U:44:GLN:OE1	2.51	0.53
20:K:734:G:H1	20:K:929:A:H62	1.56	0.53
1:1:218:HIS:O	1:1:222:THR:OG1	2.19	0.53
56:w:56:ILE:HD13	56:w:365:LEU:HD22	1.90	0.53
1:1:120:GLY:O	1:1:124:THR:N	2.41	0.53
7:7:77:TYR:OH	7:7:142:ASN:OD1	2.20	0.53
34:Y:76:LYS:NZ	55:v:74:U:OP1	2.41	0.53
53:r:56:ASP:O	53:r:58:LYS:N	2.40	0.53
7:7:39:VAL:HA	7:7:42:ILE:HD12	1.90	0.53
10:A:199:VAL:HG21	20:K:1631:A:N7	2.24	0.53
13:D:259:ARG:NH2	54:u:119:U:OP2	2.41	0.53
14:E:107:THR:O	14:E:108:ARG:NH1	2.38	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:128:MET:HE1	17:H:161:ILE:HD11	1.89	0.53
20:K:3873:G:H2'	20:K:3874:G:C8	2.44	0.53
20:K:4572:U:O2'	20:K:4573:G:O4'	2.25	0.53
20:K:734:G:C2	20:K:735:G:C8	2.97	0.53
35:Z:84:ARG:NH1	42:g:99:GLU:OE2	2.42	0.53
55:v:123:U:H1'	55:v:124:U:H2'	1.91	0.53
5:5:87:ILE:HG13	5:5:105:VAL:HG22	1.90	0.52
13:D:225:GLN:O	13:D:229:ASN:ND2	2.34	0.52
17:H:137:SER:HB3	17:H:143:GLU:HB3	1.91	0.52
20:K:3713:U:O2'	20:K:3714:G:OP2	2.24	0.52
20:K:4897:G:O6	20:K:4924:C:N4	2.41	0.52
1:1:454:ILE:HG21	3:3:40:THR:HG23	1.90	0.52
20:K:1174:G:O2'	20:K:1175:A:P	2.67	0.52
20:K:3938:G:H4'	20:K:3939:G:O5'	2.09	0.52
20:K:67:C:OP2	20:K:312:G:N2	2.41	0.52
20:K:480:C:O2'	20:K:481:G:O5'	2.25	0.52
20:K:1339:U:H2'	20:K:1340:C:C6	2.44	0.52
20:K:1502:G:H22	36:a:77:LYS:CE	2.22	0.52
20:K:4992:G:H2'	20:K:4993:G:C8	2.45	0.52
22:M:29:ASP:OD1	22:M:30:VAL:N	2.42	0.52
56:w:322:HIS:O	56:w:342:LYS:NZ	2.26	0.52
20:K:480:C:O2'	20:K:481:G:P	2.67	0.52
20:K:2465:C:H2'	20:K:2466:G:O4'	2.09	0.52
28:S:94:TYR:OH	28:S:96:GLU:OE2	2.23	0.52
17:H:173:ARG:NH2	20:K:4475:G:OP2	2.41	0.52
20:K:3641:U:H5	20:K:3646:A:N7	2.08	0.52
20:K:4948:C:H3'	20:K:4949:G:H5''	1.92	0.52
20:K:1314:C:O2'	20:K:1315:C:OP2	2.21	0.52
31:V:27:ASN:ND2	31:V:100:ASP:OD2	2.41	0.52
8:8:48:VAL:HG22	8:8:91:SER:CB	2.40	0.52
20:K:409:G:OP2	25:P:2:VAL:N	2.42	0.52
20:K:1633:G:H5'	20:K:1634:A:OP1	2.10	0.52
24:O:81:TRP:HB2	24:O:104:VAL:HG21	1.92	0.52
55:v:71:A:N1	55:v:83:C:O2'	2.39	0.52
20:K:2054:U:OP2	24:O:44:SER:OG	2.21	0.52
20:K:408:A:O2'	20:K:411:G:OP2	2.14	0.52
20:K:1766:A:H2'	20:K:1767:A:C8	2.45	0.52
12:C:209:VAL:HB	12:C:229:LEU:HD13	1.92	0.51
19:J:102:THR:HG21	20:K:4261:C:O2'	2.10	0.51
20:K:156:G:OP2	43:h:109:ARG:NH2	2.43	0.51
20:K:2844:A:O2'	20:K:4631:G:H4'	2.10	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5:108:THR:OG1	6:6:22:ARG:NH2	2.42	0.51
20:K:485:C:O2'	20:K:486:C:P	2.68	0.51
15:F:161:ILE:HD12	15:F:166:ILE:HB	1.92	0.51
20:K:132:G:H2'	20:K:133:C:O4'	2.10	0.51
20:K:691:C:H2'	20:K:692:A:C8	2.44	0.51
20:K:968:C:O2'	20:K:969:C:O4'	2.29	0.51
20:K:1541:C:C2	20:K:1619:G:C2	2.98	0.51
20:K:4591:U:H2'	20:K:4592:C:C6	2.46	0.51
20:K:4735:G:O2'	20:K:4736:C:OP2	2.24	0.51
35:Z:29:ILE:HD11	35:Z:98:LYS:HD2	1.93	0.51
55:v:123:U:O2'	55:v:124:U:O5'	2.22	0.51
20:K:4761:G:OP2	24:O:37:ARG:NH1	2.41	0.51
54:u:28:C:O2'	54:u:54:A:N1	2.41	0.51
13:D:62:CYS:HB3	13:D:105:LEU:HD22	1.92	0.51
20:K:3625:G:O2'	20:K:3626:G:P	2.67	0.51
20:K:3671:G:H2'	20:K:3672:G:C8	2.46	0.51
20:K:4478:G:O2'	20:K:4602:A:N1	2.42	0.51
20:K:5047:C:O2'	20:K:5047:C:O2	2.27	0.51
20:K:2550:G:O2'	20:K:2587:A:N1	2.38	0.51
43:h:52:LYS:NZ	55:v:62:A:OP1	2.43	0.51
20:K:4111:U:OP2	20:K:4112:C:N4	2.43	0.51
43:h:16:GLU:OE1	43:h:16:GLU:O	2.28	0.51
52:q:75:C:H2'	52:q:76:A:O4'	2.11	0.51
20:K:68:U:OP1	23:N:178:HIS:ND1	2.32	0.51
20:K:1517:G:H2'	20:K:1518:A:N7	2.26	0.51
51:p:56:HIS:HE1	51:p:61:MET:HE3	1.76	0.51
20:K:1972:G:C6	20:K:1995:G:O6	2.64	0.51
20:K:3654:G:O2'	20:K:3693:U:OP1	2.24	0.50
40:e:80:HIS:N	40:e:84:GLU:OE1	2.37	0.50
5:5:83:ALA:HB1	5:5:107:PHE:HE2	1.76	0.50
20:K:4763:U:O2'	28:S:174:THR:OG1	2.25	0.50
24:O:48:TYR:HE1	24:O:52:LEU:HD11	1.76	0.50
30:U:50:ASN:CG	30:U:50:ASN:O	2.55	0.50
39:d:54:MET:O	39:d:58:GLY:N	2.43	0.50
30:U:24:ASP:C	30:U:24:ASP:OD2	2.54	0.50
56:w:35:ASP:OD2	56:w:193:LYS:NZ	2.31	0.50
1:1:38:THR:HG23	1:1:165:LEU:HB3	1.93	0.50
1:1:93:LEU:HD21	11:B:77:LEU:HD11	1.93	0.50
6:6:158:LEU:O	6:6:162:GLY:N	2.44	0.50
20:K:2259:G:C3'	20:K:2260:C:H5'	2.41	0.50
20:K:2415:U:H2'	20:K:2416:G:O4'	2.12	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:I:193:ASP:OD1	18:I:193:ASP:C	2.55	0.50
20:K:3711:A:N6	20:K:3736:A:OP2	2.44	0.50
40:e:113:GLU:OE2	40:e:113:GLU:O	2.29	0.50
55:v:79:G:O2'	55:v:82:A:N7	2.37	0.50
19:J:167:GLN:O	19:J:171:ASP:N	2.42	0.50
20:K:2422:C:OP1	25:P:127:ARG:NH2	2.40	0.50
20:K:4195:G:OP1	20:K:4221:C:O2'	2.21	0.50
20:K:4728:U:OP2	56:w:132:LYS:NZ	2.38	0.50
23:N:90:ASN:O	50:o:48:TYR:OH	2.26	0.50
43:h:2:ALA:N	55:v:82:A:OP2	2.45	0.50
5:5:146:VAL:HG22	5:5:152:ALA:HB2	1.93	0.50
20:K:1377:G:H21	20:K:1380:G:H5'	1.76	0.50
1:1:140:PRO:O	1:1:144:GLY:N	2.32	0.50
4:4:2:VAL:HG13	4:4:6:ARG:HH11	1.77	0.50
12:C:204:ARG:NH1	20:K:2299:G:OP2	2.42	0.49
20:K:418:A:C2	55:v:17:A:H1'	2.46	0.49
20:K:1211:G:HO2'	20:K:1212:G:P	2.33	0.49
20:K:2019:C:H2'	20:K:2020:U:C6	2.47	0.49
5:5:85:THR:HG21	5:5:175:LEU:HD23	1.94	0.49
54:u:111:C:H2'	54:u:112:U:O4'	2.12	0.49
55:v:123:U:HO2'	55:v:124:U:P	2.34	0.49
1:1:343:HIS:O	1:1:360:HIS:NE2	2.37	0.49
10:A:108:PRO:O	10:A:111:THR:OG1	2.28	0.49
13:D:208:MET:HE1	13:D:226:TYR:CD2	2.47	0.49
20:K:62:A:N3	20:K:77:U:O2'	2.39	0.49
20:K:435:A:O2'	40:e:26:ASP:OD2	2.18	0.49
20:K:4735:G:O2'	20:K:4736:C:P	2.70	0.49
22:M:96:GLU:OE1	22:M:100:ARG:NE	2.45	0.49
18:I:66:GLU:OE1	18:I:69:ARG:NH1	2.45	0.49
20:K:1355:G:OP1	26:Q:108:ARG:NH2	2.41	0.49
20:K:4572:U:H2'	20:K:4573:G:C8	2.48	0.49
35:Z:22:LYS:NZ	35:Z:129:TRP:O	2.39	0.49
55:v:110:U:O2'	55:v:111:U:P	2.70	0.49
46:k:8:ILE:HG23	46:k:56:LEU:CD1	2.42	0.49
20:K:481(A):C:H4'	20:K:482:G:OP1	2.12	0.49
17:H:93:ARG:HD2	17:H:143:GLU:HG3	1.95	0.49
20:K:1174:G:HO2'	20:K:1175:A:P	2.35	0.49
20:K:1307:A:H2'	20:K:1308:C:C6	2.48	0.49
20:K:2856:C:O2	56:w:242:ARG:NH2	2.42	0.49
20:K:3720:G:H22	20:K:3733:A:H2	1.61	0.49
29:T:118:GLU:C	29:T:118:GLU:OE2	2.55	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:106:A:H2'	20:K:107:G:O4'	2.13	0.49
20:K:406:C:HO2'	20:K:407:A:P	2.36	0.49
20:K:4266:G:H2'	20:K:4266:G:N3	2.26	0.49
20:K:4947:U:HO2'	20:K:4948:C:P	2.36	0.49
46:k:24:LYS:HB3	46:k:69:LEU:HD11	1.95	0.49
56:w:29:VAL:HG13	56:w:348:ARG:HD3	1.95	0.49
20:K:325:U:H2'	20:K:326:C:C6	2.48	0.49
20:K:5007:A:N7	20:K:5042:A:O2'	2.29	0.49
30:U:33:ILE:CG2	30:U:96:LEU:HD21	2.42	0.49
20:K:406:C:O2'	20:K:407:A:OP1	2.29	0.49
20:K:2858:A:H2'	20:K:2859:G:O4'	2.13	0.49
20:K:3625:G:HO2'	20:K:3626:G:P	2.36	0.49
20:K:4304:A:OP2	20:K:4305:G:N2	2.43	0.49
20:K:4660:G:C2'	20:K:4661:G:H5'	2.42	0.49
40:e:89:LEU:HD13	40:e:118:LEU:HD22	1.94	0.49
55:v:140:C:H2'	55:v:141:C:C6	2.48	0.49
20:K:1435:G:O2'	20:K:2105:A:N1	2.32	0.48
20:K:1445:U:O2'	20:K:1446:C:P	2.71	0.48
20:K:3777:G:O2'	20:K:3815:G:O6	2.29	0.48
20:K:4660:G:H2'	20:K:4661:G:H5'	1.94	0.48
38:c:37:MET:HE3	38:c:37:MET:HA	1.94	0.48
20:K:1577:G:O2'	20:K:1612:G:H4'	2.13	0.48
20:K:2639:U:O2'	20:K:2640:G:P	2.70	0.48
20:K:4260:U:H2'	20:K:4261:C:C6	2.48	0.48
20:K:4524:G:H4'	20:K:4524:G:OP2	2.14	0.48
25:P:99:GLU:OE1	25:P:109:VAL:HG11	2.13	0.48
6:6:153:PHE:CE1	7:7:46:LEU:HD11	2.47	0.48
10:A:101:VAL:C	10:A:102:LEU:HD12	2.38	0.48
16:G:270:LYS:HD3	16:G:270:LYS:N	2.28	0.48
20:K:1440:U:O2'	20:K:1441:C:OP1	2.28	0.48
20:K:2448:G:H2'	20:K:2449:A:C8	2.48	0.48
20:K:3868:G:H22	20:K:3900:G:H1'	1.78	0.48
30:U:39:PHE:CE1	30:U:43:LEU:HD11	2.48	0.48
20:K:2258:C:H2'	20:K:2258:C:O2	2.13	0.48
20:K:2639:U:H2'	20:K:2694:G:H1	1.79	0.48
20:K:2706:G:N2	20:K:2708:U:O2'	2.46	0.48
26:Q:177:ALA:O	26:Q:184:ARG:HB2	2.14	0.48
35:Z:29:ILE:HD12	35:Z:40:HIS:NE2	2.29	0.48
15:F:127:ALA:O	20:K:1726:U:O2'	2.31	0.48
18:I:207:ASP:OD2	18:I:207:ASP:N	2.46	0.48
20:K:1552:G:O2'	20:K:1574:G:N2	2.35	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:4232:U:H4'	20:K:4233:A:O5'	2.13	0.48
20:K:4237:C:OP1	20:K:4327:C:O2'	2.31	0.48
43:h:109:ARG:HH11	43:h:109:ARG:HB2	1.78	0.48
20:K:3837:C:H2'	20:K:3838:U:O4'	2.13	0.48
24:O:34:VAL:HG22	24:O:103:LYS:HB2	1.95	0.48
2:2:79:LEU:HD12	2:2:79:LEU:C	2.37	0.48
11:B:118:THR:HG21	12:C:67:TRP:CH2	2.49	0.48
20:K:922(B):C:H2'	20:K:923:C:O4'	2.14	0.48
20:K:2089:G:H1'	20:K:2090:U:OP2	2.13	0.48
20:K:3736:A:H2'	20:K:3737:A:C8	2.49	0.48
20:K:3764:U:H2'	20:K:3765:G:O4'	2.14	0.48
20:K:4947:U:O2'	20:K:4948:C:P	2.71	0.48
56:w:87:VAL:O	56:w:107:ALA:N	2.43	0.48
20:K:69:A:N1	20:K:324:A:O2'	2.44	0.48
20:K:275:C:HO2'	20:K:276:C:P	2.33	0.48
20:K:1920:C:H3'	20:K:1921:C:H5''	1.95	0.48
20:K:1984:A:O2'	20:K:1985:G:OP1	2.30	0.48
30:U:60:VAL:HG11	30:U:76:VAL:HG13	1.95	0.48
30:U:63:LEU:HD21	30:U:70:ILE:CG2	2.44	0.48
37:b:65:MET:HE2	37:b:65:MET:HA	1.96	0.48
1:1:255:VAL:O	1:1:259:GLN:N	2.46	0.48
10:A:5:ILE:HG22	10:A:208:GLU:O	2.14	0.48
14:E:133:LYS:NZ	20:K:713:C:O2	2.47	0.48
20:K:440:U:O2'	41:f:91:ASN:O	2.26	0.48
20:K:3890:A:N6	20:K:4570:G:O2'	2.40	0.48
20:K:4412:C:H2'	20:K:4413:C:O2	2.14	0.48
20:K:4459:U:H2'	20:K:4460:U:O4'	2.14	0.48
43:h:109:ARG:HB2	43:h:109:ARG:NH1	2.28	0.48
50:o:36:GLN:O	50:o:36:GLN:NE2	2.44	0.48
55:v:125:C:H2'	55:v:126:C:O5'	2.13	0.48
20:K:964:A:H2'	20:K:965:G:O4'	2.14	0.48
20:K:1502:G:OP2	26:Q:65:ARG:NH1	2.43	0.48
20:K:4305:G:C6	29:T:80:VAL:HG11	2.49	0.48
5:5:122:ALA:O	5:5:137:PHE:N	2.47	0.47
17:H:189:GLN:N	17:H:189:GLN:OE1	2.47	0.47
18:I:53:VAL:HG21	29:T:160:ALA:HB1	1.95	0.47
20:K:99:A:H2'	20:K:100:C:O2	2.14	0.47
20:K:1197:C:O2'	20:K:1198:G:C5'	2.62	0.47
42:g:45:ALA:HB3	42:g:82:MET:HE2	1.95	0.47
5:5:122:ALA:HB3	5:5:137:PHE:HB2	1.95	0.47
14:E:62:SER:HB2	20:K:1238:A:C2	2.49	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:36:ARG:HB3	17:H:80:MET:HE2	1.95	0.47
20:K:1771:U:H2'	20:K:1772:C:O4'	2.13	0.47
33:X:153:ILE:O	33:X:153:ILE:HG22	2.14	0.47
51:p:52:VAL:HG13	51:p:52:VAL:O	2.14	0.47
3:3:53:PHE:HA	3:3:56:LEU:HD12	1.96	0.47
5:5:209:PHE:O	5:5:212:MET:HE3	2.13	0.47
6:6:71:ILE:HG12	6:6:95:LEU:HD22	1.96	0.47
14:E:289:LEU:HD12	14:E:289:LEU:C	2.39	0.47
20:K:445:U:H2'	20:K:446:C:O4'	2.14	0.47
20:K:1411(B):C:H2'	20:K:1411(C):C:C6	2.48	0.47
38:c:38:ILE:HG21	38:c:63:TYR:HB3	1.96	0.47
9:9:510:SER:O	9:9:513:VAL:HG22	2.14	0.47
1:1:288:ASN:OD1	1:1:288:ASN:N	2.47	0.47
8:8:115:LEU:CD1	8:8:125:ILE:HG23	2.44	0.47
10:A:65:ASP:OD2	10:A:72:ARG:NE	2.40	0.47
20:K:303:C:OP2	23:N:68:ARG:NH2	2.44	0.47
20:K:968:C:HO2'	20:K:969:C:P	2.32	0.47
20:K:969:C:N4	20:K:2095:A:H61	2.13	0.47
20:K:2706:G:N2	20:K:2710:C:OP2	2.46	0.47
20:K:2306:G:H1'	20:K:2332:A:N6	2.30	0.47
20:K:37:U:H2'	20:K:38:A:O4'	2.15	0.47
20:K:1617:G:H1'	20:K:2513:A:N6	2.29	0.47
20:K:1733:G:N3	20:K:4214:A:H2'	2.29	0.47
1:1:41:ILE:N	1:1:41:ILE:HD13	2.29	0.47
7:7:76:ALA:O	7:7:80:VAL:HG23	2.15	0.47
20:K:1592:G:O2'	20:K:2840:A:OP1	2.28	0.47
20:K:1961:G:H5'	20:K:1962:A:OP1	2.15	0.47
20:K:1962:A:H2'	20:K:1962:A:N3	2.29	0.47
20:K:4920:C:O2'	20:K:4921:C:H2'	2.14	0.47
38:c:103:ASP:OD1	38:c:103:ASP:C	2.57	0.47
55:v:102:G:OP2	55:v:104:A:O2'	2.29	0.47
20:K:406:C:O2'	20:K:407:A:P	2.73	0.47
20:K:504:G:O2'	20:K:505:G:P	2.73	0.47
20:K:966:A:H62	20:K:2096:G:H2'	1.80	0.47
35:Z:95:VAL:HG13	35:Z:96:VAL:HG23	1.95	0.47
20:K:230:G:OP1	34:Y:15:ARG:NH1	2.46	0.47
20:K:352:G:O2'	55:v:22:U:O4	2.29	0.47
20:K:4977:A:O2'	20:K:4982:A:N1	2.47	0.47
50:o:99:ARG:HG2	50:o:99:ARG:HH11	1.79	0.47
1:1:77:MET:O	1:1:80:GLY:N	2.47	0.46
4:4:23:ASN:OD1	4:4:23:ASN:C	2.58	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:1072:C:C2	20:K:1073:G:C8	3.03	0.46
20:K:1846:G:H2'	20:K:1847:C:C6	2.49	0.46
20:K:2695:A:O2'	20:K:2696:A:OP2	2.22	0.46
20:K:4446:U:O2'	20:K:4450:U:OP1	2.32	0.46
20:K:4625:C:O2'	20:K:4626:A:H5'	2.16	0.46
39:d:46:LEU:HD22	39:d:72:VAL:HG11	1.97	0.46
19:J:13:ARG:O	19:J:136:ARG:NH1	2.38	0.46
20:K:4390:A:H2'	20:K:4391:G:O4'	2.16	0.46
20:K:4571:A:C2	20:K:4572:U:C5	3.04	0.46
20:K:4897:G:C6	20:K:4924:C:N3	2.83	0.46
28:S:84:TYR:CE1	28:S:93:MET:HE3	2.49	0.46
6:6:58:GLU:OE2	8:8:81:GLN:NE2	2.44	0.46
20:K:109:G:OP2	21:L:74:ARG:NH2	2.46	0.46
20:K:172:C:HO2'	20:K:173:C:P	2.39	0.46
20:K:1927:U:OP1	20:K:1949:U:O2'	2.14	0.46
20:K:2835:A:O2'	56:w:228:TYR:O	2.28	0.46
20:K:4212:A:H4'	20:K:4213:A:O5'	2.15	0.46
22:M:36:ALA:HB2	22:M:52:PHE:CE1	2.51	0.46
35:Z:87:VAL:HG12	35:Z:89:ILE:HD12	1.96	0.46
1:1:16:LEU:HD13	1:1:117:LYS:HE3	1.97	0.46
10:A:198:ARG:NH2	20:K:3688:U:OP2	2.42	0.46
20:K:320:C:OP1	44:i:84:LYS:NZ	2.37	0.46
20:K:1308:C:H2'	20:K:1309:C:C6	2.51	0.46
20:K:1893:C:H1'	20:K:1937:C:O2	2.15	0.46
20:K:2358:G:H2'	20:K:2359:U:O4'	2.15	0.46
20:K:4524:G:C2	56:w:252:ALA:HB1	2.50	0.46
23:N:43:THR:OG1	23:N:131:GLU:OE2	2.23	0.46
35:Z:102:ARG:HG2	35:Z:102:ARG:HH11	1.80	0.46
1:1:93:LEU:C	1:1:93:LEU:HD23	2.40	0.46
20:K:2045:G:O6	20:K:3870:C:O2'	2.32	0.46
20:K:2258:C:C2'	20:K:2259:G:OP1	2.63	0.46
20:K:2519:U:H1'	20:K:2520:C:C6	2.51	0.46
20:K:3653:A:C2	20:K:3692:A:O4'	2.68	0.46
20:K:4572:U:H2'	20:K:4573:G:H8	1.80	0.46
33:X:105:ASN:OD1	33:X:107:HIS:N	2.49	0.46
10:A:123:ARG:NH1	20:K:4083:U:OP1	2.48	0.46
19:J:155:HIS:HB2	54:u:55:A:H4'	1.97	0.46
20:K:1440:U:HO2'	20:K:1441:C:P	2.39	0.46
20:K:1666:C:O2'	20:K:1688:G:OP1	2.27	0.46
20:K:2504:C:C2'	20:K:2505:C:O5'	2.63	0.46
20:K:4933:C:H2'	20:K:4934:A:C1'	2.46	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5:171:LEU:HD11	5:5:173:ILE:HD11	1.98	0.46
20:K:704:C:C2'	20:K:705:G:OP1	2.64	0.46
20:K:1173:G:H2'	20:K:1174:G:O4'	2.15	0.46
20:K:1272:C:OP1	37:b:117:ARG:NH2	2.49	0.46
20:K:1877:G:O6	37:b:10:HIS:NE2	2.49	0.46
20:K:1882:U:C4	20:K:2279:A:C2	3.04	0.46
20:K:2878:G:OP2	20:K:2879:A:O2'	2.28	0.46
20:K:4208:U:OP2	29:T:4:THR:OG1	2.30	0.46
20:K:4230:C:O2'	20:K:4234:A:N1	2.39	0.46
20:K:4345:C:O2'	50:o:82:MET:HE3	2.16	0.46
20:K:4448:G:H4'	20:K:4449:A:OP2	2.16	0.46
20:K:4759:C:H2'	20:K:4760:G:O4'	2.16	0.46
20:K:4884:G:C2'	20:K:4885:U:O5'	2.63	0.46
56:w:37:PRO:HA	56:w:187:GLY:O	2.16	0.46
56:w:291:TYR:HB3	56:w:298:LEU:HD11	1.98	0.46
7:7:127:GLU:CD	7:7:127:GLU:C	2.84	0.46
8:8:61:VAL:HG12	8:8:62:GLN:N	2.31	0.46
12:C:261:ASP:O	12:C:265:GLY:N	2.46	0.46
20:K:424:U:H2'	20:K:425:U:C6	2.50	0.46
20:K:1197:C:O2'	20:K:1198:G:H8	1.99	0.46
20:K:2627:C:O4'	20:K:2627:C:O2	2.32	0.46
20:K:2630:U:O4	30:U:89:LYS:NZ	2.49	0.46
20:K:2700:G:H2'	20:K:2701:U:O4'	2.15	0.46
20:K:3635:A:C8	20:K:3692:A:C8	3.04	0.46
20:K:4293:U:O2'	50:o:81:ARG:NH2	2.49	0.46
39:d:97:ASP:OD1	39:d:97:ASP:C	2.59	0.46
20:K:1655:C:OP2	36:a:26:ARG:NH1	2.49	0.46
20:K:3625:G:O2'	20:K:3626:G:OP1	2.29	0.46
20:K:4977:A:H2'	20:K:4978:G:O4'	2.16	0.46
1:1:161:ILE:O	1:1:165:LEU:HG	2.16	0.46
10:A:241:ARG:NH1	20:K:3659:G:OP1	2.49	0.46
20:K:1767:A:N7	20:K:1769:G:N7	2.63	0.46
20:K:2098:G:O2'	20:K:2099:C:H5'	2.16	0.46
20:K:3693:U:C4	20:K:3694:U:C5	3.03	0.46
20:K:4522:G:O2'	20:K:4525:C:OP2	2.34	0.46
50:o:36:GLN:OE1	50:o:39:ARG:NH2	2.49	0.46
20:K:1590:C:H5''	20:K:1591:U:O5'	2.15	0.45
20:K:2376:A:H2'	20:K:2377:C:C6	2.51	0.45
20:K:4183:G:H4'	20:K:4184:G:OP1	2.16	0.45
35:Z:102:ARG:HG2	35:Z:102:ARG:NH1	2.31	0.45
8:8:98:HIS:O	8:8:102:TYR:OH	2.26	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:206:PRO:HG3	10:A:213:GLY:HA3	1.97	0.45
20:K:327:U:O2'	44:i:30:ARG:NH1	2.49	0.45
20:K:644:G:OP2	21:L:162:LYS:NZ	2.49	0.45
20:K:921:C:H2'	20:K:922:C:O4'	2.16	0.45
20:K:1477:C:O2'	20:K:1478:C:P	2.75	0.45
20:K:4508:C:N3	20:K:4512:U:H5	2.13	0.45
7:7:119:GLU:OE1	7:7:119:GLU:C	2.60	0.45
18:I:210:ARG:O	18:I:214:SER:HB2	2.16	0.45
20:K:158:A:N1	20:K:276:C:O2'	2.42	0.45
20:K:711:A:H2'	20:K:712:C:C6	2.52	0.45
20:K:922(B):C:C2'	20:K:923:C:OP1	2.63	0.45
25:P:138:PRO:HB3	25:P:140:MET:HE3	1.98	0.45
35:Z:88:ASP:OD2	35:Z:88:ASP:N	2.40	0.45
56:w:213:GLN:HG3	56:w:214:ASP:OD2	2.16	0.45
20:K:23:C:H2'	20:K:24:G:O4'	2.16	0.45
20:K:58:G:H4'	20:K:59:A:OP1	2.17	0.45
20:K:964:A:H2'	20:K:965:G:O5'	2.16	0.45
20:K:1866:U:H2'	20:K:1867:A:O4'	2.16	0.45
20:K:4085:A:OP1	33:X:45:THR:OG1	2.31	0.45
20:K:4966:A:H2'	20:K:4967:A:O4'	2.16	0.45
29:T:137:GLU:OE2	29:T:137:GLU:N	2.39	0.45
20:K:1976:G:H1'	20:K:2002:A:H62	1.81	0.45
20:K:2258:C:H3'	20:K:2259:G:H8	1.81	0.45
20:K:2308:A:N3	55:v:19:C:O2'	2.45	0.45
20:K:4413:C:O2	20:K:4413:C:O4'	2.33	0.45
20:K:4661:G:N2	20:K:5004:C:O3'	2.49	0.45
39:d:59:THR:HG21	39:d:103:TYR:HA	1.98	0.45
45:j:18:LEU:HD21	47:l:51:LEU:HD13	1.98	0.45
9:9:514:GLU:HG3	9:9:515:TYR:N	2.31	0.45
20:K:1297:U:H2'	20:K:1298:C:H6	1.80	0.45
20:K:2563:C:H2'	20:K:2564:G:O4'	2.15	0.45
20:K:4097:G:N2	20:K:4111:U:O4	2.49	0.45
24:O:181:ALA:O	24:O:185:VAL:HG22	2.17	0.45
56:w:214:ASP:OD1	56:w:363:ILE:N	2.39	0.45
1:1:138:GLY:HA3	1:1:143:MET:HE3	1.98	0.45
1:1:180:SER:O	1:1:453:ILE:HD13	2.17	0.45
12:C:143:ARG:NH1	20:K:2300:A:N7	2.62	0.45
18:I:84:GLY:O	18:I:140:THR:OG1	2.28	0.45
20:K:1201:U:H2'	20:K:1202:C:O4'	2.17	0.45
20:K:1211:G:O2'	20:K:1212:G:P	2.74	0.45
28:S:71:SER:O	28:S:76:LYS:NZ	2.49	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:44:GLU:OE2	22:M:2:VAL:N	2.50	0.45
20:K:1196:G:H2'	20:K:1197:C:O4'	2.17	0.45
20:K:1432:G:HO2'	20:K:1433:A:P	2.39	0.45
20:K:2408:U:OP1	47:l:42:ARG:NH1	2.42	0.45
20:K:4478:G:N2	20:K:4608:G:O2'	2.50	0.45
20:K:1072:C:O2'	20:K:1073:G:O5'	2.26	0.45
20:K:1433:A:H2'	20:K:1434:G:O4'	2.17	0.45
43:h:4:ILE:O	43:h:4:ILE:HG22	2.17	0.45
20:K:280:G:OP2	23:N:44:ARG:NH1	2.49	0.45
20:K:1804:A:O4'	20:K:1806:G:C8	2.70	0.45
20:K:2468:U:C2	20:K:2506:G:N7	2.85	0.45
20:K:4633:G:O2'	20:K:4635:A:OP2	2.16	0.45
20:K:281:U:C2	20:K:282:C:C6	3.06	0.44
20:K:485:C:O2'	20:K:486:C:O5'	2.31	0.44
20:K:962:C:N4	20:K:963:G:O6	2.50	0.44
20:K:1607:C:O2'	20:K:3828:A:N3	2.32	0.44
20:K:4069:U:H2'	20:K:4070:U:C6	2.52	0.44
37:b:89:VAL:HG23	37:b:90:SER:N	2.32	0.44
1:1:272:TYR:OH	11:B:104:VAL:HG22	2.17	0.44
5:5:109:ASN:O	5:5:149:GLN:N	2.42	0.44
20:K:125:C:O2'	20:K:126:C:P	2.75	0.44
20:K:914:U:H5	20:K:917:A:N7	2.14	0.44
20:K:966:A:N3	20:K:966:A:H2'	2.33	0.44
20:K:2457:G:N3	20:K:3672:G:N2	2.65	0.44
20:K:3733:A:C5	20:K:3734:U:C5	3.05	0.44
30:U:38:ASN:C	30:U:38:ASN:OD1	2.59	0.44
52:q:44:A:H2'	52:q:45:G:O4'	2.17	0.44
55:v:123:U:O2'	55:v:124:U:P	2.75	0.44
17:H:128:MET:HE1	17:H:161:ILE:CD1	2.47	0.44
20:K:155:C:OP1	43:h:109:ARG:NH1	2.48	0.44
20:K:2395:A:OP1	20:K:2395:A:O4'	2.35	0.44
20:K:4254:G:H2'	20:K:4254:G:N3	2.32	0.44
1:1:40:PHE:O	1:1:44:VAL:HG23	2.18	0.44
1:1:305:SER:OG	1:1:324:TRP:NE1	2.50	0.44
5:5:165:GLY:HA2	5:5:196:ILE:HG22	1.99	0.44
20:K:488:G:H2'	20:K:489:C:C6	2.52	0.44
20:K:964:A:C2'	20:K:965:G:O5'	2.65	0.44
20:K:1315:C:N4	20:K:1316:G:O6	2.51	0.44
20:K:2418:A:C5	20:K:2419:C:C5	3.06	0.44
20:K:4621:C:OP1	31:V:48:ARG:HD2	2.18	0.44
20:K:4670:C:O2'	20:K:4672:A:OP2	2.27	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:M:49:ALA:HB2	28:S:100:LEU:HD11	2.00	0.44
20:K:360:A:H4'	20:K:361:C:OP2	2.17	0.44
20:K:4320:G:H2'	20:K:4321:U:O4'	2.17	0.44
37:b:112:ILE:O	37:b:116:LEU:N	2.38	0.44
39:d:65:ASP:OD1	39:d:66:THR:N	2.51	0.44
44:i:4:ARG:HB2	44:i:4:ARG:CZ	2.47	0.44
14:E:95:VAL:O	14:E:95:VAL:HG13	2.17	0.44
20:K:2399:G:O2'	20:K:2822:G:O2'	2.32	0.44
20:K:2465:C:H1'	20:K:3672:G:H1	1.82	0.44
20:K:4769:G:H5'	24:O:176:ARG:HD3	2.00	0.44
28:S:13:VAL:O	28:S:62:VAL:N	2.41	0.44
7:7:15:LEU:HD22	9:9:514:GLU:OE1	2.18	0.44
12:C:108:TRP:O	23:N:204:ARG:NH2	2.50	0.44
20:K:1279:A:O2'	20:K:1281:G:N7	2.33	0.44
7:7:157:LEU:HA	7:7:160:PHE:CD2	2.53	0.44
8:8:46:GLU:HG2	8:8:93:ASP:HA	1.99	0.44
13:D:38:ILE:HD12	29:T:30:TYR:HB2	2.00	0.44
17:H:128:MET:CE	17:H:161:ILE:HD11	2.48	0.44
20:K:115:C:O2	20:K:115:C:O5'	2.36	0.44
20:K:1833:G:N2	20:K:1835:G:O4'	2.50	0.44
20:K:2098:G:C6	20:K:2107:A:C5	3.06	0.44
20:K:2395:A:C2'	20:K:2806:A:HO2'	2.31	0.44
20:K:2581:A:N3	20:K:2654:C:O2'	2.46	0.44
20:K:4277:G:O2'	20:K:4282:A:N1	2.45	0.44
20:K:4896:G:N2	20:K:4927:G:O6	2.41	0.44
20:K:4907:G:N2	20:K:4915:G:C6	2.86	0.44
20:K:4907:G:C6	20:K:4913:G:O6	2.70	0.44
20:K:4916:G:C5	20:K:4917:C:C5	3.06	0.44
20:K:5003:U:H2'	20:K:5004:C:C6	2.53	0.44
36:a:85:GLN:HA	36:a:88:VAL:HG22	1.99	0.44
20:K:745:G:H2'	20:K:746:A:O4'	2.18	0.44
20:K:2436:U:C4	33:X:130:PRO:HG3	2.53	0.44
31:V:92:ASP:OD1	31:V:94:VAL:HG23	2.18	0.44
40:e:21:ILE:CD1	40:e:53:ILE:HD11	2.47	0.44
17:H:141:LYS:NZ	17:H:142:ASP:OD2	2.49	0.43
20:K:489:C:H2'	20:K:490:C:O4'	2.18	0.43
20:K:512:U:O2	20:K:647:G:O6	2.36	0.43
20:K:1317:U:OP1	36:a:21:ARG:NH2	2.47	0.43
20:K:1928:C:C4	24:O:133:ARG:CZ	3.01	0.43
20:K:2021:G:C6	20:K:2022:C:N4	2.86	0.43
20:K:2258:C:H3'	20:K:2259:G:C8	2.53	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:2409:U:H4'	20:K:2428:A:H4'	2.00	0.43
20:K:2815:A:C6	20:K:2816:G:C6	3.05	0.43
40:e:84:GLU:O	40:e:87:VAL:HG22	2.18	0.43
55:v:91:A:H2'	55:v:92:U:O4'	2.18	0.43
10:A:30:ARG:O	10:A:163:ARG:NH1	2.49	0.43
20:K:222:C:H2'	20:K:223:G:O4'	2.17	0.43
20:K:307:A:N3	20:K:310:G:O2'	2.46	0.43
20:K:2810:U:H2'	20:K:2811:G:O4'	2.18	0.43
20:K:3856:A:H5''	25:P:83:TRP:O	2.18	0.43
20:K:4189:U:H2'	20:K:4190:U:O4'	2.18	0.43
20:K:4699:U:H4'	20:K:4700:A:OP1	2.17	0.43
30:U:90:TYR:O	30:U:94:ASN:ND2	2.49	0.43
1:1:145:ALA:O	1:1:149:LEU:N	2.46	0.43
1:1:271:ARG:NH2	1:1:398:GLN:OE1	2.47	0.43
1:1:362:VAL:O	1:1:366:VAL:HG12	2.19	0.43
7:7:112:MET:SD	7:7:116:GLU:HB2	2.59	0.43
18:I:143:GLN:CD	18:I:143:GLN:H	2.26	0.43
20:K:1396:G:O2'	20:K:1468:C:O2'	2.29	0.43
20:K:1660:U:H3'	36:a:13:GLY:HA2	2.00	0.43
20:K:3930:U:H2'	20:K:3931:C:C6	2.53	0.43
51:p:8:VAL:O	51:p:11:VAL:HG22	2.19	0.43
1:1:43:LEU:HB3	3:3:54:VAL:HG11	2.01	0.43
1:1:252:PHE:CD1	1:1:447:ILE:HG23	2.53	0.43
3:3:29:ASP:OD1	3:3:30:ARG:NH1	2.51	0.43
16:G:218:GLU:OE2	23:N:11:TRP:NE1	2.51	0.43
17:H:128:MET:SD	17:H:157:SER:HB3	2.59	0.43
20:K:100:C:H2'	20:K:101:A:O4'	2.18	0.43
20:K:145:G:H2'	20:K:146:G:O4'	2.19	0.43
20:K:466:A:O2'	20:K:468:U:OP2	2.36	0.43
20:K:1493:G:OP1	37:b:44:ARG:NE	2.49	0.43
20:K:1824:G:C6	20:K:1825:A:C6	3.06	0.43
20:K:1941:A:C2	20:K:4434:C:H5'	2.53	0.43
12:C:283:LYS:HD3	26:Q:103:LEU:HD22	2.01	0.43
20:K:1988:G:N3	20:K:1988:G:H2'	2.34	0.43
20:K:2109:A:H2'	20:K:2110:G:C1'	2.48	0.43
20:K:2519:U:OP2	42:g:36:LYS:NZ	2.37	0.43
20:K:3880:G:H2'	20:K:3881:G:C8	2.53	0.43
20:K:4949:G:H4'	20:K:4950:U:C5'	2.49	0.43
51:p:85:ARG:HG3	51:p:85:ARG:HH11	1.83	0.43
5:5:181:ASN:OD1	5:5:181:ASN:N	2.50	0.43
7:7:11:SER:OG	9:9:514:GLU:OE2	2.29	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:7:50:ILE:O	7:7:52:HIS:ND1	2.51	0.43
7:7:54:ASP:C	7:7:54:ASP:OD2	2.61	0.43
20:K:1771:U:H2'	20:K:1772:C:C1'	2.48	0.43
20:K:4301:U:H4'	29:T:54:HIS:CE1	2.54	0.43
20:K:4459:U:H2'	20:K:4460:U:C6	2.53	0.43
20:K:4489:G:N3	20:K:4708:A:H2'	2.34	0.43
20:K:5001:U:H2'	20:K:5002:U:O4'	2.19	0.43
24:O:22:ILE:HD13	24:O:120:VAL:HG11	2.01	0.43
42:g:111:ALA:O	42:g:115:LYS:N	2.48	0.43
55:v:108:A:C2	55:v:112:G:C6	3.07	0.43
1:1:75:THR:O	1:1:78:GLU:N	2.50	0.43
1:1:256:ILE:HG23	3:3:36:ILE:CG2	2.49	0.43
7:7:31:LEU:O	7:7:35:ASN:ND2	2.52	0.43
17:H:112:VAL:CG2	17:H:128:MET:HE3	2.48	0.43
20:K:669:C:O2'	20:K:670:G:OP2	2.28	0.43
20:K:1990:A:H3'	20:K:1991:A:H5''	1.99	0.43
20:K:2095:A:H2'	20:K:2096:G:C8	2.53	0.43
20:K:2258:C:H2'	20:K:2259:G:OP1	2.18	0.43
20:K:2546:G:O2'	20:K:2547:G:OP2	2.37	0.43
20:K:3759:A:C8	20:K:3765:G:N2	2.87	0.43
20:K:4168:G:H2'	20:K:4169:G:H5'	2.00	0.43
20:K:4684:A:H2'	20:K:4685:U:O4'	2.19	0.43
26:Q:178:ARG:O	36:a:51:GLY:N	2.45	0.43
40:e:35:TRP:CZ2	40:e:56:PRO:HD2	2.54	0.43
1:1:120:GLY:O	1:1:124:THR:OG1	2.35	0.43
20:K:2276:A:H2'	20:K:2277:C:O4'	2.18	0.43
20:K:4274:A:H2'	20:K:4275:G:C8	2.54	0.43
20:K:4467:A:O2'	20:K:4510:A:N3	2.49	0.43
20:K:4758:U:O2	20:K:4758:U:O4'	2.37	0.43
34:Y:117:LYS:NZ	55:v:70:G:OP2	2.48	0.43
35:Z:90:PRO:O	35:Z:117:LYS:NZ	2.51	0.43
51:p:56:HIS:CE1	51:p:61:MET:HE3	2.54	0.43
1:1:230:LEU:HD11	5:5:210:MET:HB2	2.01	0.43
5:5:107:PHE:CE1	5:5:175:LEU:HD21	2.53	0.43
6:6:58:GLU:OE1	6:6:79:LYS:NZ	2.37	0.43
17:H:36:ARG:CB	17:H:80:MET:HE2	2.49	0.43
20:K:172:C:O2'	20:K:173:C:P	2.77	0.43
20:K:300:A:H2'	20:K:301:G:H8	1.84	0.43
20:K:481:G:O2'	20:K:482:G:OP2	2.37	0.43
20:K:1194:G:H2'	20:K:1195:G:O4'	2.19	0.43
20:K:2292:C:H2'	20:K:2293:U:C6	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:2379:A:H2'	20:K:2380:G:O4'	2.19	0.43
20:K:2502:A:H4'	20:K:2503:G:OP1	2.19	0.43
20:K:2537:A:H2'	20:K:2538:U:O4'	2.19	0.43
20:K:3910:C:H2'	20:K:3911:C:C6	2.54	0.43
20:K:4584:A:H2'	20:K:4585:U:O4'	2.19	0.43
20:K:4882:U:O2'	20:K:4883:C:H4'	2.19	0.43
55:v:139:G:H2'	55:v:140:C:O4'	2.19	0.43
56:w:113:GLU:OE1	56:w:168:MET:N	2.51	0.43
1:1:394:LEU:HD13	1:1:409:MET:HE1	2.00	0.43
10:A:27:ALA:O	10:A:128:ARG:NH1	2.38	0.43
11:B:118:THR:HG23	11:B:118:THR:O	2.18	0.43
20:K:12:A:H5'	20:K:13:U:OP2	2.19	0.43
20:K:21:G:H1'	55:v:103:A:N3	2.34	0.43
20:K:199:G:H2'	20:K:238:C:OP1	2.17	0.43
20:K:964:A:HO2'	20:K:965:G:P	2.42	0.43
20:K:1075:G:H1	20:K:1235:G:H1	1.67	0.43
20:K:3641:U:OP2	20:K:3646:A:N6	2.45	0.43
20:K:3707:U:H2'	20:K:3708:C:C6	2.54	0.43
25:P:54:LYS:HA	25:P:83:TRP:CD1	2.54	0.43
40:e:90:MET:CA	40:e:90:MET:HE2	2.48	0.43
54:u:13:A:OP2	54:u:66:G:N2	2.50	0.43
55:v:141:C:H2'	55:v:142:U:C6	2.54	0.43
3:3:55:LYS:O	3:3:59:ILE:HG12	2.18	0.42
6:6:156:MET:HE3	7:7:45:TRP:HD1	1.84	0.42
8:8:104:VAL:CG1	8:8:106:PHE:CE1	3.03	0.42
13:D:238:GLU:OE1	13:D:238:GLU:N	2.52	0.42
20:K:26:C:H42	20:K:56:A:N6	2.17	0.42
20:K:66:A:O2'	20:K:326:C:O2	2.34	0.42
20:K:281:U:N3	20:K:282:C:C5	2.87	0.42
20:K:742:G:O2'	20:K:743:G:H5'	2.20	0.42
20:K:1444:G:N2	20:K:2110:G:H1	2.17	0.42
20:K:1669:A:H4'	20:K:1685:G:N2	2.33	0.42
20:K:2407:G:O6	47:l:2:SER:N	2.52	0.42
20:K:2440:U:O2'	20:K:2441:C:P	2.73	0.42
20:K:2627:C:H41	20:K:4649:G:H1	1.67	0.42
20:K:4476:C:O2'	20:K:4478:G:OP2	2.35	0.42
20:K:4948:C:H3'	20:K:4949:G:C5'	2.49	0.42
25:P:2:VAL:HG13	25:P:2:VAL:O	2.19	0.42
8:8:53:ILE:HD11	8:8:134:VAL:HG21	2.00	0.42
20:K:195:C:O2'	34:Y:125:SER:OG	2.35	0.42
20:K:382:G:N1	20:K:385:A:OP2	2.45	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:2730:U:H2'	20:K:2731:C:C6	2.54	0.42
20:K:4928:C:O2	20:K:4928:C:O4'	2.37	0.42
20:K:5004:C:H2'	20:K:5005:G:O4'	2.18	0.42
22:M:81:ASP:OD2	22:M:84:THR:OG1	2.30	0.42
39:d:68:LEU:CD2	39:d:106:VAL:HG12	2.49	0.42
55:v:127:U:O2	55:v:127:U:O4'	2.37	0.42
1:1:359:VAL:O	1:1:362:VAL:HG22	2.19	0.42
3:3:52:PHE:O	3:3:56:LEU:HD12	2.20	0.42
12:C:32:ILE:O	26:Q:23:ILE:HD11	2.19	0.42
13:D:234:ASP:OD2	13:D:234:ASP:C	2.61	0.42
16:G:139:VAL:HG21	16:G:238:LYS:HE3	2.00	0.42
20:K:419:A:N6	55:v:15:G:H1'	2.34	0.42
20:K:703:G:H2'	20:K:704:C:H4'	2.00	0.42
20:K:1391:A:H2'	20:K:1392:A:O4'	2.19	0.42
20:K:2502:A:HO2'	20:K:2503:G:P	2.40	0.42
20:K:4122:G:O2'	35:Z:136:PHE:OXT	2.31	0.42
20:K:4303:C:O2'	20:K:4304:A:H2'	2.18	0.42
52:q:19:G:H4'	52:q:20:U:OP2	2.19	0.42
56:w:317:LEU:CD2	56:w:382:VAL:HG13	2.50	0.42
1:1:64:TRP:CD1	1:1:64:TRP:H	2.37	0.42
1:1:142:GLU:HB2	1:1:143:MET:HE2	2.02	0.42
13:D:79:TYR:N	13:D:82:GLU:OE2	2.48	0.42
20:K:39:A:O2'	20:K:1654:G:O6	2.34	0.42
20:K:649:A:C5	20:K:650:C:C5	3.07	0.42
20:K:1981:G:C2'	20:K:1982:G:O5'	2.67	0.42
20:K:2409:U:H5	20:K:2783:A:N1	2.18	0.42
20:K:3706:C:H2'	20:K:3707:U:O4'	2.19	0.42
20:K:4242:U:H4'	20:K:4243:C:OP1	2.19	0.42
20:K:4417:C:H2'	20:K:4418:G:O4'	2.20	0.42
20:K:4570:G:C2	20:K:4571:A:C8	3.07	0.42
56:w:156:TYR:O	56:w:158:GLN:NE2	2.52	0.42
20:K:705:G:OP2	40:e:5:ARG:NH2	2.49	0.42
20:K:956:A:H8	20:K:957:G:C8	2.37	0.42
20:K:1477:C:HO2'	20:K:1478:C:P	2.36	0.42
20:K:1693:U:H2'	20:K:1694:C:O4'	2.20	0.42
20:K:2503:G:H3'	20:K:2504:C:O4'	2.19	0.42
20:K:4762:A:H2'	20:K:4763:U:O4'	2.20	0.42
35:Z:47:ASP:N	35:Z:69:LYS:O	2.52	0.42
39:d:97:ASP:OD1	39:d:97:ASP:O	2.37	0.42
4:4:14:HIS:ND1	4:4:17:ASN:OD1	2.53	0.42
8:8:69:ASP:N	8:8:105:ARG:O	2.46	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:423:G:H2'	20:K:424:U:O4'	2.20	0.42
20:K:499:G:N3	20:K:499:G:H2'	2.35	0.42
20:K:1541:C:C2	20:K:1619:G:N2	2.87	0.42
20:K:1767:A:N7	20:K:1769:G:C8	2.88	0.42
20:K:1811:G:H2'	20:K:1812:C:C6	2.54	0.42
20:K:1830:G:O2'	20:K:1831:G:H5'	2.20	0.42
20:K:1980:U:N3	20:K:1983:A:OP2	2.52	0.42
20:K:2104:A:O2'	20:K:2105:A:P	2.78	0.42
20:K:2380:G:N2	20:K:2425:U:OP1	2.46	0.42
20:K:2702:C:O2'	20:K:2703:G:H5'	2.20	0.42
20:K:3727:A:H2'	20:K:3728:A:C8	2.53	0.42
20:K:3771:C:H2'	20:K:3772:U:O4'	2.19	0.42
22:M:86:TRP:O	22:M:89:THR:OG1	2.35	0.42
7:7:119:GLU:OE2	9:9:515:TYR:OH	2.34	0.42
13:D:163:LEU:HD23	13:D:163:LEU:C	2.45	0.42
20:K:1604:G:H2'	20:K:1605:G:C8	2.55	0.42
20:K:1670:G:O2'	20:K:1853:G:H4'	2.19	0.42
20:K:1804:A:H4'	20:K:1805:A:O5'	2.19	0.42
20:K:4716:C:OP1	56:w:276:HIS:ND1	2.51	0.42
20:K:4882:U:HO2'	20:K:4883:C:H4'	1.85	0.42
50:o:11:PHE:O	50:o:81:ARG:NH1	2.50	0.42
1:1:117:LYS:HD2	1:1:117:LYS:C	2.44	0.42
7:7:14:ASP:OD2	9:9:517:LYS:NZ	2.51	0.42
16:G:305:LYS:NZ	20:K:4090:G:OP1	2.47	0.42
20:K:132:G:C2	20:K:137:G:C6	3.08	0.42
20:K:262:G:N3	20:K:263:G:C8	2.88	0.42
20:K:1853:G:OP1	36:a:22:ILE:HG21	2.19	0.42
20:K:1893:C:O2'	20:K:1936:C:N3	2.42	0.42
20:K:2079:G:OP2	40:e:64:LYS:NZ	2.44	0.42
20:K:2362:U:OP1	25:P:82:ARG:NH2	2.42	0.42
20:K:4691:A:H2'	20:K:4692:A:O4'	2.19	0.42
20:K:4716:C:OP2	56:w:30:LYS:HG3	2.20	0.42
20:K:4909:A:OP1	24:O:163:LYS:NZ	2.51	0.42
22:M:40:GLY:HA3	22:M:45:VAL:HB	2.02	0.42
24:O:48:TYR:CE1	24:O:52:LEU:HD11	2.54	0.42
20:K:686:A:H2'	20:K:686:A:N3	2.34	0.42
20:K:960:A:H4'	20:K:961:G:OP2	2.19	0.42
20:K:1190:C:N3	20:K:1191:C:C5	2.88	0.42
20:K:1996:C:H2'	20:K:1997:U:H1'	2.02	0.42
20:K:3603:G:N2	20:K:3604:A:N1	2.67	0.42
20:K:4771:C:C2'	20:K:4773:C:H41	2.33	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:U:61:VAL:HG22	30:U:74:SER:CB	2.49	0.42
38:c:17:ARG:NE	38:c:103:ASP:OD1	2.53	0.42
1:1:39:LEU:HD13	1:1:39:LEU:O	2.19	0.42
14:E:71:TYR:CE2	20:K:1072:C:C4	3.08	0.42
20:K:351:C:H2'	20:K:352:G:O4'	2.20	0.42
20:K:1411(A):G:H2'	20:K:1411(B):C:H6	1.84	0.42
20:K:2467:U:H4'	20:K:2468:U:H5'	2.02	0.42
20:K:3765:G:C4'	20:K:3766:A:OP1	2.68	0.42
20:K:4457:U:O2	56:w:252:ALA:HB3	2.19	0.42
20:K:4949:G:H4'	20:K:4950:U:OP1	2.20	0.42
20:K:4971:A:C5	20:K:4972:U:C5	3.08	0.42
42:g:13:TYR:O	42:g:18:ASN:ND2	2.42	0.42
3:3:51:GLY:O	3:3:54:VAL:HG12	2.19	0.41
20:K:968:C:HO2'	20:K:969:C:C5'	2.23	0.41
20:K:1087:A:H2'	20:K:1088:C:C6	2.55	0.41
20:K:2458:C:H5''	23:N:67:ARG:HD2	2.02	0.41
20:K:2729:C:H2'	20:K:2730:U:O4'	2.20	0.41
20:K:3816:A:OP1	20:K:3818:U:H5	2.03	0.41
36:a:39:HIS:O	36:a:41:HIS:N	2.53	0.41
20:K:119:G:H3'	20:K:120:A:C5'	2.49	0.41
20:K:4423:U:O2	20:K:4423:U:O4'	2.36	0.41
40:e:124:ASN:OD1	40:e:124:ASN:N	2.53	0.41
15:F:89:ALA:HB2	15:F:124:LEU:HD21	2.01	0.41
20:K:481(A):C:O5'	20:K:482:G:P	2.78	0.41
20:K:965:G:N2	20:K:2096:G:O2'	2.53	0.41
20:K:3888:G:O2'	20:K:3889:G:P	2.76	0.41
20:K:4092:G:C4	20:K:4093:G:C8	3.08	0.41
20:K:4350:C:C2	20:K:4351:U:C5	3.08	0.41
20:K:4918:C:C2	20:K:4919:G:C8	3.08	0.41
44:i:26:HIS:O	44:i:29:ARG:HG3	2.19	0.41
56:w:19:ARG:HB2	56:w:234:ARG:NH2	2.34	0.41
5:5:134:ILE:HD12	5:5:169:PHE:HD2	1.85	0.41
9:9:485:TRP:O	9:9:489:VAL:HG23	2.20	0.41
20:K:1978:C:H3'	20:K:1979:A:C8	2.55	0.41
20:K:4582:C:O2'	20:K:4583:C:H5'	2.20	0.41
24:O:84:VAL:HG11	24:O:102:LEU:HD22	2.03	0.41
26:Q:43:PHE:CD2	26:Q:133:GLY:HA3	2.55	0.41
52:q:4:U:H2'	52:q:5:C:O4'	2.19	0.41
11:B:117:GLY:O	11:B:118:THR:HG22	2.20	0.41
20:K:732:A:H2'	20:K:733:A:O4'	2.20	0.41
20:K:970:G:H2'	20:K:971:U:O4'	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:1398:A:H61	20:K:1419:G:H2'	1.86	0.41
20:K:1460:C:H5''	26:Q:144:LYS:HG2	2.01	0.41
20:K:1660:U:C2	20:K:2346:C:C5	3.08	0.41
20:K:2338:C:OP1	53:r:19:LYS:NZ	2.45	0.41
20:K:2882:A:H2'	20:K:2883:G:H5'	2.02	0.41
20:K:4298:A:OP1	26:Q:160:HIS:NE2	2.54	0.41
20:K:4476:C:O2	20:K:4476:C:O4'	2.37	0.41
20:K:4948:C:H2'	20:K:4949:G:N2	2.35	0.41
55:v:125:C:C2'	55:v:126:C:O5'	2.67	0.41
7:7:54:ASP:OD2	7:7:55:LEU:N	2.52	0.41
7:7:167:ILE:O	7:7:171:SER:OG	2.24	0.41
13:D:289:ARG:NH1	20:K:1180:C:OP2	2.52	0.41
17:H:155:SER:OG	20:K:4688:C:O2'	2.35	0.41
20:K:275:C:O2'	20:K:276:C:P	2.78	0.41
20:K:1449:C:O2	20:K:2105:A:O2'	2.29	0.41
20:K:1858:A:C2	20:K:1859:C:C5	3.08	0.41
20:K:2529:A:O2'	20:K:2531:C:C6	2.74	0.41
20:K:2562:G:C4	20:K:2564:G:OP2	2.74	0.41
20:K:2659:A:C2	20:K:2676:A:N9	2.88	0.41
20:K:2744:A:H2'	20:K:2745:A:C8	2.56	0.41
20:K:2787:A:N3	20:K:2787:A:C2'	2.83	0.41
1:1:243:MET:SD	1:1:244:ASN:N	2.94	0.41
5:5:126:TYR:HA	5:5:134:ILE:HD11	2.02	0.41
20:K:1930:U:OP2	24:O:49:ARG:NH1	2.46	0.41
20:K:2489:C:H1'	20:K:2490:U:P	2.61	0.41
20:K:2701:U:H2'	20:K:2702:C:C6	2.55	0.41
1:1:289:ILE:N	1:1:290:PRO:CD	2.83	0.41
6:6:61:ASP:HB3	6:6:76:LEU:HB3	2.03	0.41
12:C:101:MET:SD	12:C:104:PRO:HA	2.61	0.41
18:I:51:HIS:ND1	18:I:137:SER:OG	2.47	0.41
20:K:119:G:H3'	20:K:120:A:H5''	2.02	0.41
20:K:419:A:N3	20:K:1332:C:O2'	2.48	0.41
20:K:756:G:O2'	20:K:757:G:H5'	2.21	0.41
20:K:1667:A:N1	20:K:2281:U:OP2	2.54	0.41
20:K:1957:U:O2'	20:K:1958:A:H8	2.04	0.41
20:K:2045:G:OP2	20:K:4461:C:H4'	2.21	0.41
20:K:2485:U:C2	20:K:2486:G:C8	3.08	0.41
20:K:3945:A:C6	20:K:3946:G:N7	2.89	0.41
27:R:51:ILE:HG22	27:R:52:ARG:N	2.36	0.41
34:Y:74:TYR:OH	55:v:75:G:OP2	2.29	0.41
45:j:39:TYR:CD1	45:j:40:PRO:HA	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:q:31:C:O2	52:q:31:C:H2'	2.21	0.41
1:1:153:ILE:O	1:1:157:VAL:HG23	2.21	0.41
12:C:191:ALA:HB2	20:K:2334:C:C5	2.56	0.41
13:D:146:LEU:HD22	13:D:163:LEU:HD12	2.02	0.41
14:E:290:VAL:O	22:M:109:ARG:NH2	2.54	0.41
19:J:97:ASN:OD1	19:J:98:ASN:N	2.54	0.41
20:K:100:C:O2	20:K:100:C:O4'	2.36	0.41
20:K:125:C:H2'	20:K:126:C:H6	1.86	0.41
20:K:650:C:C2	20:K:651:C:C5	3.09	0.41
20:K:709:C:H1'	20:K:4942:C:H5	1.85	0.41
20:K:1236:C:O2'	20:K:1237:C:P	2.79	0.41
20:K:1411:C:C4	20:K:1411(A):G:N7	2.89	0.41
20:K:1455:G:O2'	20:K:1456:C:P	2.79	0.41
20:K:1662:C:H2'	20:K:1663:C:C6	2.56	0.41
20:K:1773:U:H2'	20:K:1774:C:C6	2.55	0.41
20:K:2341:A:OP2	36:a:4:ARG:NH2	2.48	0.41
20:K:2412:A:H2'	20:K:2413:U:C6	2.56	0.41
20:K:2580:U:OP1	35:Z:36:ARG:NH1	2.42	0.41
20:K:3656:A:H2'	20:K:3657:U:H6	1.86	0.41
20:K:3861:A:C2	20:K:3862:A:C5	3.09	0.41
20:K:4515:G:C2	20:K:4516:G:C8	3.09	0.41
30:U:35:ASP:OD1	30:U:37:ALA:N	2.51	0.41
32:W:2:LYS:HB2	32:W:2:LYS:HE2	1.93	0.41
36:a:39:HIS:O	36:a:42:ARG:N	2.54	0.41
55:v:27:U:H2'	55:v:28:C:C6	2.56	0.41
55:v:124:U:O2'	55:v:125:C:OP2	2.37	0.41
56:w:317:LEU:HD21	56:w:382:VAL:HG13	2.02	0.41
11:B:106:GLY:N	11:B:107:PRO:CD	2.84	0.41
20:K:1236:C:HO2'	20:K:1237:C:P	2.44	0.41
20:K:2875:C:H5'	51:p:8:VAL:HG13	2.03	0.41
20:K:3710:G:H1'	20:K:3712:A:N6	2.36	0.41
20:K:3717:A:H2'	20:K:3718:A:C8	2.55	0.41
20:K:4188:U:H2'	20:K:4189:U:C6	2.56	0.41
20:K:4468:U:O2	20:K:4708:A:C8	2.74	0.41
20:K:4884:G:O2'	20:K:4885:U:O5'	2.37	0.41
30:U:26:THR:HG22	30:U:68:SER:HB2	2.03	0.41
33:X:105:ASN:OD1	33:X:105:ASN:C	2.64	0.41
55:v:80:A:H3'	55:v:81:C:C5'	2.51	0.41
55:v:84:A:H4'	55:v:85:U:C5'	2.51	0.41
1:1:245:LEU:HD11	1:1:249:ILE:HD11	2.03	0.40
11:B:72:LEU:HG	11:B:76:LEU:HD13	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:77:LEU:HD22	11:B:77:LEU:O	2.22	0.40
20:K:90:G:OP2	20:K:92:C:N4	2.48	0.40
20:K:424:U:C2	20:K:425:U:C5	3.10	0.40
20:K:1355:G:H2'	20:K:1356:U:O4'	2.22	0.40
20:K:1513:U:H2'	20:K:1514:U:O4'	2.21	0.40
20:K:1673:U:O2'	20:K:4304:A:N7	2.48	0.40
20:K:2104:A:O2'	20:K:2105:A:O4'	2.33	0.40
20:K:2830:G:C6	20:K:3856:A:N6	2.88	0.40
20:K:3911:C:H2'	20:K:3912:U:C6	2.56	0.40
20:K:4077:A:N1	20:K:4171:C:N4	2.63	0.40
20:K:4173:G:H2'	20:K:4174:U:C6	2.56	0.40
20:K:4884:G:O2'	20:K:4885:U:P	2.79	0.40
30:U:23:LEU:HD23	30:U:110:TYR:HB2	2.04	0.40
38:c:36:LYS:O	38:c:40:GLN:HG2	2.21	0.40
39:d:27:ILE:HD11	39:d:86:VAL:HG21	2.01	0.40
55:v:31:G:H2'	55:v:32:C:O4'	2.22	0.40
55:v:62:A:H4'	55:v:63:U:O5'	2.21	0.40
19:J:128:LEU:N	19:J:128:LEU:HD23	2.35	0.40
20:K:1479:G:H2'	20:K:1480:C:C6	2.57	0.40
20:K:2267:U:C2'	20:K:2268:A:OP1	2.69	0.40
20:K:2341:A:O2'	20:K:2342:G:H5'	2.21	0.40
21:L:90:VAL:O	21:L:90:VAL:HG12	2.21	0.40
25:P:170:ILE:HD12	25:P:170:ILE:N	2.35	0.40
27:R:95:TRP:CZ2	27:R:99:MET:SD	3.14	0.40
30:U:27:HIS:O	30:U:30:GLU:HG2	2.21	0.40
42:g:73:HIS:CD2	42:g:73:HIS:C	2.98	0.40
55:v:5:U:H2'	55:v:6:C:H6	1.86	0.40
56:w:294:LYS:O	56:w:297:LYS:HG2	2.22	0.40
16:G:318:LEU:HD23	16:G:318:LEU:H	1.86	0.40
20:K:433:A:C2	20:K:3867:A:H4'	2.56	0.40
20:K:453:G:N3	20:K:453:G:H2'	2.36	0.40
20:K:651:C:H2'	20:K:652:G:H8	1.86	0.40
20:K:1545:G:H2'	20:K:1546:C:C6	2.57	0.40
20:K:1957:U:O2'	20:K:1958:A:P	2.79	0.40
20:K:2543:A:H5''	20:K:2544:G:OP2	2.21	0.40
20:K:4915:G:C6	20:K:4916:G:C5	3.09	0.40
42:g:103:VAL:O	42:g:107:LEU:HD23	2.21	0.40
54:u:11:A:N1	54:u:66:G:O2'	2.42	0.40
1:1:196:PHE:CE1	1:1:213:ILE:HG21	2.56	0.40
6:6:55:LEU:HD23	6:6:82:ARG:HG3	2.04	0.40
7:7:46:LEU:HD22	7:7:50:ILE:HD12	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:7:119:GLU:OE1	7:7:120:ARG:N	2.54	0.40
20:K:24:G:N7	45:j:46:LYS:NZ	2.67	0.40
20:K:969:C:H5''	20:K:2259:G:O6	2.22	0.40
20:K:1479:G:O2'	20:K:1480:C:H5'	2.21	0.40
20:K:2018:C:H2'	20:K:2019:C:C6	2.57	0.40
20:K:2486:G:H2'	20:K:2487:G:C8	2.56	0.40
20:K:2750:G:H2'	20:K:2751:G:O4'	2.22	0.40
20:K:2753:G:H5'	35:Z:135:ARG:CZ	2.51	0.40
20:K:2857:A:H2'	20:K:2858:A:O4'	2.21	0.40
20:K:3939:G:N7	20:K:4170:A:H2'	2.36	0.40
20:K:4348:A:O2'	20:K:4350:C:OP2	2.39	0.40
20:K:4967:A:H2'	20:K:4968:A:C8	2.57	0.40
54:u:45:U:H2'	54:u:46:C:O4'	2.22	0.40
56:w:77:THR:HG21	56:w:337:VAL:HG22	2.03	0.40
56:w:153:MET:HE3	56:w:194:LEU:HD21	2.03	0.40
1:1:39:LEU:HD23	1:1:181:LEU:HD23	2.04	0.40
1:1:189:GLU:C	1:1:189:GLU:OE2	2.65	0.40
5:5:162:GLU:N	5:5:163:PRO:HD2	2.37	0.40
12:C:69:THR:HG21	20:K:3906:A:H2'	2.03	0.40
20:K:65:A:N6	20:K:75:G:H1'	2.36	0.40
20:K:88:A:O2'	20:K:292:G:O2'	2.35	0.40
20:K:966:A:H1'	20:K:968:C:N4	2.37	0.40
20:K:1411(B):C:H2'	20:K:1411(C):C:H6	1.86	0.40
20:K:2046:G:H1'	20:K:2047:A:OP2	2.22	0.40
20:K:2683:C:H2'	20:K:2684:C:C6	2.57	0.40
20:K:4084:G:H4'	20:K:4085:A:OP2	2.21	0.40
24:O:54:TYR:OH	24:O:73:PHE:O	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	1	455/476 (96%)	442 (97%)	13 (3%)	0	100	100
2	2	30/96 (31%)	30 (100%)	0	0	100	100
3	3	64/68 (94%)	64 (100%)	0	0	100	100
4	4	29/66 (44%)	28 (97%)	1 (3%)	0	100	100
5	5	174/286 (61%)	170 (98%)	4 (2%)	0	100	100
6	6	160/183 (87%)	156 (98%)	4 (2%)	0	100	100
7	7	177/185 (96%)	172 (97%)	5 (3%)	0	100	100
8	8	148/173 (86%)	146 (99%)	2 (1%)	0	100	100
9	9	34/593 (6%)	34 (100%)	0	0	100	100
10	A	246/257 (96%)	238 (97%)	8 (3%)	0	100	100
11	B	57/229 (25%)	45 (79%)	11 (19%)	1 (2%)	6	25
12	C	360/425 (85%)	350 (97%)	10 (3%)	0	100	100
13	D	291/297 (98%)	288 (99%)	3 (1%)	0	100	100
14	E	215/291 (74%)	207 (96%)	8 (4%)	0	100	100
15	F	223/247 (90%)	217 (97%)	6 (3%)	0	100	100
16	G	229/319 (72%)	225 (98%)	4 (2%)	0	100	100
17	H	188/192 (98%)	186 (99%)	2 (1%)	0	100	100
18	I	201/214 (94%)	198 (98%)	3 (2%)	0	100	100
19	J	168/178 (94%)	166 (99%)	2 (1%)	0	100	100
21	L	208/211 (99%)	203 (98%)	5 (2%)	0	100	100
22	M	136/218 (62%)	130 (96%)	6 (4%)	0	100	100
23	N	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
24	O	197/203 (97%)	193 (98%)	4 (2%)	0	100	100
25	P	179/184 (97%)	176 (98%)	3 (2%)	0	100	100
26	Q	185/187 (99%)	180 (97%)	5 (3%)	0	100	100
27	R	153/196 (78%)	151 (99%)	2 (1%)	0	100	100
28	S	174/176 (99%)	172 (99%)	2 (1%)	0	100	100
29	T	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
30	U	100/128 (78%)	97 (97%)	3 (3%)	0	100	100
31	V	129/140 (92%)	129 (100%)	0	0	100	100
32	W	61/157 (39%)	60 (98%)	1 (2%)	0	100	100
33	X	116/156 (74%)	113 (97%)	3 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	Y	132/145 (91%)	127 (96%)	5 (4%)	0	100	100
35	Z	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
36	a	145/148 (98%)	137 (94%)	7 (5%)	1 (1%)	18	48
37	b	100/226 (44%)	94 (94%)	6 (6%)	0	100	100
38	c	96/115 (84%)	95 (99%)	1 (1%)	0	100	100
39	d	105/125 (84%)	104 (99%)	1 (1%)	0	100	100
40	e	126/135 (93%)	122 (97%)	4 (3%)	0	100	100
41	f	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
42	g	112/116 (97%)	111 (99%)	1 (1%)	0	100	100
43	h	120/123 (98%)	117 (98%)	3 (2%)	0	100	100
44	i	100/105 (95%)	97 (97%)	3 (3%)	0	100	100
45	j	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
46	k	67/70 (96%)	67 (100%)	0	0	100	100
47	l	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
48	m	50/102 (49%)	50 (100%)	0	0	100	100
49	n	23/25 (92%)	23 (100%)	0	0	100	100
50	o	102/106 (96%)	99 (97%)	3 (3%)	0	100	100
51	p	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
53	r	122/137 (89%)	117 (96%)	5 (4%)	0	100	100
56	w	392/403 (97%)	385 (98%)	7 (2%)	0	100	100
All	All	7698/9662 (80%)	7512 (98%)	184 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
36	a	40	HIS
11	B	120	VAL

