



Full wwPDB EM Validation Report ⓘ

Jul 8, 2026 – 01:52 PM JST

PDB ID : 9KMX / pdb_00009kmx
EMDB ID : EMD-62448
Title : Bat MERsSr-CoV NeoCoV Nsp1 bound to the Human 40S Ribosomal subunit-State1
Authors : Yuan, S.; Yan, R.; Wu, M.
Deposited on : 2024-11-18
Resolution : 2.89 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.dev133
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) : 2.50

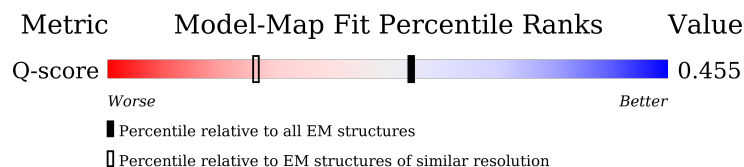
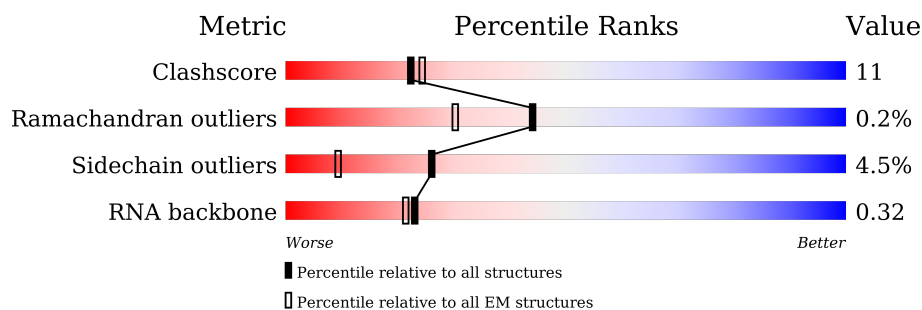
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.89 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.



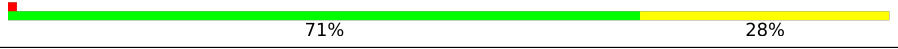
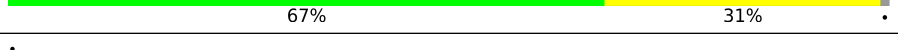
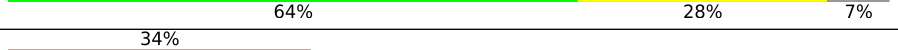
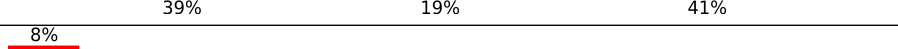
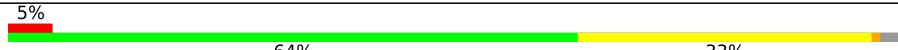
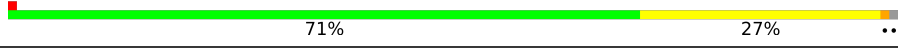
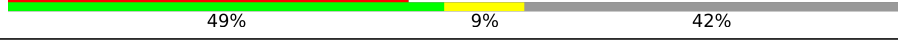
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12148 (2.39 - 3.39)

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

Mol	Chain	Length	Quality of chain
1	2	1869	10% 32% 40% 15% 13%
2	A	295	54% 18% 28%
3	B	264	60% 20% 19%

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Mol	Chain	Length	Quality of chain
4	C	293	
5	D	243	
6	E	263	
7	F	204	
8	G	249	
9	H	194	
10	I	208	
11	J	194	
12	K	165	
13	L	158	
14	M	132	
15	N	151	
16	O	151	
17	P	145	
18	Q	146	
19	R	135	
20	S	152	
21	T	145	
22	U	119	
23	V	83	
24	W	130	
25	X	143	
26	Y	130	
27	Z	125	
28	a	101	

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Mol	Chain	Length	Quality of chain
29	b	82	
30	c	62	
31	d	55	
32	e	56	
33	f	74	
34	g	315	
35	h	25	
36	n	193	

2 Entry composition [i](#)

There are 36 unique types of molecules in this entry. The entry contains 73974 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1633	Total	C	N	O	P	0	0
			34852	15567	6268	11392	1625		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	213	Total	C	N	O	S	0	0
			1686	1072	295	311	8		

- Molecule 3 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 4 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	218	Total	C	N	O	S	0	0
			1690	1094	289	297	10		

- Molecule 5 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	225	Total	C	N	O	S	0	0
			1752	1117	315	313	7		

- Molecule 6 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 8 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	230	Total	C	N	O	S	0	0
			1864	1164	373	320	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	221	ARG	LYS	variant	UNP P62753

- Molecule 9 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	186	Total	C	N	O	S	0	0
			1501	957	276	267	1		

- Molecule 10 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	205	Total	C	N	O	S	0	0
			1682	1056	331	290	5		

- Molecule 11 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	180	Total	C	N	O	S	0	0
			1499	955	300	242	2		

- Molecule 12 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	97	Total	C	N	O	S	0	0
			816	533	144	133	6		

- Molecule 13 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	151	Total	C	N	O	S	0	0
			1229	782	230	211	6		

- Molecule 14 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	121	Total	C	N	O	S	0	0
			935	586	165	175	9		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 16 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	135	Total	C	N	O	S	0	0
			1010	618	198	188	6		

- Molecule 17 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	126	Total	C	N	O	S	0	0
			1037	659	196	175	7		

- Molecule 18 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	138	Total	C	N	O	S	0	0
			1097	698	206	190	3		

- Molecule 19 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 20 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	143	Total	C	N	O	S	0	0
			1184	743	240	200	1		

- Molecule 21 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	144	Total	C	N	O	S	0	0
			1123	703	217	200	3		

- Molecule 22 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	101	Total	C	N	O	S	0	0
			803	504	153	142	4		

- Molecule 23 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 24 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 25 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 26 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	124	Total	C	N	O	S	0	0
			1014	641	198	170	5		

- Molecule 27 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	72	Total	C	N	O	S	0	0
			574	368	104	101	1		

- Molecule 28 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	99	Total	C	N	O	S	0	0
			794	494	165	130	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	78	VAL	ALA	conflict	UNP P62854

- Molecule 29 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	82	Total	C	N	O	S	0	0
			641	402	118	114	7		

- Molecule 30 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	62	Total	C	N	O	S	0	0
			489	297	97	93	2		

- Molecule 31 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 32 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	56	Total	C	N	O	S	0	0
			442	273	96	72	1		

- Molecule 33 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	74	Total	C	N	O	S	0	0
			611	385	117	102	7		

- Molecule 34 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	314	Total	C	N	O	S	0	0
			2441	1537	425	467	12		

- Molecule 35 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	22	Total	C	N	O	S	0	0
			213	130	57	23	3		

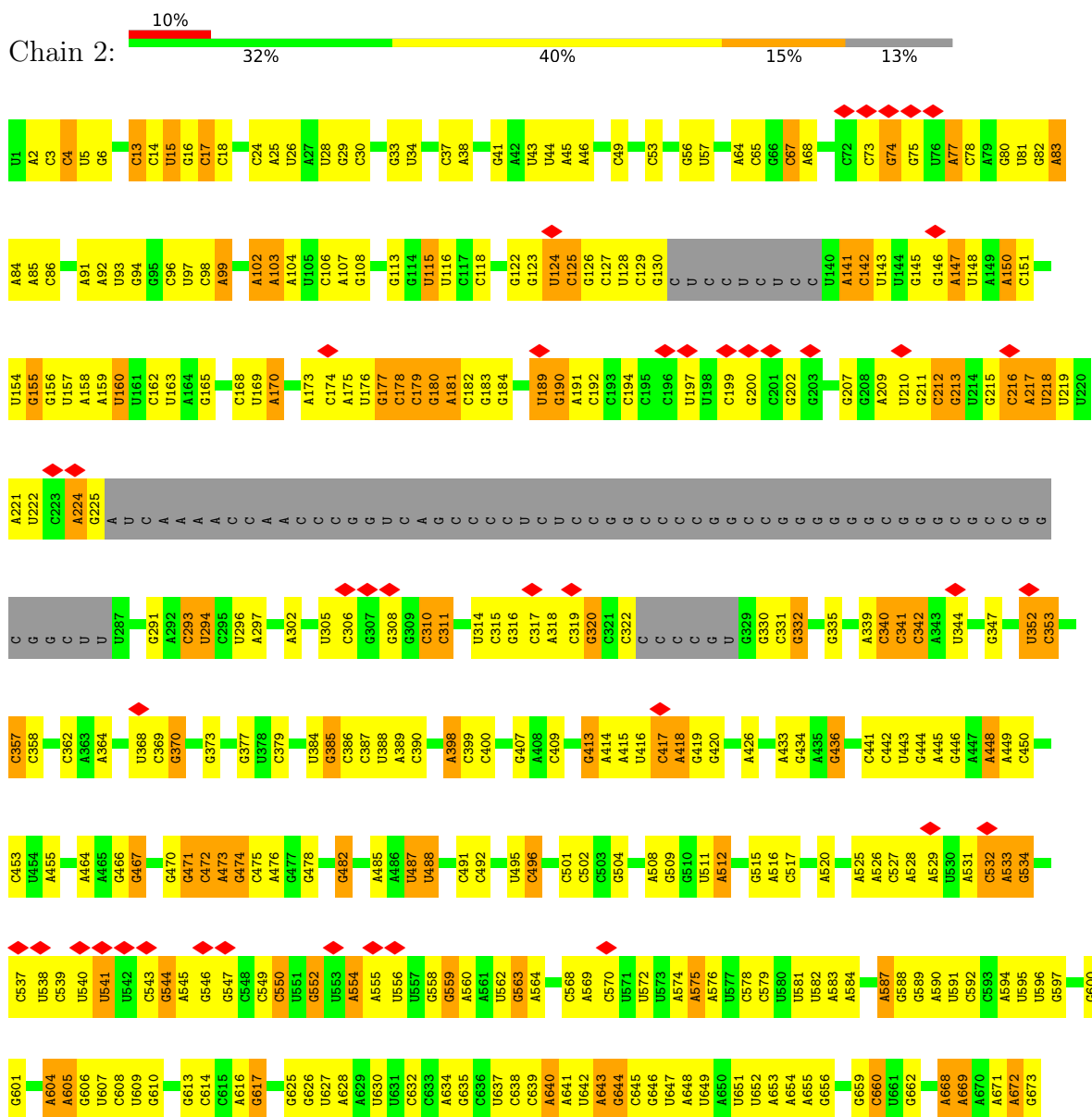
- Molecule 36 is a protein called ORF1ab polyprotein.

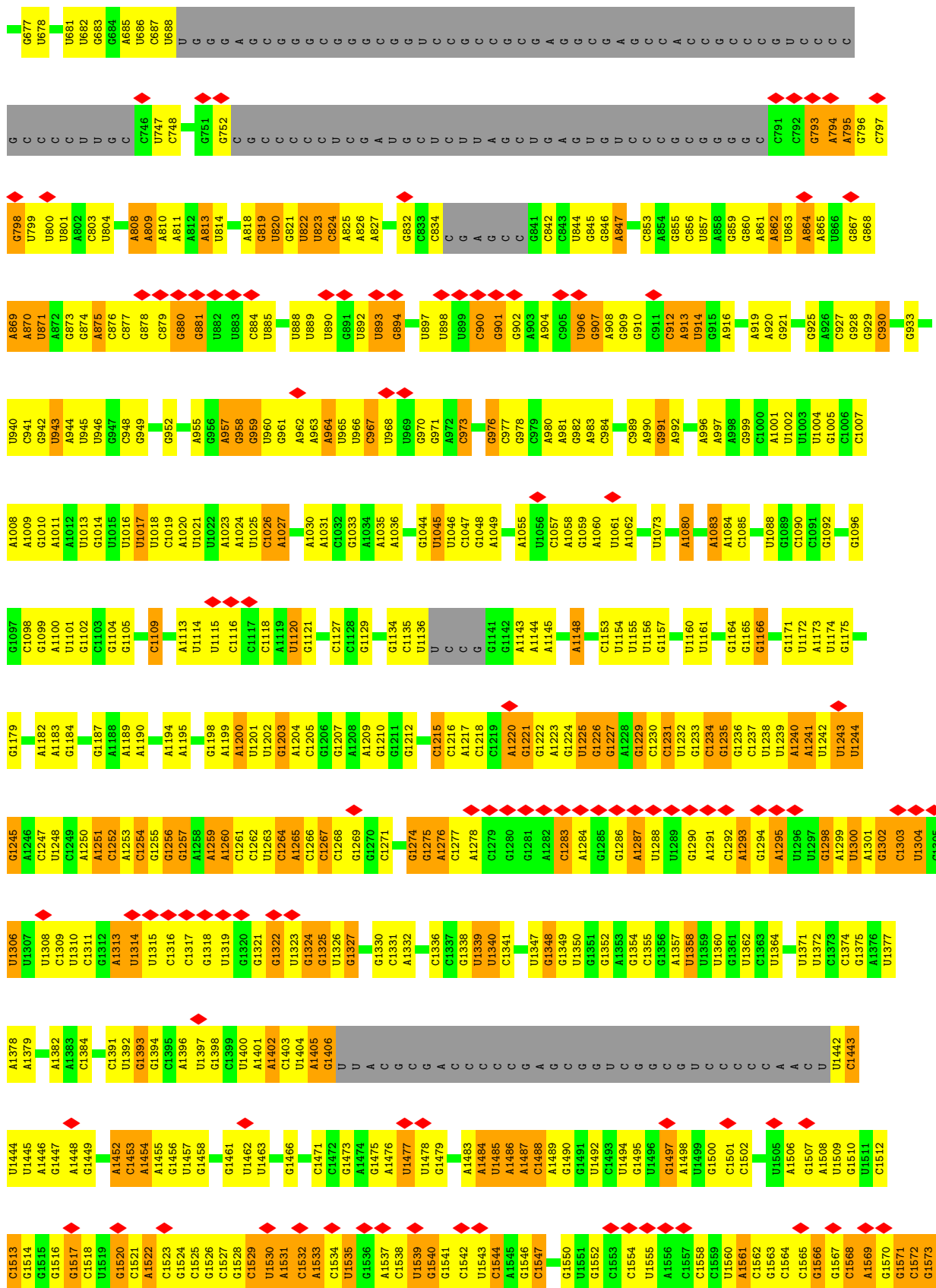
Mol	Chain	Residues	Atoms				AltConf	Trace
36	n	26	Total	C	N	O	0	0
			209	136	33	40		

3 Residue-property plots

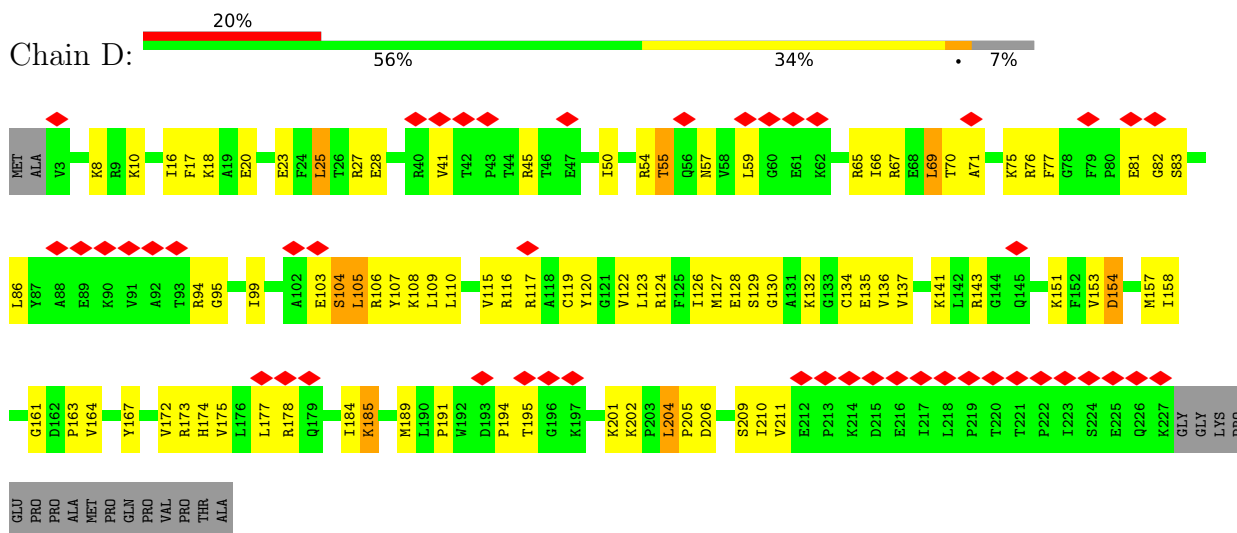
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 18S ribosomal RNA

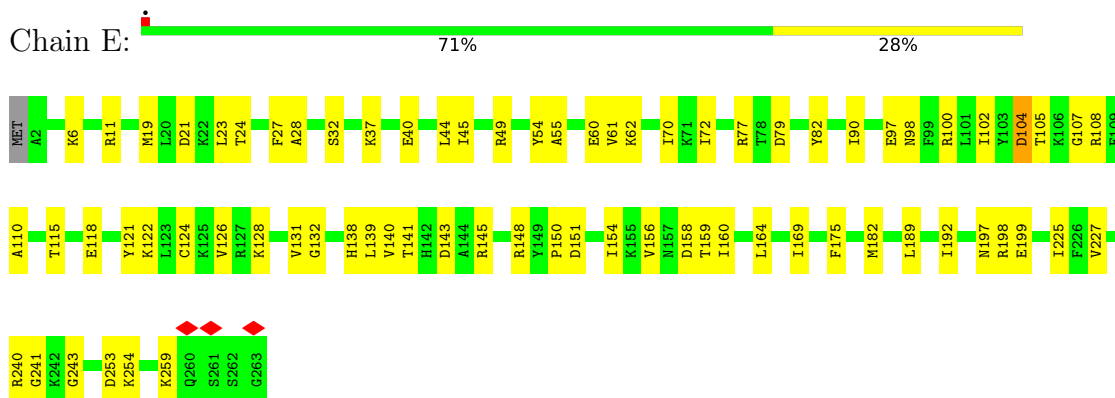




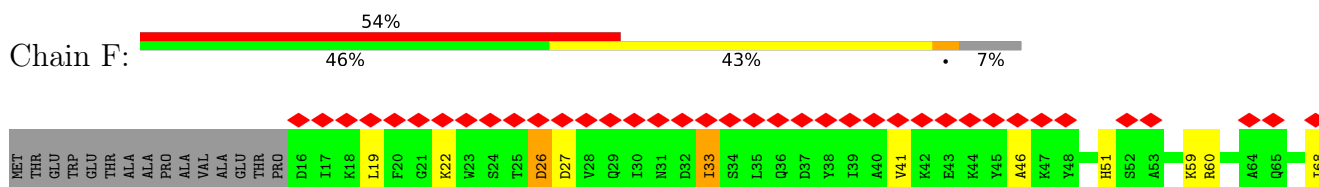
- Molecule 5: Small ribosomal subunit protein uS3