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	388/398 (98%)	382 (98%)	6 (2%)	57	84
2	2	28/74 (38%)	25 (89%)	3 (11%)	6	22
3	3	59/59 (100%)	57 (97%)	2 (3%)	32	66
4	4	26/55 (47%)	26 (100%)	0	100	100
5	5	157/249 (63%)	154 (98%)	3 (2%)	50	79
6	6	135/152 (89%)	134 (99%)	1 (1%)	76	92
7	7	161/164 (98%)	160 (99%)	1 (1%)	78	93
8	8	130/146 (89%)	130 (100%)	0	100	100
9	9	35/526 (7%)	35 (100%)	0	100	100
10	A	190/199 (96%)	189 (100%)	1 (0%)	81	93
11	B	48/172 (28%)	47 (98%)	1 (2%)	47	77
12	C	302/347 (87%)	296 (98%)	6 (2%)	48	78
13	D	247/250 (99%)	245 (99%)	2 (1%)	73	90
14	E	197/251 (78%)	197 (100%)	0	100	100
15	F	196/215 (91%)	194 (99%)	2 (1%)	68	89
16	G	200/272 (74%)	195 (98%)	5 (2%)	42	74
17	H	169/171 (99%)	169 (100%)	0	100	100
18	I	175/181 (97%)	175 (100%)	0	100	100
19	J	143/149 (96%)	140 (98%)	3 (2%)	47	77
21	L	175/176 (99%)	175 (100%)	0	100	100
22	M	117/161 (73%)	117 (100%)	0	100	100
23	N	171/172 (99%)	170 (99%)	1 (1%)	78	93
24	O	171/173 (99%)	167 (98%)	4 (2%)	44	76
25	P	160/163 (98%)	159 (99%)	1 (1%)	78	93
26	Q	164/164 (100%)	163 (99%)	1 (1%)	78	93
27	R	138/175 (79%)	138 (100%)	0	100	100
28	S	157/157 (100%)	157 (100%)	0	100	100
29	T	139/140 (99%)	137 (99%)	2 (1%)	59	85
30	U	92/114 (81%)	89 (97%)	3 (3%)	33	67
31	V	101/107 (94%)	100 (99%)	1 (1%)	68	89
32	W	55/126 (44%)	55 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	X	106/134 (79%)	106 (100%)	0	100	100
34	Y	124/135 (92%)	123 (99%)	1 (1%)	73	90
35	Z	117/118 (99%)	116 (99%)	1 (1%)	70	90
36	a	119/120 (99%)	119 (100%)	0	100	100
37	b	84/172 (49%)	83 (99%)	1 (1%)	63	86
38	c	84/98 (86%)	83 (99%)	1 (1%)	63	86
39	d	98/110 (89%)	94 (96%)	4 (4%)	27	61
40	e	114/121 (94%)	113 (99%)	1 (1%)	70	90
41	f	88/89 (99%)	86 (98%)	2 (2%)	44	76
42	g	98/99 (99%)	98 (100%)	0	100	100
43	h	109/110 (99%)	107 (98%)	2 (2%)	51	80
44	i	86/89 (97%)	85 (99%)	1 (1%)	63	86
45	j	73/80 (91%)	73 (100%)	0	100	100
46	k	64/65 (98%)	62 (97%)	2 (3%)	35	69
47	l	47/48 (98%)	47 (100%)	0	100	100
48	m	48/90 (53%)	47 (98%)	1 (2%)	47	77
49	n	24/24 (100%)	24 (100%)	0	100	100
50	o	92/94 (98%)	90 (98%)	2 (2%)	45	77
51	p	74/75 (99%)	74 (100%)	0	100	100
53	r	108/121 (89%)	105 (97%)	3 (3%)	38	72
56	w	342/348 (98%)	342 (100%)	0	100	100
All	All	6725/8198 (82%)	6654 (99%)	71 (1%)	63	88