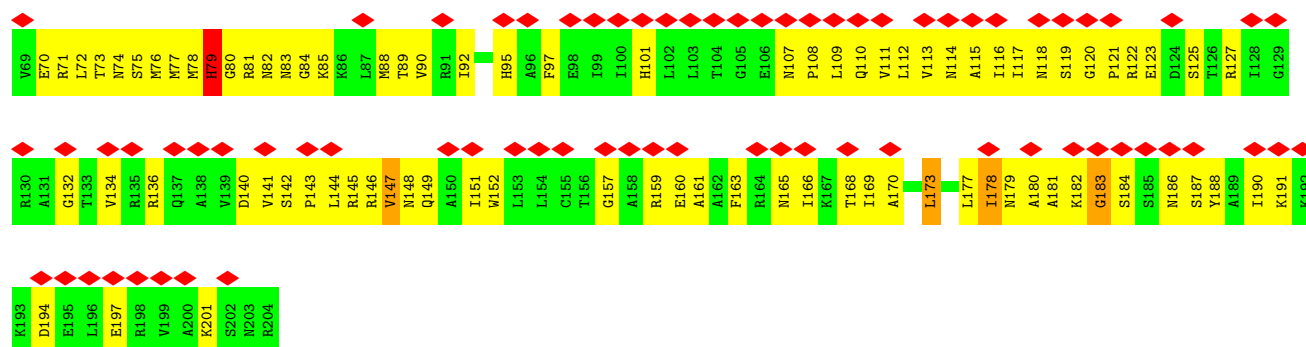


- Molecule 6: Small ribosomal subunit protein eS4, X isoform

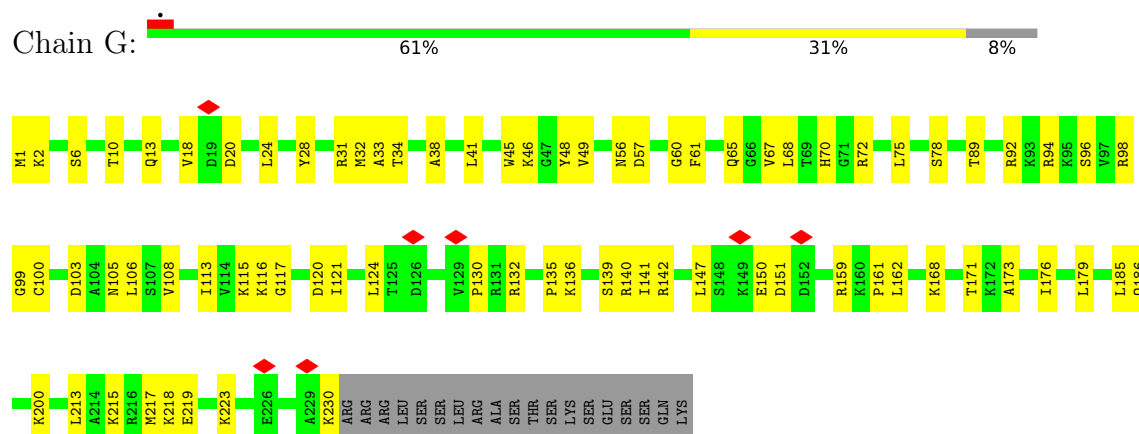


- Molecule 7: Small ribosomal subunit protein uS7

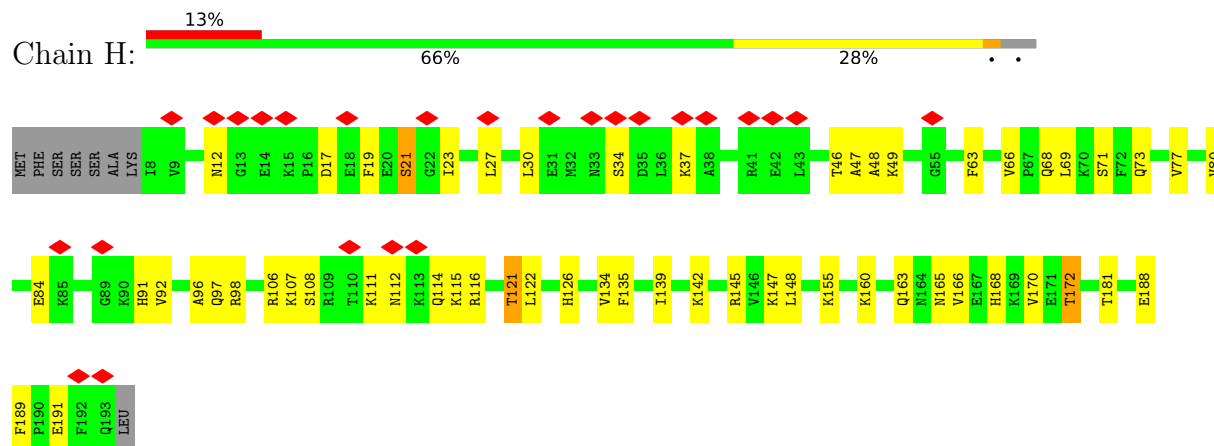




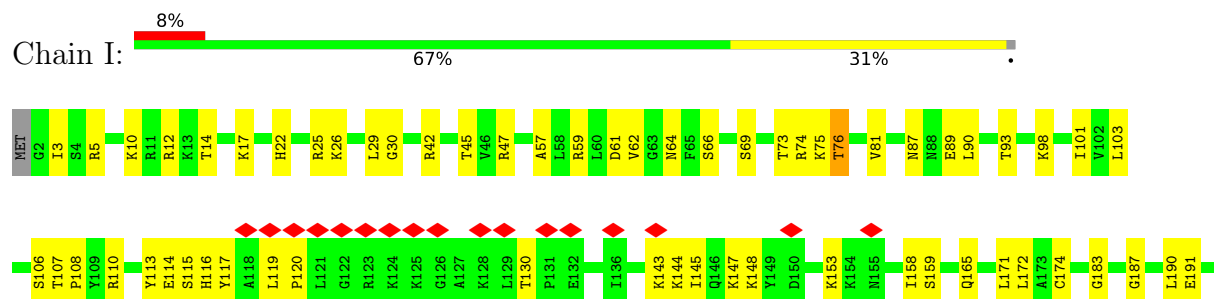
• Molecule 8: Small ribosomal subunit protein eS6



• Molecule 9: Small ribosomal subunit protein eS7

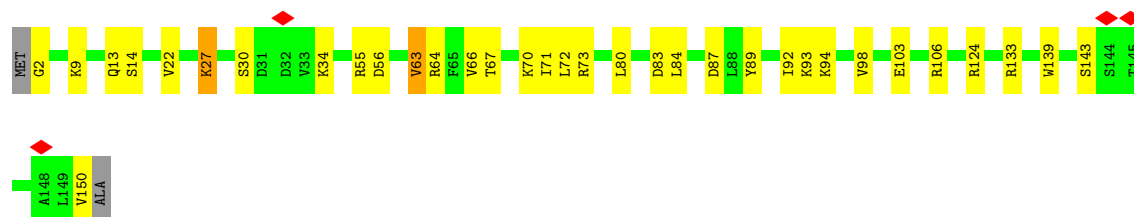
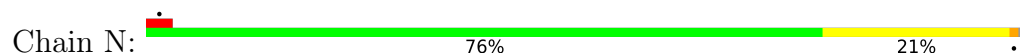


• Molecule 10: Small ribosomal subunit protein eS8

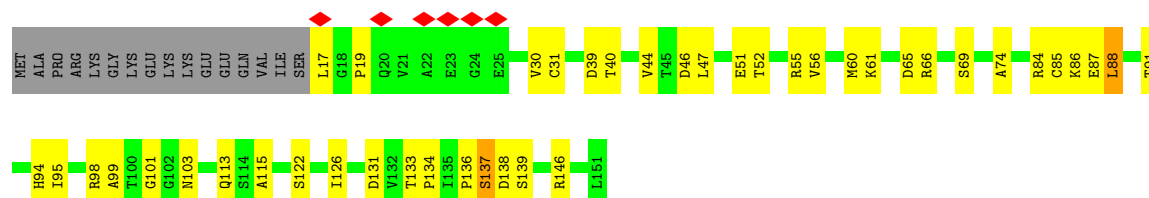




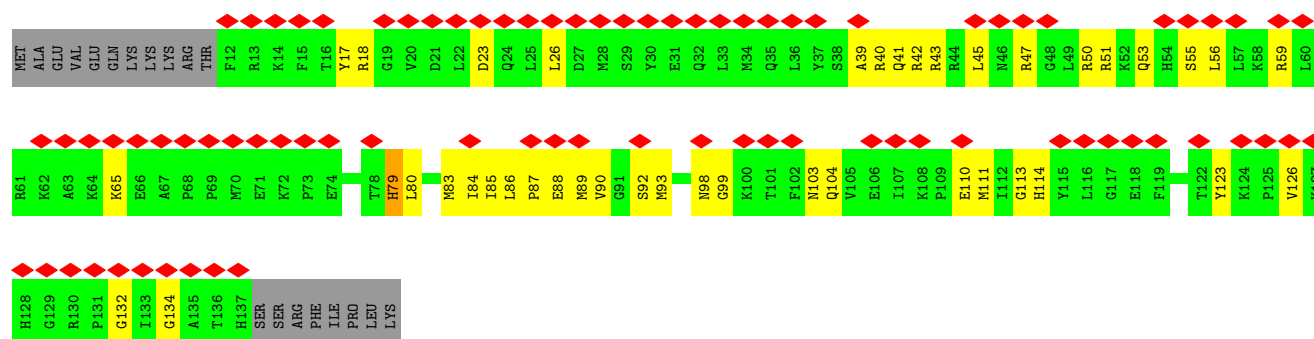
- Molecule 15: Small ribosomal subunit protein uS15



- Molecule 16: Small ribosomal subunit protein uS11

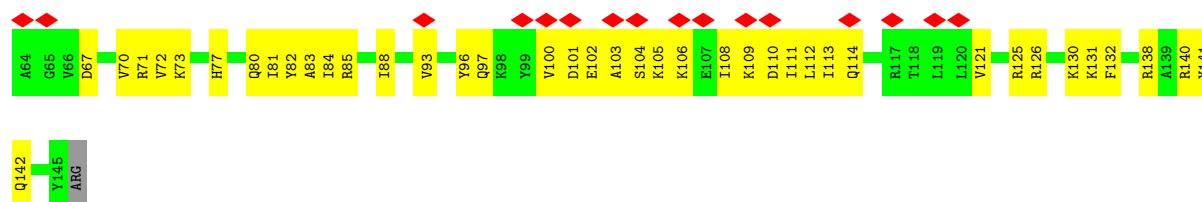


- Molecule 17: Small ribosomal subunit protein uS19

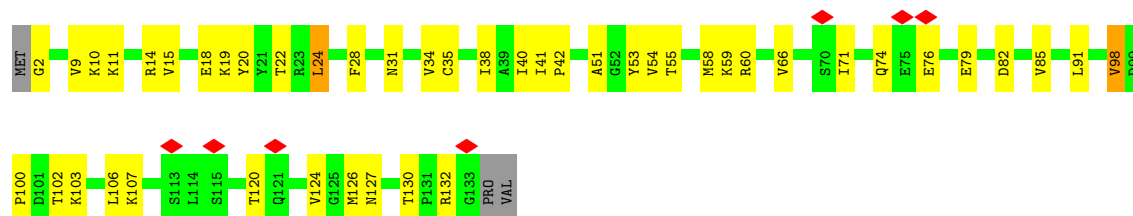


- Molecule 18: Small ribosomal subunit protein uS9

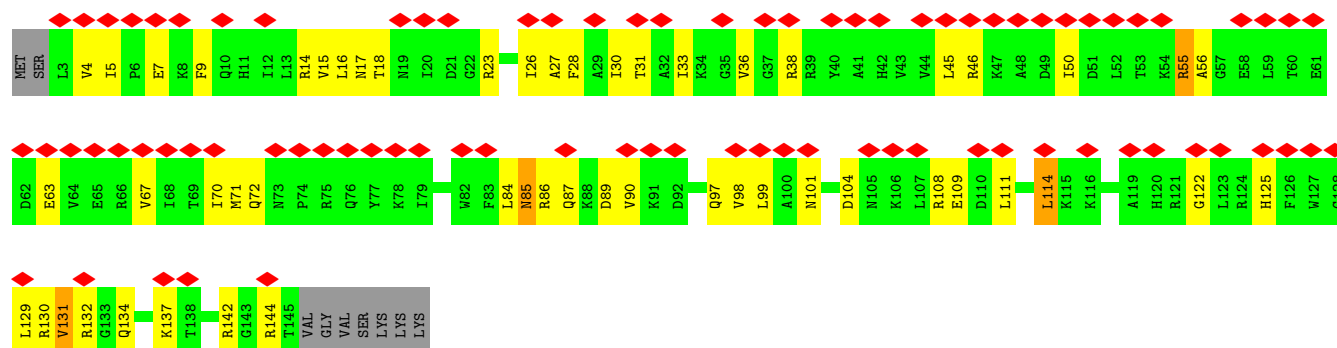




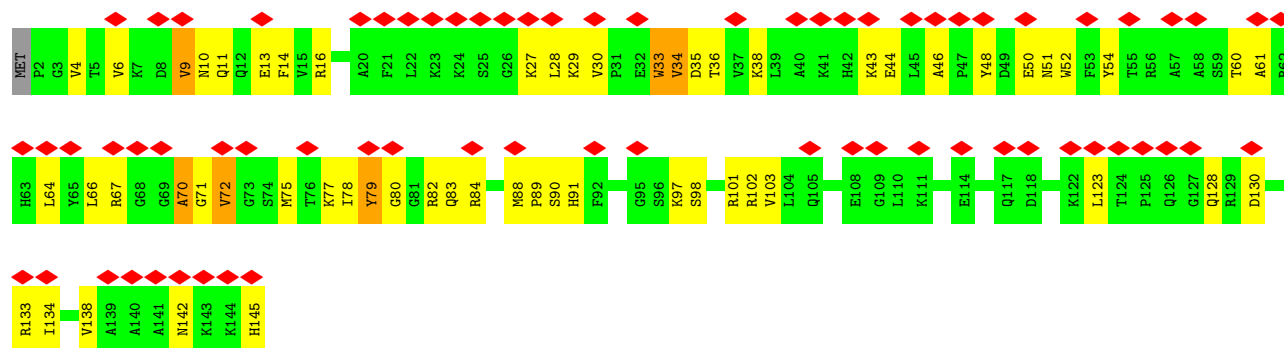
- Molecule 19: Small ribosomal subunit protein eS17



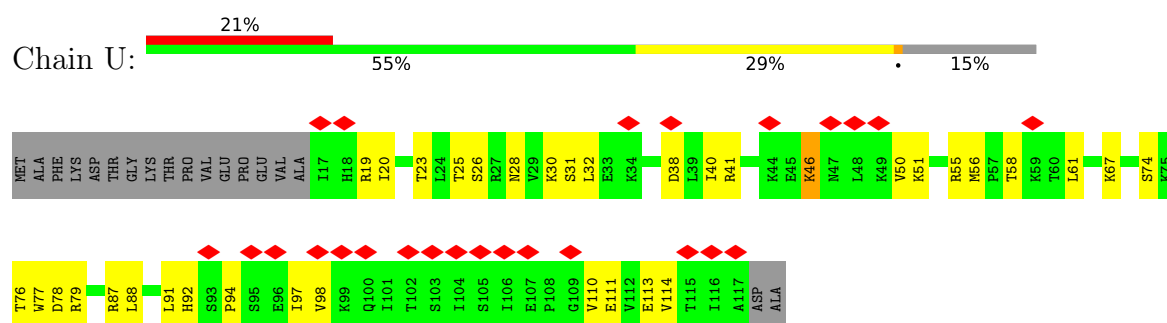
- Molecule 20: Small ribosomal subunit protein uS13



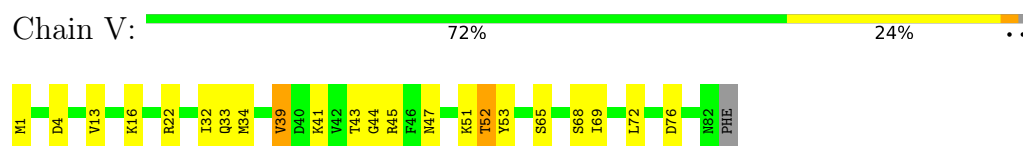
- Molecule 21: Small ribosomal subunit protein eS19



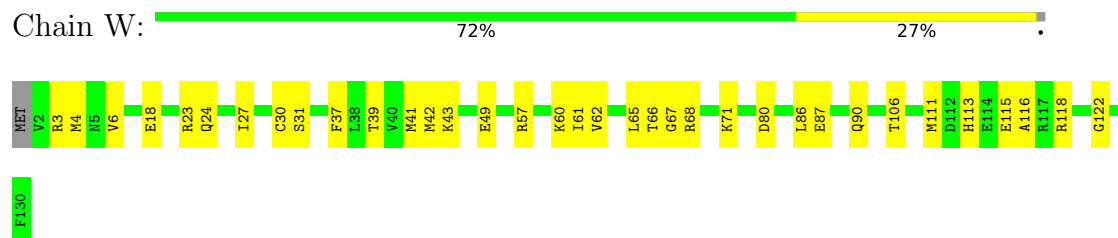
- Molecule 22: Small ribosomal subunit protein uS10



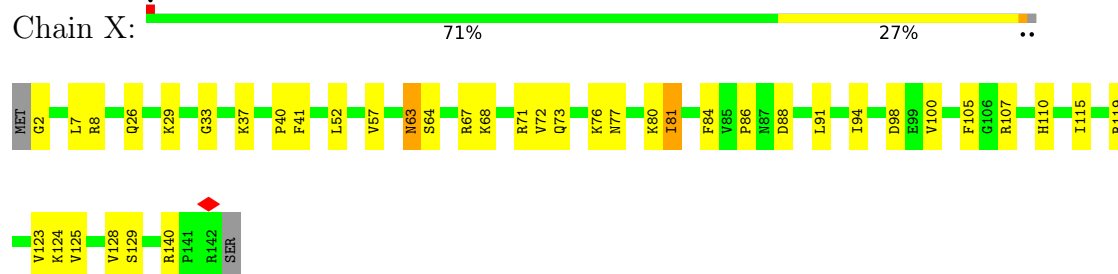
- Molecule 23: Small ribosomal subunit protein eS21



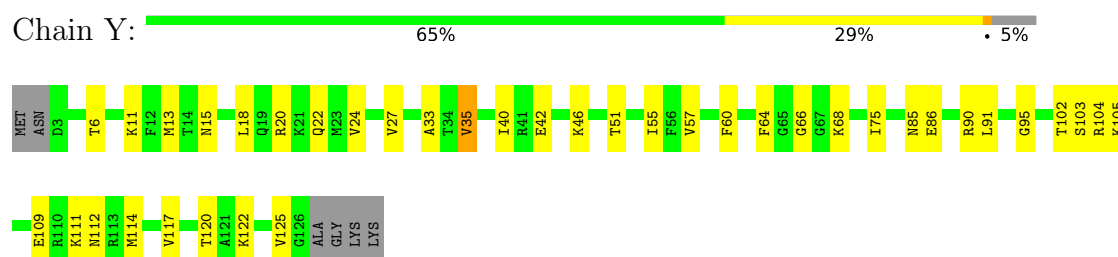
- Molecule 24: Small ribosomal subunit protein uS8