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	46	CYS
1	1	65	MET
1	1	246	ILE
1	1	288	ASN
1	1	433	VAL
1	1	438	LEU
2	2	77	SER
2	2	85	PHE
2	2	89	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	3	11	SER
3	3	58	HIS
5	5	86	THR
5	5	176	ASN
5	5	181	ASN
6	6	169	TYR
7	7	184	SER
10	A	208	GLU
11	B	91	PHE
12	C	14	LYS
12	C	69	THR
12	C	101	MET
12	C	150	LEU
12	C	158	VAL
12	C	349	LEU
13	D	51	MET
13	D	186	GLU
15	F	100	VAL
15	F	241	ARG
16	G	139	VAL
16	G	168	LEU
16	G	195	THR
16	G	262	SER
16	G	284	ASP
19	J	100	SER
19	J	102	THR
19	J	163	MET
23	N	60	VAL
24	O	43	ILE
24	O	49	ARG
24	O	108	ILE
24	O	118	MET
25	P	57	CYS
26	Q	42	THR
29	T	76	VAL
29	T	114	GLN
30	U	26	THR
30	U	106	THR
30	U	111	GLU
31	V	71	GLU
34	Y	46	SER
35	Z	35	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
37	b	9	THR
38	c	10	SER
39	d	18	ASN
39	d	84	ILE
39	d	101	LYS
39	d	123	ASP
40	e	53	ILE
41	f	2	SER
41	f	24	HIS
43	h	8	ASP
43	h	112	ARG
44	i	81	ILE
46	k	58	GLN
46	k	64	LEU
48	m	87	LYS
50	o	26	TYR
50	o	77	CYS
53	r	26	SER
53	r	76	SER
53	r	103	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	47	GLN
1	1	343	HIS
3	3	62	ASN
8	8	87	GLN
8	8	98	HIS
10	A	22	HIS
12	C	212	ASN
12	C	223	ASN
12	C	329	ASN
12	C	347	HIS
13	D	111	ASN
13	D	198	HIS
13	D	244	HIS
14	E	271	GLN
15	F	57	HIS
15	F	118	ASN
16	G	135	GLN
16	G	212	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
17	H	98	HIS
19	J	110	GLN
22	M	66	HIS
22	M	125	ASN
24	O	42	ASN
24	O	50	ASN
27	R	75	HIS
28	S	108	GLN
30	U	38	ASN
30	U	41	GLN
33	X	111	GLN
33	X	151	ASN
34	Y	61	HIS
36	a	28	HIS
36	a	34	ASN
39	d	121	ASN
40	e	52	GLN
41	f	21	GLN
43	h	98	HIS
44	i	80	HIS
45	j	57	ASN
45	j	66	HIS
50	o	90	HIS
51	p	56	HIS
56	w	184	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
20	K	3521/3543 (99%)	606 (17%)	51 (1%)
52	q	74/76 (97%)	12 (16%)	0
54	u	119/120 (99%)	8 (6%)	0
55	v	155/156 (99%)	23 (14%)	0
All	All	3869/3895 (99%)	649 (16%)	51 (1%)