- Molecule 25: Small ribosomal subunit protein uS12



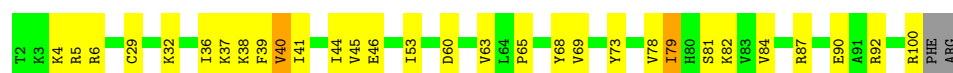
- Molecule 26: Small ribosomal subunit protein eS24



- Molecule 27: Small ribosomal subunit protein eS25



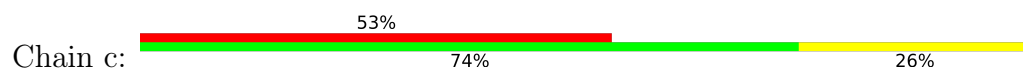
- Molecule 28: Small ribosomal subunit protein eS26



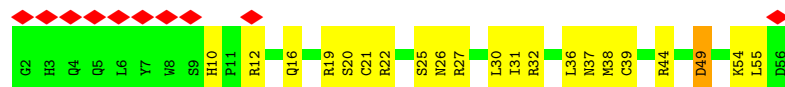
- Molecule 29: Small ribosomal subunit protein eS27



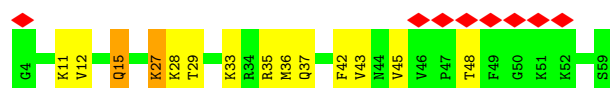
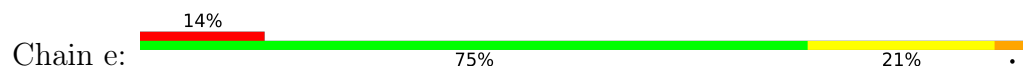
- Molecule 30: Small ribosomal subunit protein eS28



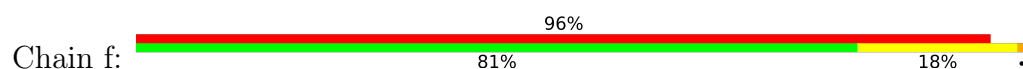
- Molecule 31: Small ribosomal subunit protein uS14



- Molecule 32: Small ribosomal subunit protein eS30

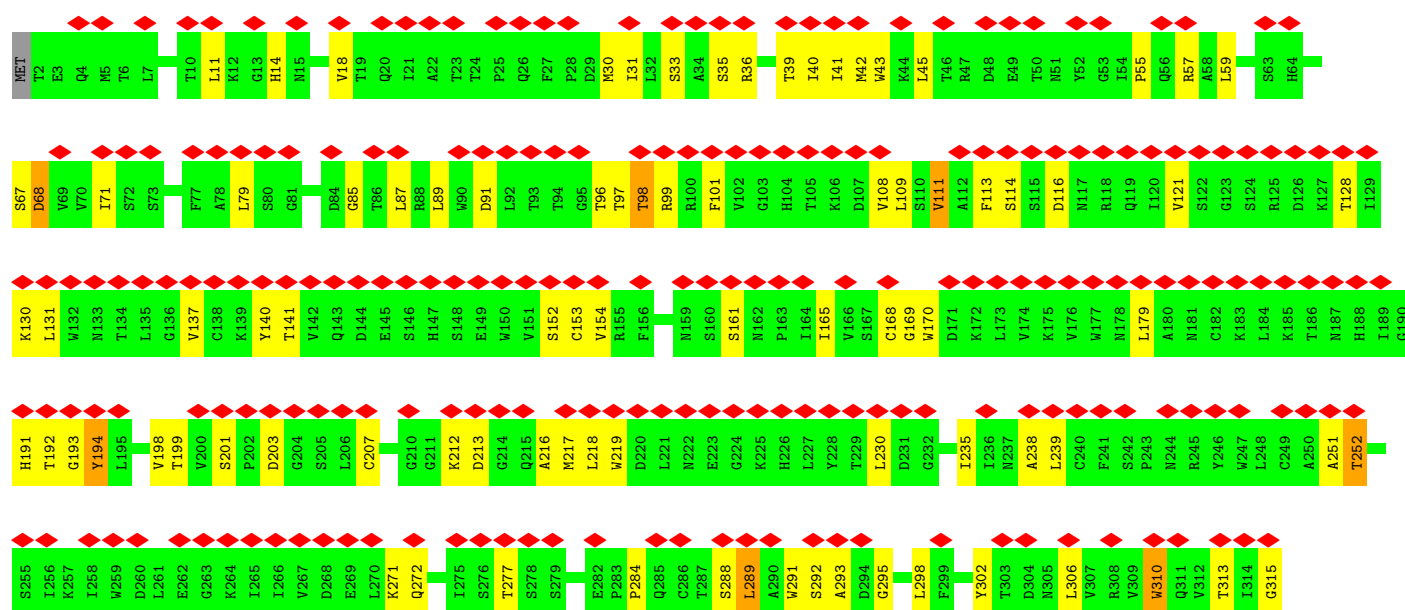


- Molecule 33: Small ribosomal subunit protein eS31

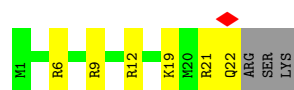




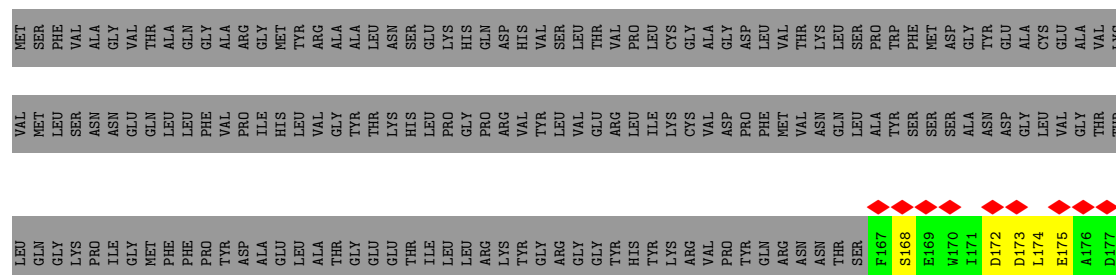
• Molecule 34: Small ribosomal subunit protein RACK1

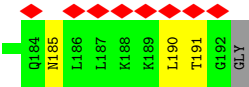


• Molecule 35: Small ribosomal subunit protein eS32



• Molecule 36: ORF1ab polypeptide





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53238	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.915	Depositor
Minimum map value	-1.093	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.056	Depositor
Recommended contour level	0.192	Depositor
Map size ($\text{\AA}$)	486.4, 486.4, 486.4	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.95, 0.95, 0.95	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	2	0.19	0/38977	0.31	0/60748
2	A	0.16	0/1723	0.30	0/2341
3	B	0.18	0/1756	0.35	0/2350
4	C	0.18	0/1726	0.32	0/2332
5	D	0.15	0/1780	0.40	0/2397
6	E	0.18	0/2118	0.32	0/2849
7	F	0.23	0/1516	0.62	1/2037 (0.0%)
8	G	0.14	0/1887	0.32	0/2513
9	H	0.14	0/1524	0.35	0/2042
10	I	0.16	0/1711	0.35	0/2282
11	J	0.16	0/1524	0.31	0/2035
12	K	0.16	0/840	0.43	0/1133
13	L	0.18	0/1250	0.31	0/1673
14	M	0.12	0/945	0.33	0/1269
15	N	0.16	0/1226	0.30	0/1649
16	O	0.15	0/1023	0.35	0/1372
17	P	0.20	0/1058	0.41	0/1414
18	Q	0.19	0/1114	0.47	0/1492
19	R	0.18	0/1082	0.41	0/1452
20	S	0.12	0/1202	0.36	0/1610
21	T	0.28	0/1143	0.67	4/1530 (0.3%)
22	U	0.15	0/813	0.37	0/1092
23	V	0.17	0/631	0.29	0/844
24	W	0.21	0/1051	0.35	0/1406
25	X	0.16	0/1116	0.30	0/1490
26	Y	0.16	0/1031	0.31	0/1370
27	Z	0.13	0/580	0.39	0/780
28	a	0.18	0/807	0.34	0/1082
29	b	0.19	0/654	0.37	1/876 (0.1%)
30	c	0.14	0/491	0.39	0/656
31	d	0.17	0/470	0.37	0/623
32	e	0.14	0/447	0.32	0/587
33	f	0.12	0/623	0.33	0/822
34	g	0.13	0/2498	0.36	0/3399

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.15	0/214	0.36	0/272
36	n	0.10	0/213	0.23	0/285
All	All	0.18	0/78764	0.34	6/114104 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
7	F	0	1
16	O	0	1
All	All	0	2

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	T	79	TYR	N-CA-C	9.29	121.41	111.28
21	T	71	GLY	N-CA-C	-7.33	103.39	112.77
21	T	80	GLY	N-CA-C	6.23	122.36	111.14
21	T	78	ILE	N-CA-C	6.09	116.84	110.62
7	F	183	GLY	N-CA-C	5.89	127.14	113.18
29	b	12	PRO	CA-N-CD	-5.17	104.76	112.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	F	180	ALA	Peptide
16	O	137	SER	Peptide

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	2	34852	0	17611	613	0
2	A	1686	0	1688	35	0
3	B	1729	0	1803	38	0
4	C	1690	0	1777	40	0
5	D	1752	0	1848	72	0
6	E	2076	0	2177	53	0
7	F	1495	0	1549	95	0
8	G	1864	0	2018	51	0
9	H	1501	0	1593	41	0
10	I	1682	0	1769	47	0
11	J	1499	0	1618	36	0
12	K	816	0	841	27	0
13	L	1229	0	1302	17	0
14	M	935	0	964	13	0
15	N	1202	0	1289	24	0
16	O	1010	0	1034	30	0
17	P	1037	0	1082	34	0
18	Q	1097	0	1161	54	0
19	R	1068	0	1121	30	0
20	S	1184	0	1244	44	0
21	T	1123	0	1153	39	0
22	U	803	0	873	29	0
23	V	625	0	628	20	0
24	W	1034	0	1080	28	0
25	X	1098	0	1167	29	0
26	Y	1014	0	1082	28	0
27	Z	574	0	627	9	0
28	a	794	0	849	23	0
29	b	641	0	665	29	0
30	c	489	0	514	12	0
31	d	459	0	452	20	0
32	e	442	0	487	10	0
33	f	611	0	638	11	0
34	g	2441	0	2396	56	0
35	h	213	0	258	5	0
36	n	209	0	207	10	0
All	All	73974	0	58565	1479	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 11.