All (649) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
20	K	5	A
20	K	13	U
20	K	25	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	39	A
20	K	42	A
20	K	56	A
20	K	59	A
20	K	64	A
20	K	65	A
20	K	66	A
20	K	71	C
20	K	73	A
20	K	91	G
20	K	98	A
20	K	109	G
20	K	110	C
20	K	117	C
20	K	118	C
20	K	119	G
20	K	120	A
20	K	122	U
20	K	126	C
20	K	135	G
20	K	136	C
20	K	150	U
20	K	157	U
20	K	159	C
20	K	171	U
20	K	173	C
20	K	195	C
20	K	197	A
20	K	200	U
20	K	203	U
20	K	210	C
20	K	219	G
20	K	224	U
20	K	234	G
20	K	246	G
20	K	250	C
20	K	262	G
20	K	265	C
20	K	266	C
20	K	271	C
20	K	275	C
20	K	276	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	280	G
20	K	297	U
20	K	306	A
20	K	309	C
20	K	315	G
20	K	316	U
20	K	322	C
20	K	334	A
20	K	340	C
20	K	347	A
20	K	387	G
20	K	399	G
20	K	407	A
20	K	409	G
20	K	410	A
20	K	412	G
20	K	432	U
20	K	440	U
20	K	444	G
20	K	449	C
20	K	450	G
20	K	452	A
20	K	453	G
20	K	463	A
20	K	464	G
20	K	467	U
20	K	472	C
20	K	481	G
20	K	481(A)	C
20	K	482	G
20	K	483	G
20	K	486	C
20	K	492	U
20	K	493	G
20	K	497	G
20	K	498	C
20	K	499	G
20	K	505	G
20	K	510	U
20	K	647	G
20	K	658	C
20	K	661	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	666	G
20	K	667	A
20	K	670	G
20	K	672	C
20	K	684	G
20	K	696	C
20	K	697	G
20	K	704	C
20	K	705	G
20	K	708	G
20	K	730	G
20	K	731	G
20	K	738	C
20	K	738(A)	C
20	K	749	G
20	K	758	G
20	K	913	U
20	K	915	A
20	K	917	A
20	K	923	C
20	K	925	C
20	K	926	G
20	K	928	C
20	K	929	A
20	K	932	A
20	K	933	G
20	K	934	C
20	K	935	A
20	K	935(A)	G
20	K	936	C
20	K	938	C
20	K	939	G
20	K	944	A
20	K	945	U
20	K	959	G
20	K	960	A
20	K	961	G
20	K	964	A
20	K	965	G
20	K	966	A
20	K	967	C
20	K	968	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	972	C
20	K	983	C
20	K	1070	G
20	K	1072	C
20	K	1073	G
20	K	1079	C
20	K	1082	C
20	K	1175	A
20	K	1179	U
20	K	1187	G
20	K	1198	G
20	K	1210	C
20	K	1211	G
20	K	1212	G
20	K	1234	G
20	K	1235	G
20	K	1236	C
20	K	1237	C
20	K	1238	A
20	K	1247	U
20	K	1272	C
20	K	1273	G
20	K	1274	A
20	K	1275	G
20	K	1280	C
20	K	1284	G
20	K	1285	U
20	K	1287	G
20	K	1294	A
20	K	1296	G
20	K	1304	C
20	K	1314	C
20	K	1326	A
20	K	1337	A
20	K	1354	A
20	K	1359	G
20	K	1371	A
20	K	1387	A
20	K	1394	G
20	K	1397	A
20	K	1398	A
20	K	1415	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	1416	G
20	K	1420	A
20	K	1421	G
20	K	1433	A
20	K	1436	C
20	K	1437	C
20	K	1438	U
20	K	1440	U
20	K	1441	C
20	K	1446	C
20	K	1448	G
20	K	1455	G
20	K	1456	C
20	K	1457	G
20	K	1458	C
20	K	1478	C
20	K	1482	G
20	K	1498	G
20	K	1502	G
20	K	1504	G
20	K	1523	A
20	K	1534	A
20	K	1535	C
20	K	1547	A
20	K	1564	A
20	K	1566	C
20	K	1578	U
20	K	1588	U
20	K	1591	U
20	K	1596	U
20	K	1613	A
20	K	1624	G
20	K	1625	G
20	K	1631	A
20	K	1633	G
20	K	1634	A
20	K	1638	A
20	K	1640	C
20	K	1641	G
20	K	1654	G
20	K	1655	C
20	K	1661	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	1676	C
20	K	1677	U
20	K	1680	G
20	K	1721	G
20	K	1726	U
20	K	1731	C
20	K	1734	G
20	K	1742	A
20	K	1750	G
20	K	1753	G
20	K	1755	C
20	K	1756	U
20	K	1757	U
20	K	1761	G
20	K	1764	G
20	K	1765	A
20	K	1766	A
20	K	1769	G
20	K	1772	C
20	K	1776	A
20	K	1777	C
20	K	1780	A
20	K	1781	U
20	K	1787	A
20	K	1792	U
20	K	1804	A
20	K	1815	G
20	K	1835	G
20	K	1836	G
20	K	1837	A
20	K	1842	G
20	K	1847	C
20	K	1855	G
20	K	1869	G
20	K	1893	C
20	K	1897	A
20	K	1910	G
20	K	1915	C
20	K	1918	U
20	K	1920	C
20	K	1921	C
20	K	1922	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	1931	C
20	K	1932	A
20	K	1940	G
20	K	1948	G
20	K	1952	G
20	K	1957	U
20	K	1958	A
20	K	1961	G
20	K	1964	A
20	K	1966	C
20	K	1972	G
20	K	1977	C
20	K	1978	C
20	K	1979	A
20	K	1980	U
20	K	1982	G
20	K	1984	A
20	K	1987	C
20	K	1988	G
20	K	1989	G
20	K	1990	A
20	K	1991	A
20	K	1992	U
20	K	1993	C
20	K	1997	U
20	K	1999	A
20	K	2001	G
20	K	2002	A
20	K	2003	G
20	K	2004	U
20	K	2007	G
20	K	2011	C
20	K	2018	C
20	K	2020	U
20	K	2026	A
20	K	2044	U
20	K	2045	G
20	K	2046	G
20	K	2047	A
20	K	2048	U
20	K	2052	G
20	K	2055	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	2056	G
20	K	2062	C
20	K	2064	G
20	K	2069	A
20	K	2084	U
20	K	2089	G
20	K	2090	U
20	K	2092	G
20	K	2093	G
20	K	2094	C
20	K	2100	G
20	K	2101	A
20	K	2102	G
20	K	2104	A
20	K	2105	A
20	K	2107	A
20	K	2108	G
20	K	2110	G
20	K	2259	G
20	K	2260	C
20	K	2267	U
20	K	2268	A
20	K	2270	G
20	K	2289	C
20	K	2300	A
20	K	2301	G
20	K	2313	A
20	K	2333	G
20	K	2348	G
20	K	2351	C
20	K	2395	A
20	K	2396	A
20	K	2402	G
20	K	2422	C
20	K	2425	U
20	K	2441	C
20	K	2450	G
20	K	2469	C
20	K	2475	G
20	K	2476	G
20	K	2483	G
20	K	2486	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	2488	C
20	K	2489	C
20	K	2490	U
20	K	2491	C
20	K	2493	G
20	K	2503	G
20	K	2504	C
20	K	2505	C
20	K	2506	G
20	K	2512	A
20	K	2513	A
20	K	2520	C
20	K	2530	U
20	K	2544	G
20	K	2545	U
20	K	2546	G
20	K	2554	U
20	K	2566	G
20	K	2583	C
20	K	2587	A
20	K	2601	A
20	K	2620	G
20	K	2627	C
20	K	2638	G
20	K	2640	G
20	K	2652	G
20	K	2653	C
20	K	2658	G
20	K	2662	G
20	K	2669	C
20	K	2673	G
20	K	2676	A
20	K	2686	G
20	K	2687	U
20	K	2694	G
20	K	2695	A
20	K	2696	A
20	K	2705	G
20	K	2708	U
20	K	2711	G
20	K	2719	C
20	K	2725	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	2726	G
20	K	2735	G
20	K	2740	U
20	K	2743	A
20	K	2753	G
20	K	2762	G
20	K	2763	U
20	K	2764	A
20	K	2769	U
20	K	2787	A
20	K	2788	U
20	K	2790	U
20	K	2794	C
20	K	2798	A
20	K	2814	C
20	K	2826	U
20	K	2827	G
20	K	2829	U
20	K	2842	G
20	K	2855	G
20	K	2875	C
20	K	3602	C
20	K	3604	A
20	K	3615	G
20	K	3617	G
20	K	3618	C
20	K	3625	G
20	K	3626	G
20	K	3635	A
20	K	3644	U
20	K	3648	A
20	K	3649	A
20	K	3662	A
20	K	3673	C
20	K	3711	A
20	K	3712	A
20	K	3740	G
20	K	3748	A
20	K	3753	G
20	K	3760	A
20	K	3766	A
20	K	3772	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	3773	U
20	K	3776	G
20	K	3777	G
20	K	3784	A
20	K	3785	A
20	K	3786	U
20	K	3811	G
20	K	3814	U
20	K	3817	A
20	K	3819	G
20	K	3822	U
20	K	3838	U
20	K	3840	U
20	K	3859	G
20	K	3876	A
20	K	3877	A
20	K	3878	C
20	K	3879	G
20	K	3885	G
20	K	3889	G
20	K	3897	G
20	K	3901	A
20	K	3905	A
20	K	3906	A
20	K	3907	G
20	K	3908	A
20	K	3915	U
20	K	3916	G
20	K	3938	G
20	K	3943	A
20	K	3946	G
20	K	4066	U
20	K	4073	A
20	K	4076	G
20	K	4085	A
20	K	4119	C
20	K	4120	U
20	K	4121	G
20	K	4122	G
20	K	4127	A
20	K	4148	C
20	K	4162	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	4163	U
20	K	4170	A
20	K	4171	C
20	K	4183	G
20	K	4184	G
20	K	4191	G
20	K	4203	A
20	K	4225	G
20	K	4228	G
20	K	4229	U
20	K	4233	A
20	K	4234	A
20	K	4251	A
20	K	4254	G
20	K	4266	G
20	K	4268	A
20	K	4271	A
20	K	4280	A
20	K	4281	A
20	K	4286	C
20	K	4291	G
20	K	4304	A
20	K	4305	G
20	K	4306	U
20	K	4314	C
20	K	4317	A
20	K	4318	C
20	K	4319	C
20	K	4330	G
20	K	4332	C
20	K	4339	A
20	K	4349	C
20	K	4350	C
20	K	4354	U
20	K	4355	G
20	K	4373	G
20	K	4376	A
20	K	4377	G
20	K	4378	A
20	K	4379	A
20	K	4387	C
20	K	4394	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	4395	U
20	K	4398	C
20	K	4415	A
20	K	4419	U
20	K	4422	A
20	K	4424	A
20	K	4443	C
20	K	4448	G
20	K	4449	A
20	K	4452	U
20	K	4464	A
20	K	4475	G
20	K	4500	U
20	K	4512	U
20	K	4513	A
20	K	4522	G
20	K	4524	G
20	K	4528	G
20	K	4532	U
20	K	4548	A
20	K	4549	G
20	K	4550	G
20	K	4560	C
20	K	4567	G
20	K	4573	G
20	K	4574	U
20	K	4581	G
20	K	4583	C
20	K	4584	A
20	K	4585	U
20	K	4590	A
20	K	4627	U
20	K	4636	U
20	K	4637	G
20	K	4656	A
20	K	4657	U
20	K	4661	G
20	K	4670	C
20	K	4672	A
20	K	4693	C
20	K	4700	A
20	K	4720	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	4736	C
20	K	4745	G
20	K	4751	G
20	K	4752	U
20	K	4754	G
20	K	4757	C
20	K	4759	C
20	K	4761	G
20	K	4765	G
20	K	4771	C
20	K	4772	C
20	K	4868	G
20	K	4870	G
20	K	4871	C
20	K	4875	G
20	K	4881	U
20	K	4882	U
20	K	4883	C
20	K	4885	U
20	K	4895	C
20	K	4896	G
20	K	4897	G
20	K	4903	G
20	K	4915	G
20	K	4921	C
20	K	4922	C
20	K	4924	C
20	K	4925	U
20	K	4926	C
20	K	4928	C
20	K	4934	A
20	K	4944	C
20	K	4945	G
20	K	4948	C
20	K	4949	G
20	K	4950	U
20	K	4951	G
20	K	4956	A
20	K	4958	C
20	K	4960	G
20	K	4965	U
20	K	4966	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	4967	A
20	K	4976	U
20	K	4985	U
20	K	4988	U
20	K	4990	C
20	K	4993	G
20	K	5014	A
20	K	5017	G
20	K	5041	G
20	K	5047	C
20	K	5050	C
20	K	5054	C
20	K	5061	A
20	K	5062	G
20	K	5069	U
52	q	9	A
52	q	20	U
52	q	20(A)	U
52	q	21	A
52	q	47	U
52	q	58	A
52	q	61	C
52	q	63	G
52	q	67	G
52	q	72	C
52	q	75	C
52	q	76	A
54	u	21	G
54	u	31	G
54	u	33	U
54	u	53	U
54	u	54	A
54	u	64	G
54	u	100	A
54	u	110	G
55	v	34	U
55	v	35	C
55	v	38	U
55	v	46	G
55	v	52	A
55	v	59	A
55	v	62	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
55	v	63	U
55	v	81	C
55	v	82	A
55	v	85	U
55	v	86	U
55	v	103	A
55	v	105	C
55	v	109	C
55	v	110	U
55	v	111	U
55	v	113	C
55	v	114	G
55	v	124	U
55	v	125	C
55	v	126	C
55	v	153	C

All (51) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
20	K	12	A
20	K	125	C
20	K	245	C
20	K	265	C
20	K	275	C
20	K	406	C
20	K	480	C
20	K	481(A)	C
20	K	485	C
20	K	504	G
20	K	696	C
20	K	922(B)	C
20	K	959	G
20	K	964	A
20	K	1072	C
20	K	1174	G
20	K	1197	C
20	K	1211	G
20	K	1236	C
20	K	1370	G
20	K	1440	U
20	K	1445	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	K	1455	G
20	K	1477	C
20	K	1590	C
20	K	1633	G
20	K	1992	U
20	K	2046	G
20	K	2089	G
20	K	2104	A
20	K	2258	C
20	K	2266	C
20	K	2489	C
20	K	2502	A
20	K	2639	U
20	K	2695	A
20	K	2762	G
20	K	3603	G
20	K	3625	G
20	K	3765	G
20	K	3876	A
20	K	3888	G
20	K	3904	G
20	K	4119	C
20	K	4170	A
20	K	4232	U
20	K	4354	U
20	K	4448	G
20	K	4699	U
20	K	4884	G
20	K	4947	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 223 ligands modelled in this entry, 223 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
20	K	23
52	q	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	2113:G	O3'	2258:C	P	41.87
1	K	1252:C	O3'	1271:G	P	35.95
1	K	1219:G	O3'	1233:G	P	24.34
1	K	990:C	O3'	1064:G	P	17.41
1	K	4138:C	O3'	4146:G	P	17.32
1	K	4777:C	O3'	4859:C	P	17.01
1	K	4101:C	O3'	4107:G	P	17.00
1	K	3948:C	O3'	4065:G	P	16.47
1	K	1406(C):G	O3'	1411:C	P	15.11
1	K	760:G	O3'	904:C	P	14.82
1	K	1364:U	O3'	1368:A	P	14.42
1	K	182:G	O3'	189:G	P	14.13
1	K	2901:G	O3'	3597:G	P	13.55
1	K	523:C	O3'	638:G	P	13.28
1	K	5022:U	O3'	5028:G	P	13.26
1	K	1696:C	O3'	1720:C	P	12.45
1	K	1100:U	O3'	1168:G	P	8.56
1	K	1180:C	O3'	1183:C	P	8.39
1	K	4729:A	O3'	4735:G	P	8.18