All (1479) 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)
1:2:190:G:N2	1:2:209:A:H62	1.56	1.03
7:F:112:LEU:HD12	7:F:177:LEU:HB3	1.45	0.99
1:2:190:G:H21	1:2:209:A:N6	1.63	0.96
18:Q:132:PHE:HZ	22:U:77:TRP:H	1.09	0.96
1:2:141:A:N6	1:2:177:G:C4	2.36	0.93
1:2:1120:U:H5'	29:b:72:ARG:HH12	1.34	0.92
1:2:531:A:H61	1:2:552:G:H1	0.94	0.91
1:2:531:A:N6	1:2:552:G:H1	1.71	0.86
1:2:1658:G:OP2	1:2:1660:C:N4	2.11	0.83
1:2:1223:A:H61	1:2:1644:C:H42	1.25	0.83
19:R:22:THR:HB	34:g:212:LYS:HG2	1.59	0.83
7:F:143:PRO:HB3	7:F:146:ARG:HH21	1.44	0.82
1:2:1735:A:H2	1:2:1799:G:H21	1.25	0.81
7:F:113:VAL:HA	7:F:182:LYS:H	1.45	0.81
1:2:919:A:OP2	15:N:64:ARG:NH2	2.13	0.81
1:2:1864:U:H5'	28:a:79:ILE:HD11	1.64	0.80
1:2:190:G:H21	1:2:209:A:H62	0.83	0.80
5:D:116:ARG:HH21	36:n:172:ASP:HA	1.47	0.79
1:2:103:A:H4'	1:2:104:A:H5'	1.63	0.79
1:2:1648:G:N2	1:2:1675:A:OP2	2.15	0.78
18:Q:102:GLU:HB2	34:g:55:PRO:HB2	1.65	0.78
3:B:28:LYS:HB3	3:B:48:LEU:HD22	1.65	0.78
3:B:104:ASP:OD1	3:B:105:LEU:N	2.16	0.78
34:g:152:SER:H	34:g:169:GLY:HA2	1.49	0.78
19:R:98:VAL:HG13	19:R:102:THR:HG23	1.66	0.78
1:2:560:A:N6	1:2:588:G:O6	2.16	0.78
16:O:30:VAL:HG12	16:O:94:HIS:HB2	1.63	0.78
1:2:1244:U:O4	1:2:1257:G:N2	2.15	0.77
1:2:1533:A:OP1	7:F:81:ARG:NH2	2.17	0.77
1:2:1614:A:N7	17:P:43:ARG:NH1	2.33	0.76
1:2:1221:G:N2	1:2:1677:U:O2	2.18	0.76
34:g:217:MET:HE3	34:g:219:TRP:HE1	1.50	0.76
7:F:125:SER:HB2	7:F:136:ARG:HB3	1.68	0.76
1:2:1610:G:H2'	1:2:1611:G:C8	2.21	0.75
2:A:81:ASN:HA	2:A:84:GLN:HG3	1.68	0.75
7:F:117:ILE:HB	7:F:183:GLY:H	1.52	0.75
7:F:159:ARG:O	7:F:163:PHE:N	2.19	0.74
17:P:56:LEU:HB2	17:P:80:LEU:HD12	1.69	0.74
1:2:1547:C:H1'	1:2:1670:C:H4'	1.69	0.74
11:J:89:GLU:OE2	11:J:89:GLU:N	2.19	0.74
1:2:928:G:H1	1:2:1013:U:H3	1.35	0.73
1:2:1406:G:N2	1:2:1442:U:O4	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:107:ASN:HB2	7:F:109:LEU:HG	1.70	0.73
12:K:27:VAL:HG13	12:K:43:LEU:HD13	1.70	0.73
7:F:145:ARG:HG3	30:c:49:PRO:HD2	1.70	0.73
1:2:880:G:O2'	1:2:881:G:OP2	2.06	0.73
7:F:113:VAL:HB	7:F:182:LYS:O	1.89	0.73
29:b:12:PRO:HD2	29:b:13:GLU:H	1.54	0.72
34:g:33:SER:HB3	34:g:43:TRP:HE1	1.54	0.72
7:F:82:ASN:HD21	7:F:88:MET:HG2	1.54	0.72
1:2:1143:A:H5'	4:C:190:SER:HB3	1.70	0.72
18:Q:82:TYR:HA	18:Q:85:ARG:HG2	1.71	0.72
1:2:1265:A:OP2	1:2:1267:C:N4	2.22	0.72
1:2:1532:C:H42	1:2:1637:A:H61	1.38	0.72
7:F:92:ILE:HG12	7:F:170:ALA:HB2	1.72	0.72
1:2:984:C:O2'	16:O:138:ASP:OD2	2.09	0.71
12:K:3:MET:HE1	12:K:51:SER:HB2	1.72	0.71
1:2:1563:G:H5'	21:T:101:ARG:HH21	1.54	0.71
8:G:2:LYS:HB2	8:G:108:VAL:HG12	1.72	0.71
1:2:433:A:H5''	10:I:22:HIS:HB3	1.72	0.71
1:2:1858:G:OP2	16:O:146:ARG:NH2	2.24	0.71
34:g:298:LEU:HB3	34:g:310:TRP:CD1	2.26	0.71
20:S:55:ARG:NH1	20:S:56:ALA:O	2.24	0.70
1:2:1327:G:H22	1:2:1502:C:H41	1.38	0.70
25:X:68:LYS:HB3	25:X:91:LEU:HD22	1.72	0.70
5:D:109:LEU:HD11	5:D:115:VAL:HG12	1.72	0.70
16:O:56:VAL:HG13	16:O:60:MET:HE2	1.71	0.70
1:2:870:A:H4'	1:2:871:U:H5'	1.74	0.70
1:2:1848:U:O4	35:h:12:ARG:NH1	2.24	0.70
1:2:370:G:O2'	10:I:10:LYS:NZ	2.24	0.69
1:2:1148:A:OP2	28:a:6:ARG:NH2	2.25	0.69
1:2:1259:A:H1'	1:2:1264:C:H41	1.55	0.69
4:C:259:THR:HG21	23:V:16:LYS:H	1.57	0.69
1:2:1581:C:H5'	1:2:1582:C:H5	1.58	0.69
5:D:177:LEU:HD12	5:D:178:ARG:H	1.56	0.69
1:2:332:G:O6	8:G:186:GLN:NE2	2.26	0.69
1:2:1233:G:H21	1:2:1252:C:H2'	1.56	0.69
1:2:1453:C:H5	1:2:1476:A:H2	1.40	0.69
1:2:1617:G:N2	1:2:1619:A:OP2	2.25	0.69
1:2:13:C:H5	1:2:1198:G:H1	1.40	0.69
1:2:867:G:O2'	1:2:868:G:N7	2.25	0.69
2:A:66:VAL:HG21	2:A:185:MET:HB2	1.73	0.69
1:2:1532:C:N4	7:F:79:HIS:O	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1179:G:N2	1:2:1182:A:OP2	2.26	0.69
19:R:14:ARG:O	19:R:18:GLU:HG2	1.92	0.69
20:S:14:ARG:HA	20:S:14:ARG:HH11	1.57	0.69
1:2:560:A:OP2	11:J:177:ASN:ND2	2.25	0.68
1:2:94:G:O2'	1:2:508:A:O2'	2.12	0.68
1:2:122:G:H1	1:2:342:C:H42	1.40	0.68
1:2:1675:A:H5'	7:F:84:GLY:HA3	1.75	0.68
3:B:125:VAL:HG22	3:B:172:MET:HE3	1.76	0.68
5:D:76:ARG:O	5:D:76:ARG:NH1	2.26	0.68
11:J:102:ILE:HD12	11:J:102:ILE:H	1.60	0.67
10:I:198:TYR:O	10:I:202:ILE:HG12	1.95	0.67
1:2:64:A:H2	1:2:83:A:H62	1.42	0.67
1:2:640:A:H2'	1:2:641:A:C8	2.29	0.67
7:F:115:ALA:O	7:F:119:SER:OG	2.10	0.67
30:c:18:LEU:HB2	30:c:29:GLN:HB3	1.76	0.67
34:g:216:ALA:HB3	34:g:230:LEU:HB2	1.77	0.67
1:2:1527:C:OP1	18:Q:142:GLN:NE2	2.28	0.67
26:Y:11:LYS:H	26:Y:24:VAL:HG22	1.60	0.67
1:2:1231:C:O2'	1:2:1232:U:O2	2.10	0.67
2:A:78:SER:HB2	2:A:87:VAL:HG21	1.77	0.67
31:d:21:CYS:HB3	31:d:26:ASN:H	1.60	0.67
1:2:1453:C:C5	1:2:1476:A:H2	2.13	0.67
6:E:54:TYR:O	26:Y:15:ASN:ND2	2.28	0.67
1:2:1290:G:N2	1:2:1302:G:O2'	2.27	0.66
7:F:115:ALA:HA	7:F:186:ASN:HD22	1.58	0.66
12:K:5:LYS:HG3	12:K:8:ARG:HE	1.60	0.66
1:2:927:C:O2	29:b:51:GLN:NE2	2.27	0.66