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	512:U	O3'	515:C	P	6.27
1	q	16:C	O3'	18:G	P	6.11
1	K	500:G	O3'	504:G	P	5.94
1	K	4740:G	O3'	4743:G	P	5.33
1	K	4899:G	O3'	4902:C	P	3.90

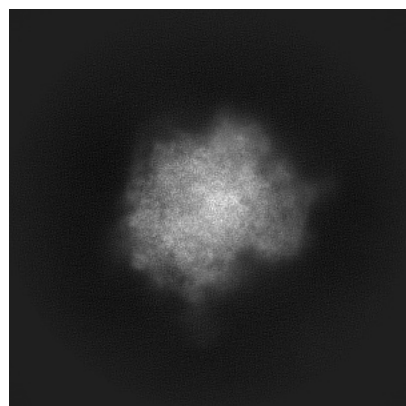
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19197. These allow visual inspection of the internal detail of the map and identification of artifacts.

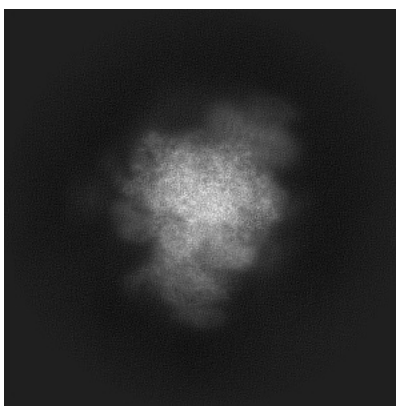
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

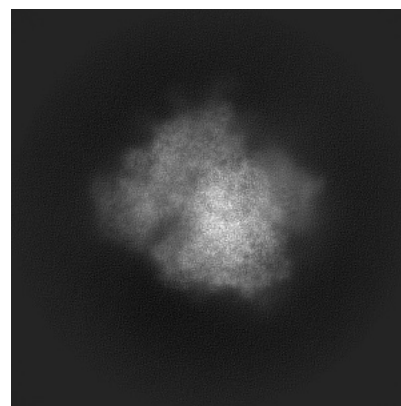
6.1.1 Primary map



X

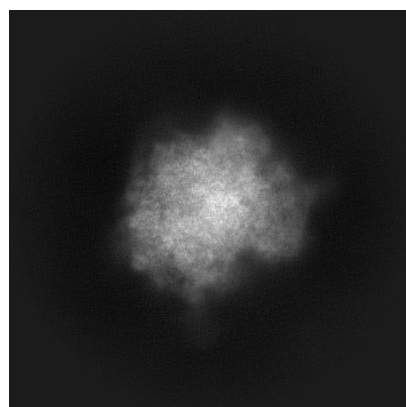


Y

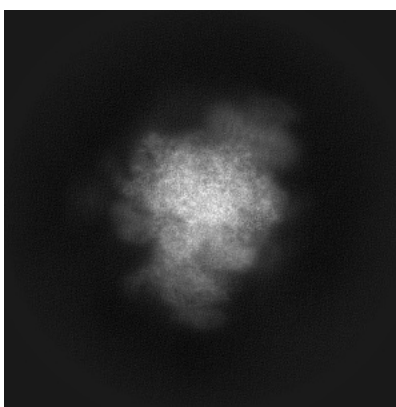


Z

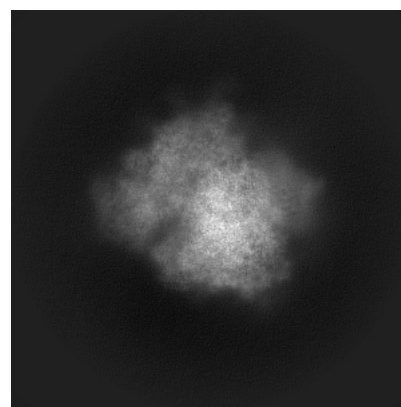
6.1.2 Raw map



X



Y

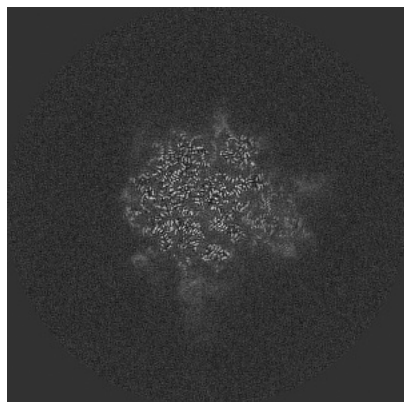


Z

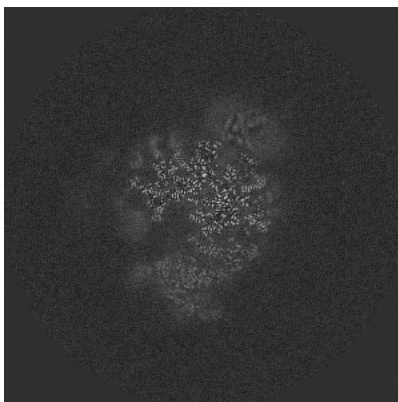
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

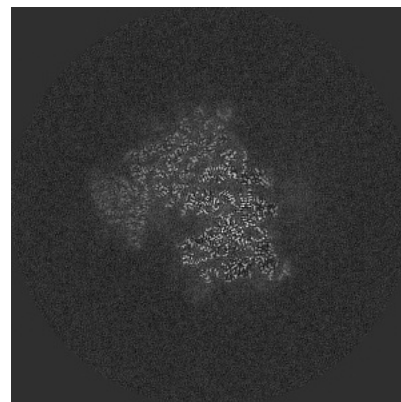
6.2.1 Primary map



X Index: 210

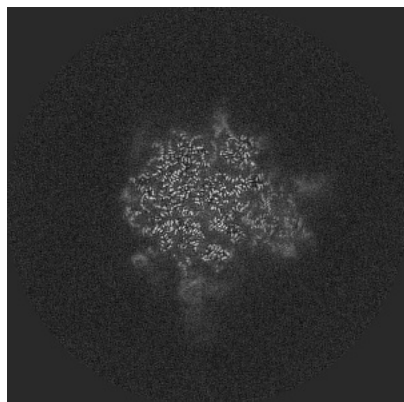


Y Index: 210

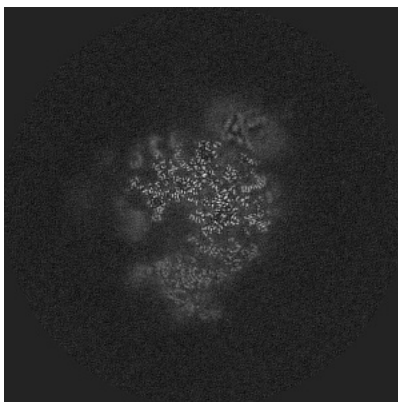


Z Index: 210

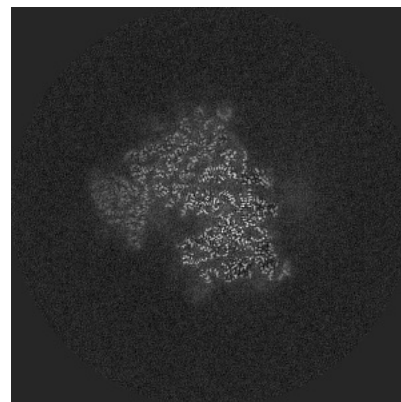
6.2.2 Raw map



X Index: 210



Y Index: 210

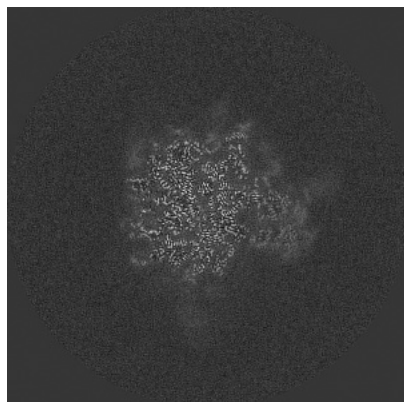


Z Index: 210

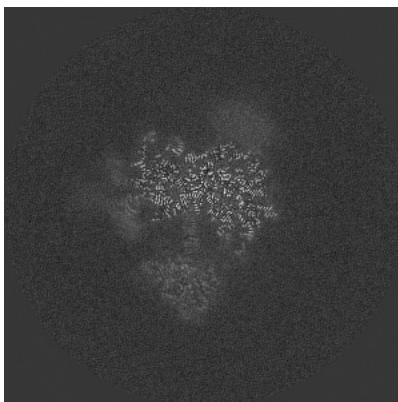
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

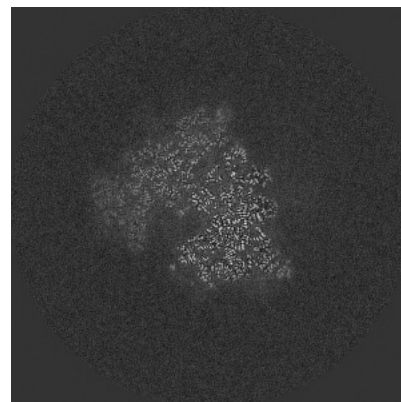
6.3.1 Primary map



X Index: 220

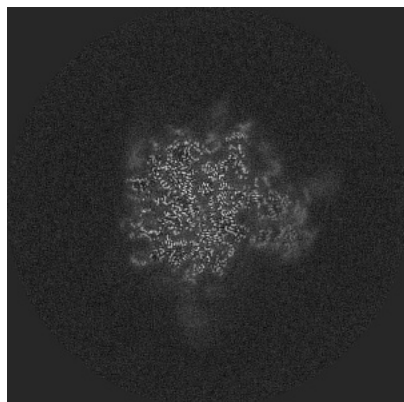


Y Index: 195

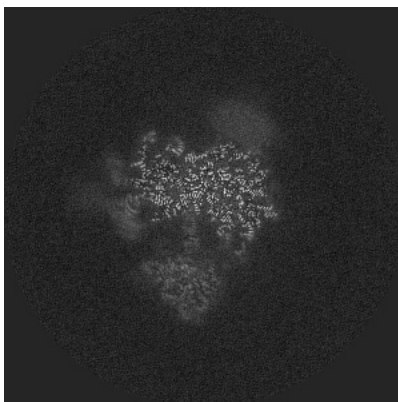


Z Index: 207

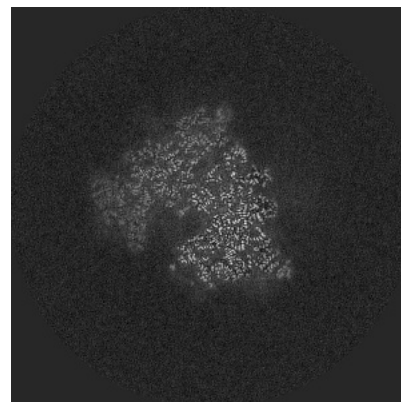
6.3.2 Raw map



X Index: 220



Y Index: 195

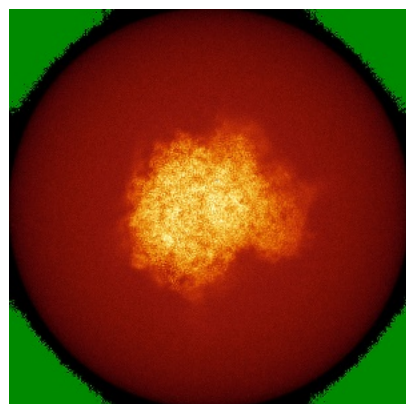


Z Index: 207

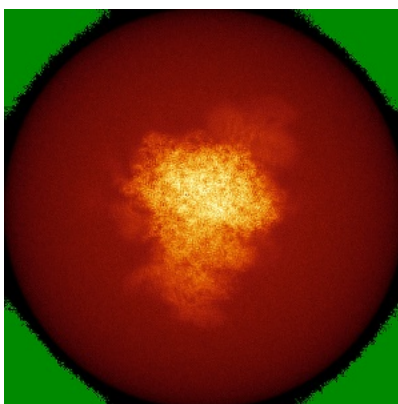
The images above show the largest variance slices of the map in three orthogonal directions.

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

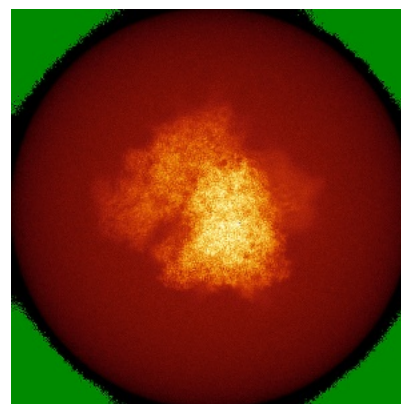
6.4.1 Primary map



X

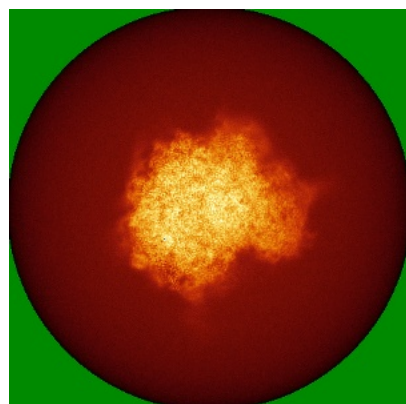


Y

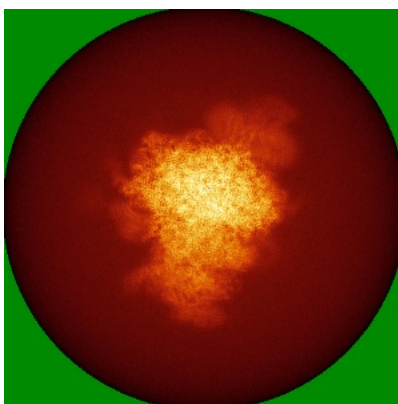


Z

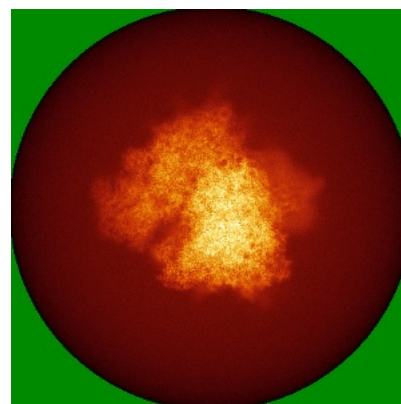
6.4.2 Raw map



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.

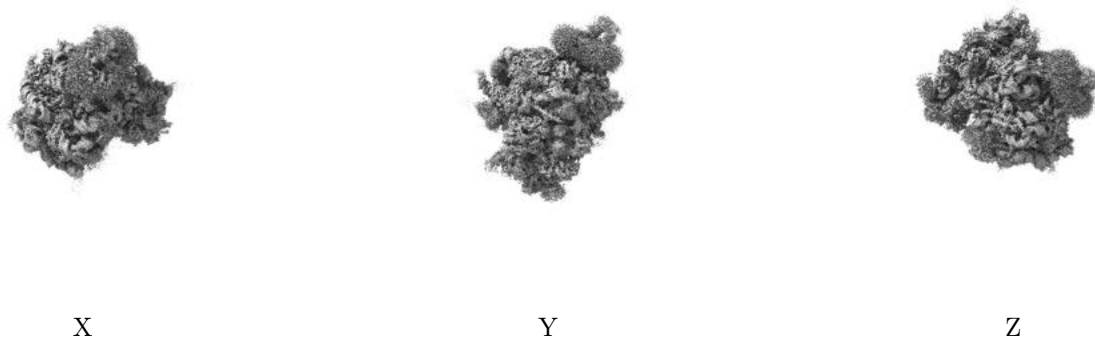
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0231. 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.

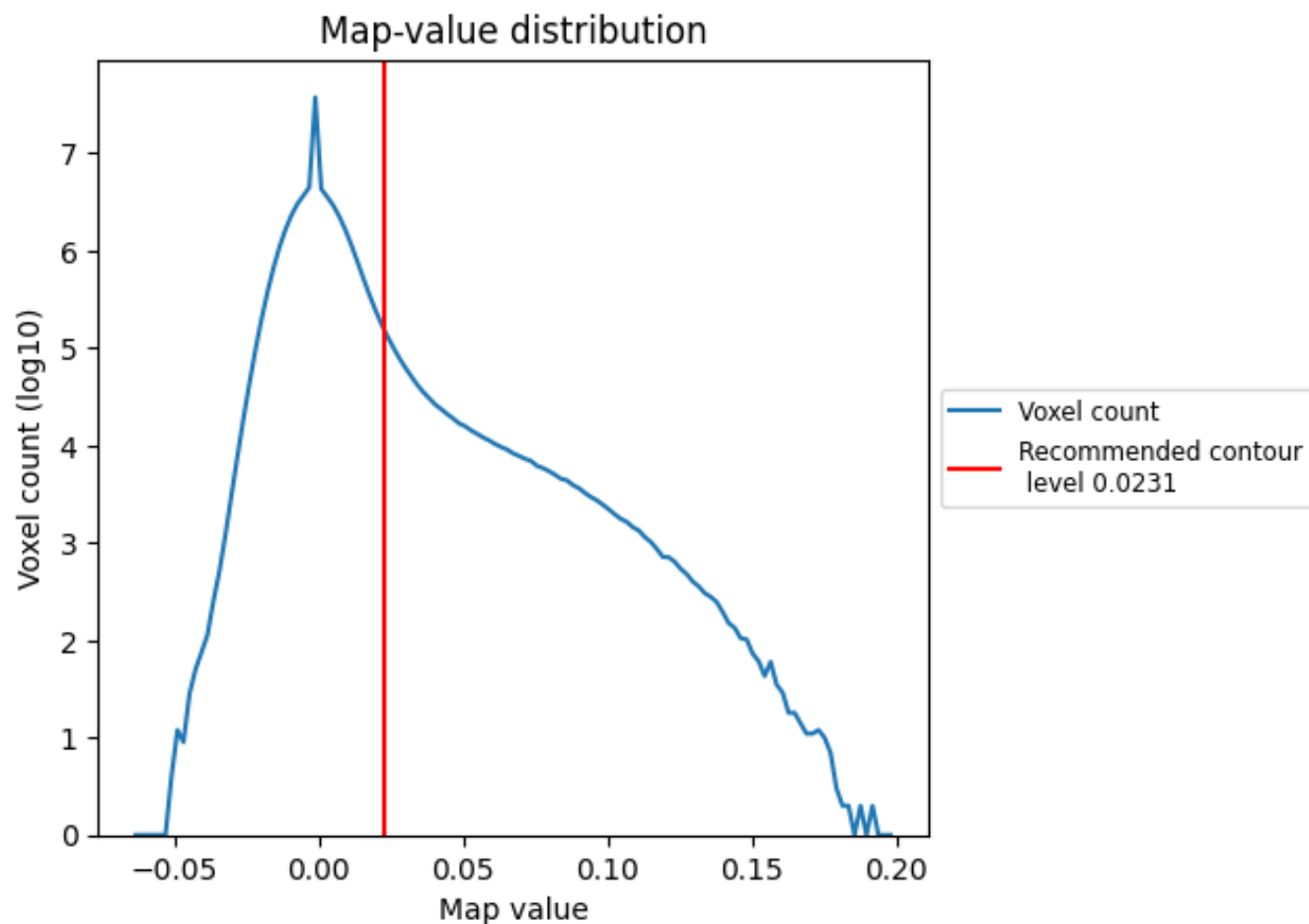
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

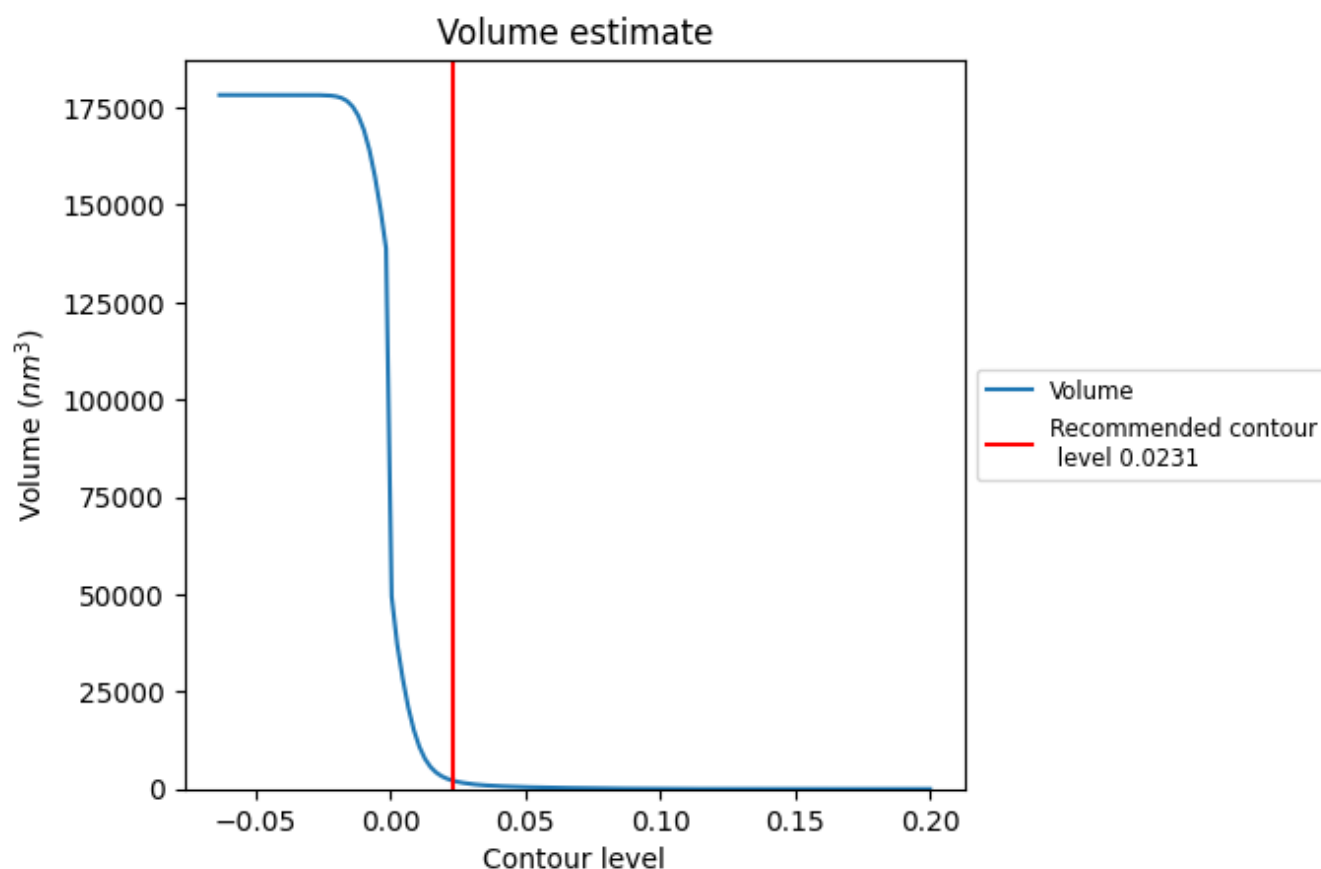
This section contains the results of statistical analysis of the map.

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.