1:2:1394:G:H5''	18:Q:126:ARG:HE	1.60	0.66
20:S:23:ARG:HH21	27:Z:43:LYS:HB2	1.60	0.66
1:2:296:U:O2'	6:E:131:VAL:O	2.12	0.66
1:2:1477:U:O2	19:R:2:GLY:N	2.28	0.66
5:D:143:ARG:NH2	36:n:173:ASP:OD1	2.27	0.66
7:F:78:MET:O	7:F:79:HIS:HB2	1.95	0.66
5:D:211:VAL:O	19:R:20:TYR:OH	2.13	0.66
1:2:630:U:H5	36:n:185:ASN:HD22	1.44	0.66
1:2:1224:G:H22	1:2:1643:U:H3	1.44	0.66
7:F:68:ILE:O	7:F:72:LEU:HG	1.96	0.66
1:2:387:C:OP2	10:I:10:LYS:NZ	2.25	0.66
1:2:973:C:N3	16:O:55:ARG:NH1	2.43	0.66
25:X:41:PHE:O	25:X:76:LYS:NZ	2.28	0.66
1:2:320:G:H22	1:2:331:C:H42	1.42	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:57:ALA:HB2	10:I:183:GLY:HA2	1.78	0.66
1:2:1669:G:OP1	22:U:79:ARG:NH1	2.29	0.65
1:2:1678:A:H2'	1:2:1679:A:H5''	1.78	0.65
1:2:855:G:O2'	13:L:71:ARG:NH1	2.29	0.65
1:2:1630:A:N6	20:S:28:PHE:O	2.22	0.65
2:A:187:GLY:HA2	23:V:45:ARG:HD2	1.77	0.65
1:2:384:U:O4	10:I:5:ARG:NH2	2.26	0.65
7:F:115:ALA:HB3	7:F:178:ILE:HG23	1.78	0.65
11:J:113:GLN:OE1	11:J:154:GLN:NE2	2.30	0.65
34:g:289:LEU:HB3	34:g:298:LEU:HD11	1.78	0.65
7:F:112:LEU:CD1	7:F:177:LEU:HB3	2.25	0.65
10:I:110:ARG:O	10:I:114:GLU:HG2	1.96	0.65
10:I:120:PRO:HD3	10:I:153:LYS:HE2	1.78	0.65
17:P:93:MET:HE1	17:P:104:GLN:HB2	1.77	0.65
1:2:846:G:H2'	6:E:19:MET:HG2	1.77	0.65
1:2:1568:C:H4'	21:T:97:LYS:HG3	1.79	0.65
18:Q:16:LYS:HB2	18:Q:83:ALA:HB2	1.78	0.65
18:Q:21:ALA:HA	18:Q:71:ARG:O	1.97	0.65
1:2:1298:G:H1'	17:P:79:HIS:HB2	1.78	0.64
1:2:1851:A:OP1	35:h:9:ARG:NH2	2.30	0.64
15:N:93:LYS:HG3	15:N:150:VAL:HG11	1.79	0.64
20:S:130:ARG:HG3	20:S:134:GLN:HB2	1.80	0.64
1:2:1570:G:O2'	1:2:1615:U:OP1	2.13	0.64
1:2:28:U:H2'	1:2:29:G:H8	1.63	0.64
20:S:86:ARG:HD2	20:S:89:ASP:HB2	1.78	0.64
1:2:141:A:N6	1:2:177:G:C5	2.66	0.64
6:E:60:GLU:OE1	26:Y:20:ARG:NH2	2.22	0.64
7:F:77:MET:HB2	7:F:84:GLY:H	1.61	0.64
1:2:1261:C:O2	31:d:12:ARG:NH2	2.31	0.64
3:B:68:GLU:OE1	3:B:68:GLU:N	2.28	0.64
17:P:50:ARG:HH12	17:P:83:MET:HE1	1.63	0.63
10:I:62:VAL:HG11	10:I:75:LYS:HZ3	1.63	0.63
1:2:1161:U:O4	25:X:2:GLY:N	2.32	0.63
13:L:150:GLY:HA2	15:N:133:ARG:NH2	2.14	0.63
1:2:377:G:H5'	10:I:98:LYS:HB3	1.80	0.63
1:2:928:G:H2'	1:2:929:G:C8	2.34	0.63
11:J:18:ARG:O	11:J:24:ARG:NH1	2.31	0.63
18:Q:104:SER:O	18:Q:108:ILE:HG22	1.98	0.63
1:2:921:G:O6	24:W:60:LYS:NZ	2.32	0.63
1:2:1121:G:O2'	3:B:204:ILE:O	2.17	0.63
5:D:195:THR:H	5:D:201:LYS:HE2	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:55:ALA:HB1	6:E:60:GLU:HB2	1.81	0.63
26:Y:57:VAL:HB	26:Y:60:PHE:HE2	1.61	0.63
1:2:861:A:H1'	1:2:862:A:H2	1.63	0.63
1:2:587:A:H5'	1:2:592:C:H41	1.62	0.63
1:2:798:G:O2'	9:H:108:SER:OG	2.16	0.63
18:Q:77:HIS:O	18:Q:81:ILE:HB	1.99	0.63
34:g:79:LEU:HG	34:g:87:LEU:HD11	1.80	0.63
1:2:1290:G:OP1	1:2:1301:A:O2'	2.16	0.62
20:S:14:ARG:HD2	20:S:17:ASN:H	1.63	0.62
34:g:109:LEU:HD11	34:g:152:SER:HA	1.79	0.62
1:2:1010:G:H2'	1:2:1011:A:C8	2.34	0.62
1:2:1694:U:HO2'	1:2:1833:C:HO2'	1.44	0.62
3:B:52:THR:HG23	3:B:57:ILE:HA	1.81	0.62
6:E:197:ASN:ND2	6:E:199:GLU:OE1	2.31	0.62
7:F:145:ARG:O	7:F:145:ARG:NH1	2.32	0.62
1:2:613:G:N2	1:2:626:G:OP1	2.33	0.62
1:2:1400:U:O4	1:2:1401:A:N6	2.32	0.62
7:F:108:PRO:O	7:F:112:LEU:HB2	1.99	0.62
1:2:617:G:H4'	25:X:88:ASP:HB3	1.81	0.62
1:2:921:G:OP2	29:b:21:LYS:NZ	2.28	0.62
1:2:1445:U:O2'	22:U:55:ARG:O	2.17	0.62
1:2:1485:U:H5'	5:D:151:LYS:NZ	2.14	0.62
18:Q:26:LYS:HD3	18:Q:27:ARG:H	1.64	0.62
1:2:1454:A:C2	1:2:1476:A:H1'	2.35	0.62
5:D:106:ARG:NH1	5:D:174:HIS:O	2.32	0.62
1:2:1647:A:N6	1:2:1677:U:O4	2.32	0.62
18:Q:132:PHE:HZ	22:U:77:TRP:N	1.91	0.62
20:S:130:ARG:HE	20:S:134:GLN:HB2	1.64	0.62
1:2:495:U:O2'	6:E:27:PHE:O	2.16	0.62
1:2:563:G:N7	11:J:172:ARG:NH2	2.48	0.62
1:2:1610:G:H2'	1:2:1611:G:H8	1.65	0.62
5:D:105:LEU:HD23	5:D:122:VAL:HG11	1.80	0.62
1:2:14:C:H2'	1:2:15:U:C6	2.35	0.61
1:2:989:C:OP2	3:B:155:TYR:OH	2.10	0.61
3:B:107:ARG:HG3	3:B:107:ARG:HH11	1.65	0.61
12:K:14:LEU:O	12:K:18:GLU:HB2	2.00	0.61
23:V:53:TYR:OH	23:V:76:ASP:OD2	2.18	0.61
1:2:224:A:N6	1:2:297:A:N1	2.48	0.61
1:2:639:C:O2'	1:2:640:A:H8	1.83	0.61
25:X:63:ASN:C	25:X:63:ASN:HD22	2.07	0.61
1:2:1538:C:H2'	1:2:1539:U:H4'	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:90:SER:OG	21:T:91:HIS:N	2.34	0.61
1:2:568:C:H2'	1:2:569:A:C8	2.35	0.61
1:2:1024:A:OP2	15:N:124:ARG:NH2	2.34	0.61
3:B:36:PRO:HB2	3:B:38:MET:HE3	1.81	0.61
6:E:21:ASP:OD2	6:E:24:THR:OG1	2.18	0.61
13:L:111:VAL:HG12	13:L:140:PHE:HB2	1.82	0.61
34:g:152:SER:OG	34:g:168:CYS:SG	2.58	0.61
18:Q:93:VAL:HG22	18:Q:109:LYS:HB2	1.81	0.61
16:O:40:THR:HG21	16:O:74:ALA:HB2	1.82	0.61
20:S:5:ILE:HG12	20:S:7:GLU:H	1.66	0.61
2:A:128:ARG:NH2	2:A:151:ASP:O	2.34	0.61
9:H:19:PHE:O	9:H:23:ILE:HG12	2.00	0.61
1:2:388:U:H2'	1:2:389:A:H8	1.66	0.60
1:2:957:A:H3'	1:2:958:G:H21	1.66	0.60
16:O:86:LYS:NZ	16:O:122:SER:O	2.32	0.60