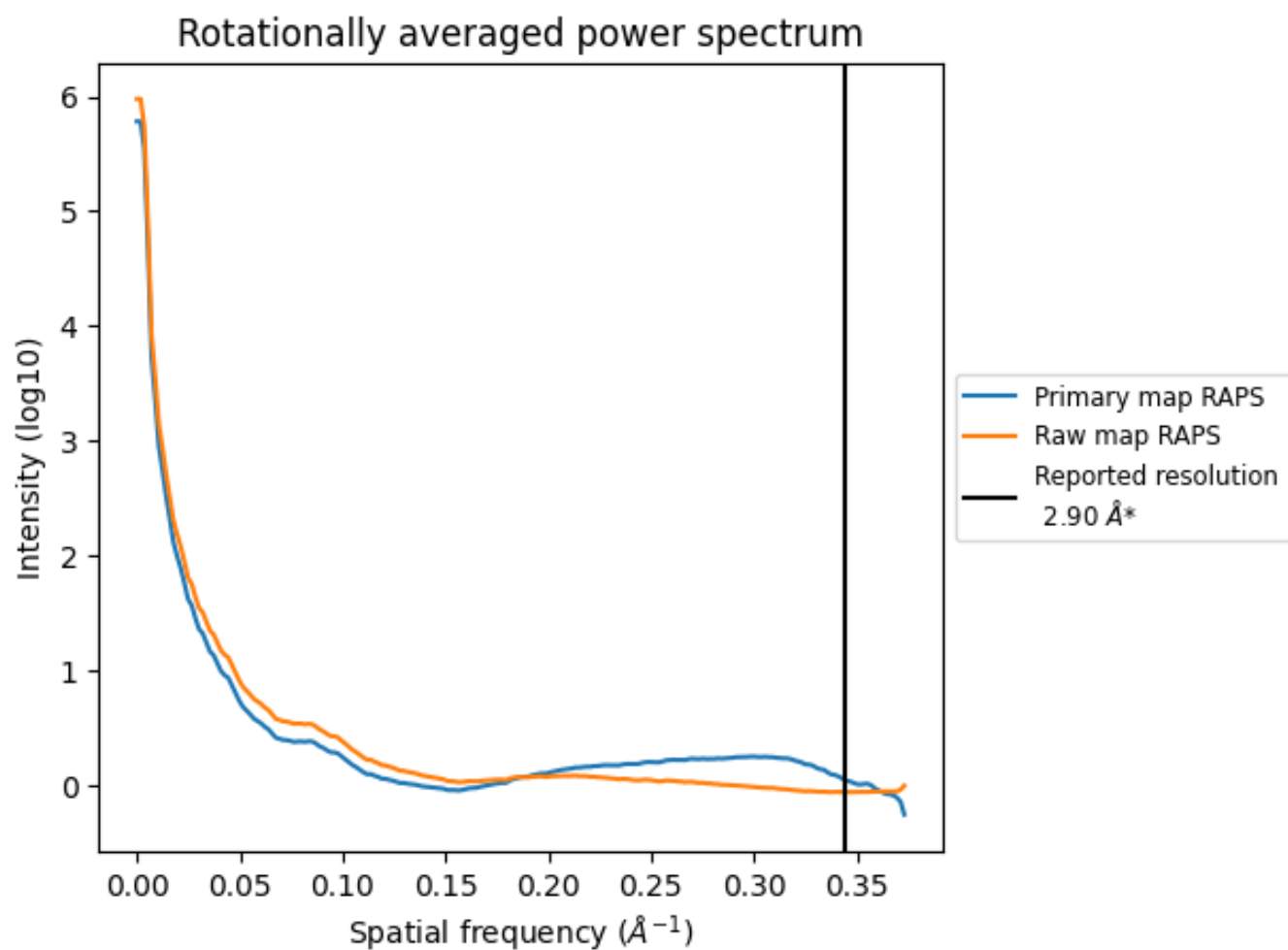
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2152 nm^3 ; this corresponds to an approximate mass of 1944 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 ⓘ

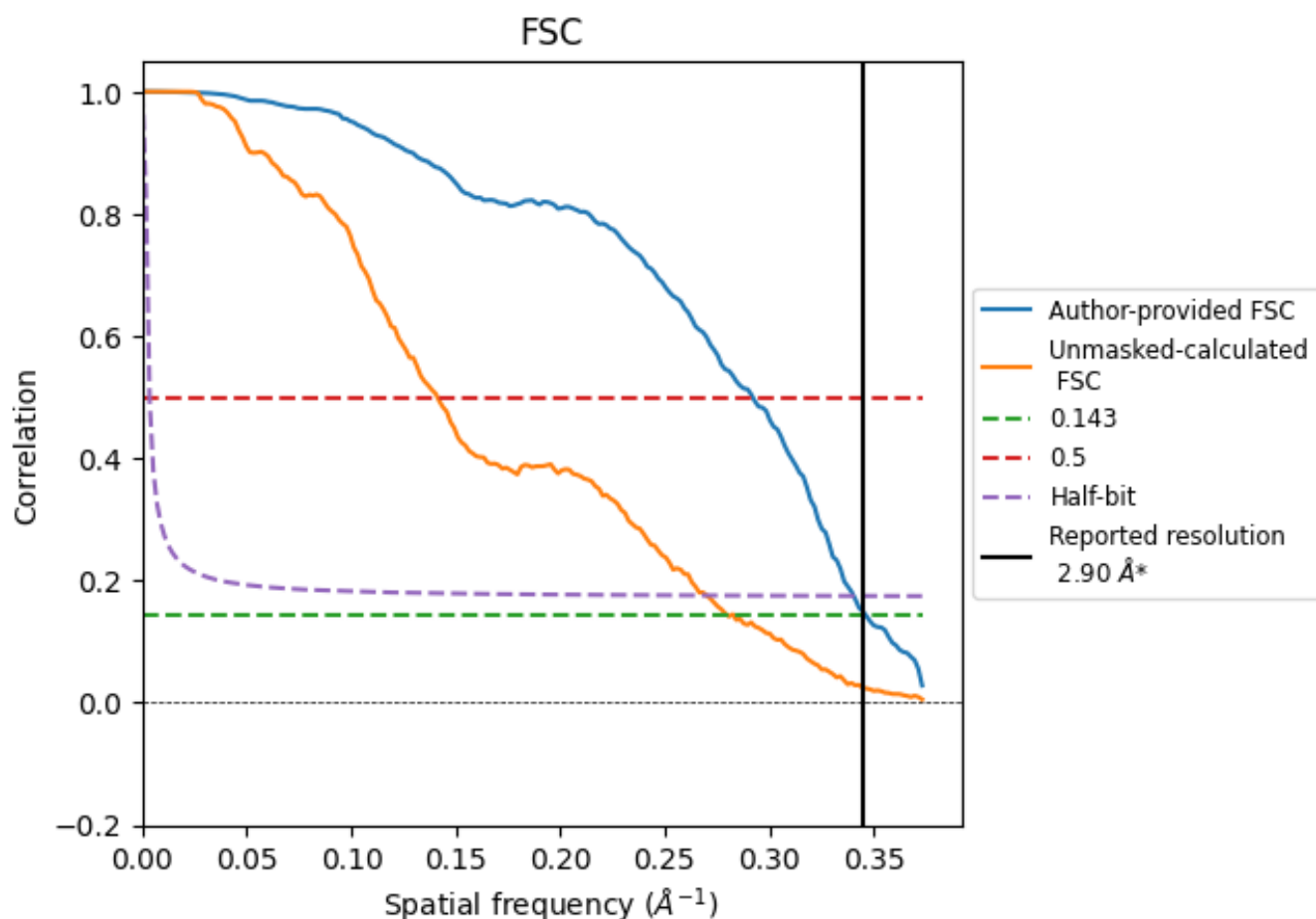


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

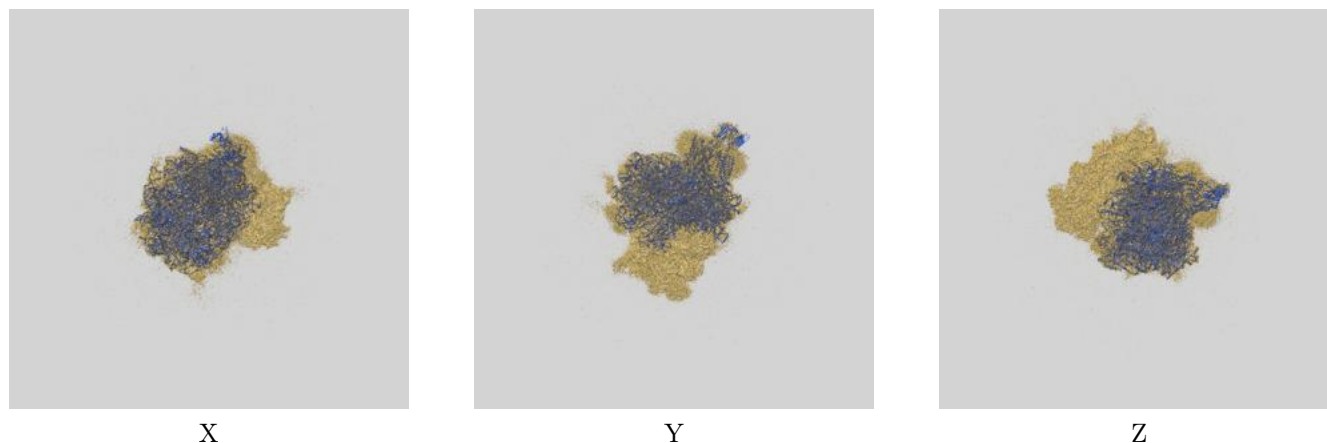
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.89	3.42	2.94
Unmasked-calculated*	3.57	7.08	3.70

*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 3.57 differs from the reported value 2.90061 by more than 10 %

9 Map-model fit [i](#)

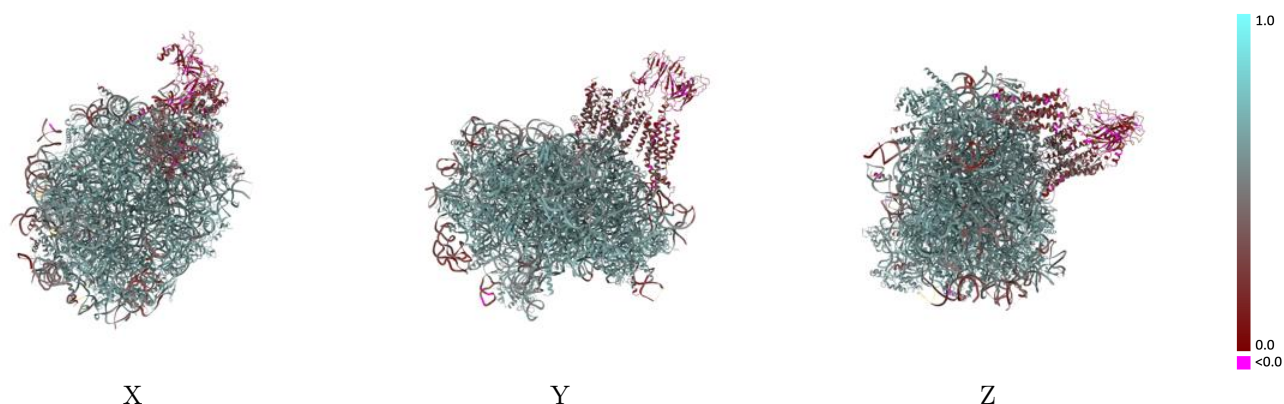
This section contains information regarding the fit between EMDB map EMD-19197 and PDB model 8RJC. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



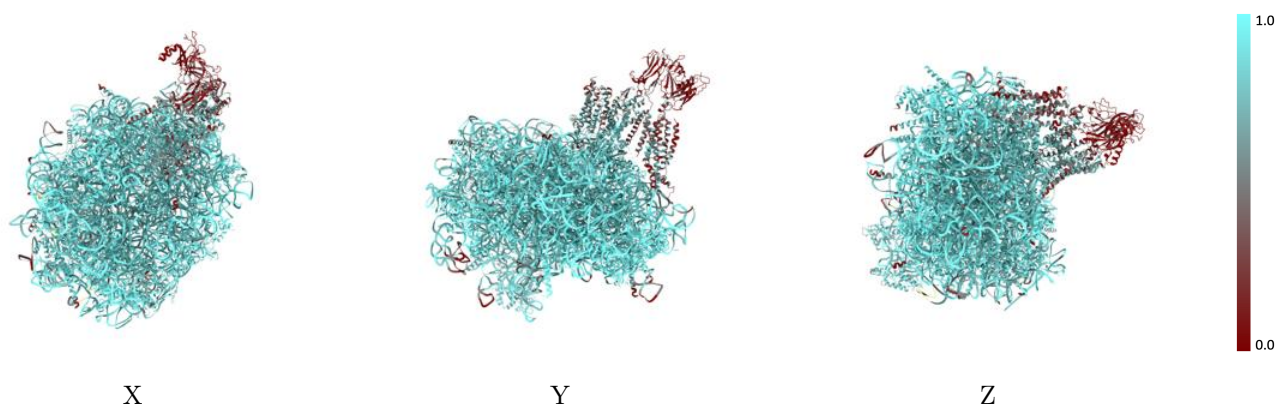
The images above show the 3D surface view of the map at the recommended contour level 0.0231 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



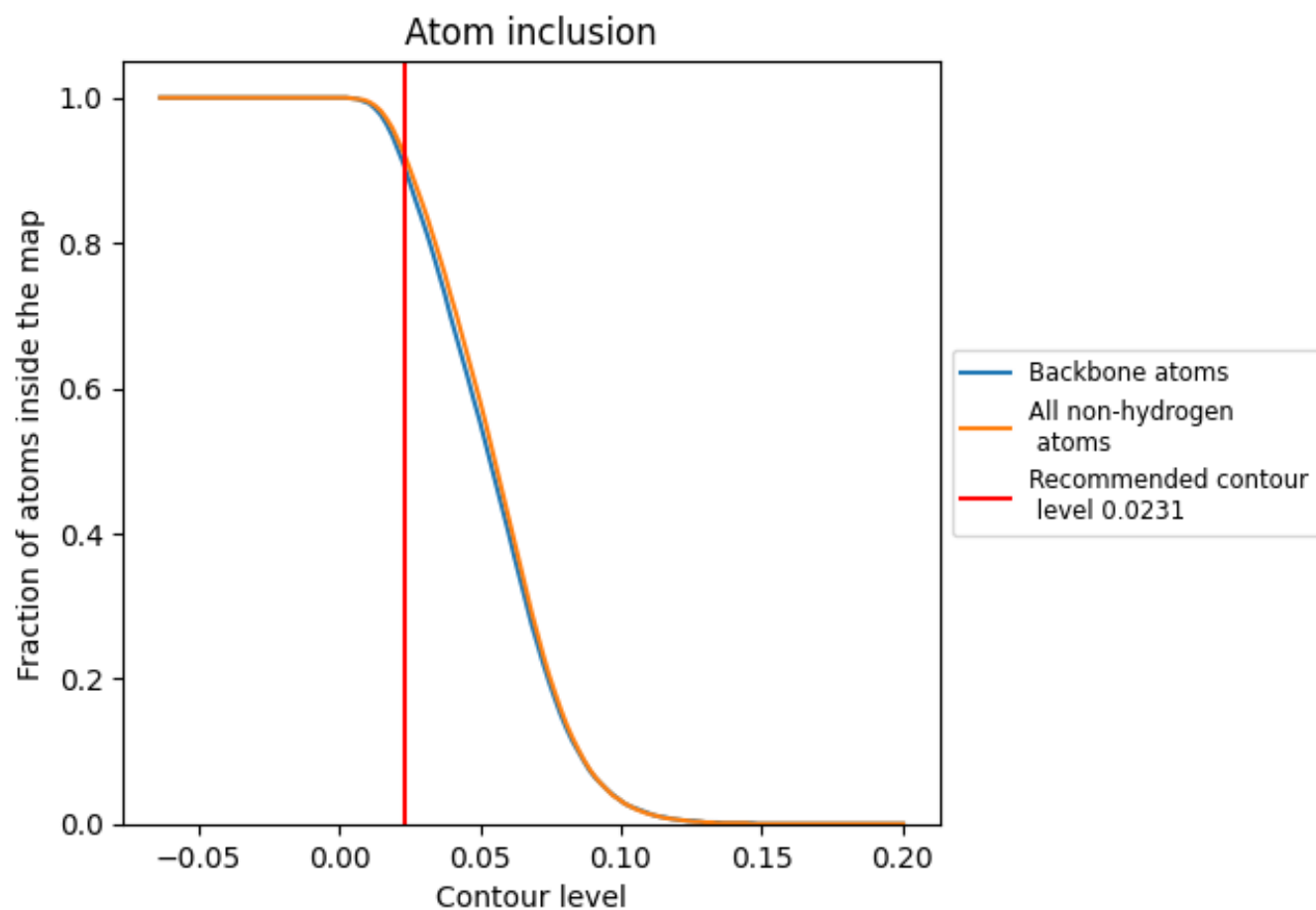
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0231).

9.4 Atom inclusion ⓘ



At the recommended contour level, 91% 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 (0.0231) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9230	 0.5680
1	 0.6560	 0.3620
2	 0.5830	 0.3360
3	 0.7660	 0.4230
4	 0.6230	 0.4960
5	 0.2650	 0.2140
6	 0.2000	 0.1640
7	 0.4590	 0.2590
8	 0.1590	 0.1770
9	 0.3030	 0.2120
A	 0.9920	 0.6440
B	 0.5900	 0.2820
C	 0.9690	 0.6260
D	 0.9290	 0.6020
E	 0.9160	 0.5890
F	 0.9800	 0.6310
G	 0.8900	 0.5820
H	 0.9520	 0.6200
I	 0.9640	 0.6220
J	 0.8910	 0.5780
K	 0.9550	 0.5740
L	 0.9140	 0.6060
M	 0.9490	 0.6170
N	 0.9990	 0.6520
O	 0.9740	 0.6350
P	 0.8550	 0.5860
Q	 0.9850	 0.6380
R	 0.9780	 0.6270
S	 0.9800	 0.6330
T	 0.9620	 0.6180
U	 0.8250	 0.5070
V	 0.9770	 0.6300
W	 0.9800	 0.6240
X	 0.9660	 0.6160
Y	 0.9520	 0.6210



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Z	 0.9530	 0.6060
a	 0.9800	 0.6400
b	 0.8830	 0.5630
c	 0.9450	 0.6110
d	 0.9520	 0.6080
e	 0.9860	 0.6380
f	 0.9860	 0.6490
g	 0.9350	 0.6110
h	 0.9410	 0.6070
i	 0.9420	 0.6000
j	 0.9990	 0.6420
k	 0.8760	 0.5900
l	 0.9860	 0.6270
m	 0.9520	 0.6220
n	 0.9860	 0.6000
o	 0.9660	 0.6250
p	 0.9680	 0.6190
q	 0.6760	 0.4560
r	 0.9760	 0.6230
u	 0.9910	 0.6150
v	 0.9750	 0.5980
w	 0.9730	 0.6320