1:2:1227:G:H21	1:2:1639:G:H21	1.48	0.60
19:R:127:ASN:ND2	19:R:127:ASN:O	2.34	0.60
1:2:413:G:H5'	1:2:813:A:H61	1.66	0.60
1:2:1240:A:N6	17:P:99:GLY:O	2.34	0.60
1:2:1610:G:N2	20:S:85:ASN:O	2.32	0.60
26:Y:27:VAL:HG11	26:Y:35:VAL:HG11	1.83	0.60
34:g:114:SER:OG	34:g:116:ASP:OD1	2.19	0.60
1:2:436:G:OP2	1:2:471:G:O2'	2.19	0.60
1:2:1453:C:O2	19:R:28:PHE:CE2	2.55	0.60
20:S:72:GLN:OE1	20:S:97:GLN:NE2	2.35	0.60
34:g:251:ALA:HB2	34:g:289:LEU:HD21	1.84	0.60
1:2:562:U:H2'	1:2:563:G:C8	2.37	0.60
20:S:71:MET:HE1	20:S:84:LEU:HG	1.83	0.60
26:Y:55:ILE:HG12	26:Y:75:ILE:HG12	1.82	0.60
21:T:11:GLN:HA	21:T:14:PHE:HB3	1.83	0.60
25:X:123:VAL:HG12	25:X:124:LYS:HG3	1.83	0.60
34:g:35:SER:OG	34:g:36:ARG:N	2.33	0.60
1:2:180:G:O2'	1:2:181:A:O5'	2.17	0.60
1:2:1098:C:H2'	1:2:1099:G:C8	2.36	0.60
1:2:212:C:H2'	1:2:213:G:H8	1.65	0.60
1:2:1649:U:O2'	18:Q:138:ARG:HG3	2.01	0.60
5:D:50:ILE:HD13	5:D:86:LEU:HB2	1.84	0.60
1:2:14:C:O2'	1:2:668:A:N1	2.34	0.59
1:2:796:G:N2	9:H:108:SER:O	2.34	0.59
1:2:1544:C:OP2	1:2:1585:U:N3	2.31	0.59
34:g:201:SER:OG	34:g:203:ASP:OD1	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:34:SER:H	9:H:37:LYS:HD3	1.67	0.59
12:K:11:ILE:HG21	12:K:48:ALA:HB1	1.84	0.59
1:2:818:A:OP1	11:J:80:ARG:NH2	2.35	0.59
1:2:643:A:OP1	11:J:39:ASN:ND2	2.35	0.59
35:h:19:LYS:O	35:h:22:GLN:NE2	2.35	0.59
1:2:104:A:OP2	1:2:352:U:N3	2.35	0.59
1:2:1603:G:O5'	1:2:1630:A:N6	2.31	0.59
5:D:135:GLU:HG3	5:D:153:VAL:HG12	1.83	0.59
26:Y:86:GLU:OE2	26:Y:90:ARG:NE	2.34	0.59
1:2:1862:G:O2'	28:a:5:ARG:NH2	2.36	0.59
6:E:11:ARG:HA	6:E:28:ALA:HB2	1.84	0.59
9:H:68:GLN:O	9:H:71:SER:OG	2.13	0.59
2:A:94:THR:O	2:A:186:ARG:NH2	2.35	0.59
8:G:56:ASN:ND2	8:G:60:GLY:O	2.36	0.59
16:O:95:ILE:HD11	16:O:126:ILE:HG13	1.82	0.59
18:Q:131:LYS:HB3	18:Q:140:ARG:HH22	1.66	0.59
20:S:30:ILE:HD12	20:S:36:VAL:HG13	1.84	0.59
1:2:1036:A:H4'	1:2:1855:G:N2	2.17	0.59
31:d:21:CYS:HB2	31:d:39:CYS:H	1.67	0.59
6:E:100:ARG:NH2	6:E:121:TYR:O	2.36	0.59
7:F:161:ALA:HA	7:F:165:ASN:HD22	1.68	0.59
25:X:98:ASP:OD2	25:X:140:ARG:NH2	2.35	0.59
1:2:93:U:H4'	6:E:6:LYS:HA	1.83	0.59
1:2:106:C:H2'	1:2:107:A:H8	1.67	0.59
1:2:558:G:H2'	1:2:559:G:C8	2.37	0.59
1:2:996:A:H2'	1:2:997:A:C8	2.38	0.59
1:2:1354:G:N2	1:2:1357:A:OP2	2.33	0.59
1:2:455:A:OP1	8:G:94:ARG:HD2	2.03	0.58
1:2:1010:G:H2'	1:2:1011:A:H8	1.68	0.58
1:2:1644:C:H4'	18:Q:140:ARG:HB2	1.85	0.58
4:C:70:VAL:HG11	4:C:93:ILE:HG23	1.85	0.58
5:D:103:GLU:OE2	5:D:173:ARG:NH1	2.36	0.58
5:D:209:SER:HB2	19:R:40:ILE:HB	1.84	0.58
7:F:76:MET:HE3	7:F:76:MET:HA	1.85	0.58
5:D:75:LYS:NZ	12:K:20:VAL:O	2.34	0.58
22:U:28:ASN:OD1	22:U:31:SER:OG	2.15	0.58
29:b:34:ASP:CG	29:b:82:LYS:HE2	2.28	0.58
1:2:1540:G:H1	21:T:77:LYS:HG3	1.68	0.58
15:N:55:ARG:NH2	29:b:51:GLN:OE1	2.36	0.58
21:T:84:ARG:NH1	21:T:88:MET:O	2.33	0.58
25:X:107:ARG:HB3	25:X:110:HIS:HB3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:107:A:H2'	1:2:108:G:C8	2.38	0.58
1:2:448:A:H5''	10:I:25:ARG:HA	1.86	0.58
1:2:453:C:O2'	8:G:92:ARG:O	2.19	0.58
1:2:643:A:OP1	11:J:41:ARG:NH2	2.36	0.58
1:2:869:A:C6	9:H:114:GLN:HG3	2.38	0.58
17:P:17:TYR:CD1	17:P:110:GLU:HG2	2.39	0.58
7:F:110:GLN:OE1	7:F:114:ASN:ND2	2.36	0.58
20:S:14:ARG:HA	20:S:14:ARG:NH1	2.19	0.58
21:T:29:LYS:HD3	21:T:30:VAL:H	1.69	0.58
4:C:146:GLU:OE1	5:D:120:TYR:OH	2.17	0.58
8:G:67:VAL:HG23	8:G:99:GLY:HA2	1.86	0.58
29:b:33:MET:HE1	29:b:73:LEU:HD11	1.86	0.58
1:2:1614:A:H8	17:P:43:ARG:HD3	1.69	0.58
1:2:1670:C:OP2	18:Q:130:LYS:N	2.26	0.58
10:I:69:SER:OG	10:I:191:GLU:OE2	2.18	0.58
16:O:98:ARG:HD2	16:O:99:ALA:O	2.04	0.58
18:Q:26:LYS:HD3	18:Q:27:ARG:N	2.18	0.58
7:F:27:ASP:N	7:F:27:ASP:OD1	2.37	0.57
34:g:193:GLY:HA3	34:g:213:ASP:HB2	1.86	0.57
1:2:1255:G:OP1	1:2:1256:G:O2'	2.22	0.57
1:2:1287:A:H61	33:f:97:LYS:HD3	1.69	0.57
1:2:1300:U:O2'	17:P:51:ARG:NH2	2.38	0.57
18:Q:110:ASP:O	18:Q:114:GLN:HB3	2.03	0.57
1:2:1153:C:OP2	24:W:71:LYS:NZ	2.37	0.57
1:2:1260:A:N1	1:2:1619:A:N6	2.48	0.57
1:2:1317:C:H2'	1:2:1318:G:C8	2.39	0.57
3:B:34:LYS:O	3:B:98:THR:OG1	2.15	0.57
28:a:60:ASP:OD1	28:a:60:ASP:N	2.38	0.57
34:g:252:THR:O	34:g:252:THR:OG1	2.22	0.57
1:2:962:A:H61	7:F:134:VAL:HG11	1.69	0.57
7:F:194:ASP:O	7:F:197:GLU:HB3	2.04	0.57
16:O:131:ASP:OD1	16:O:133:THR:HG22	2.04	0.57
1:2:1856:C:H2'	1:2:1857:G:C8	2.39	0.57
2:A:8:LEU:HD11	23:V:39:VAL:HG11	1.87	0.57
2:A:158:ASP:OD2	23:V:32:ILE:HD13	2.05	0.57
18:Q:96:TYR:HD2	18:Q:108:ILE:HG21	1.69	0.57
21:T:66:LEU:HG	21:T:67:ARG:HG2	1.87	0.57
4:C:256:TRP:CD2	24:W:68:ARG:HD3	2.39	0.57
25:X:124:LYS:HG2	25:X:129:SER:HA	1.86	0.57
1:2:1854:U:H2'	1:2:1855:G:H8	1.70	0.57
1:2:847:A:OP1	6:E:108:ARG:NH1	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1358:U:OP1	4:C:121:ARG:NH2	2.37	0.57
1:2:1572:C:H2'	1:2:1573:G:C8	2.39	0.57
6:E:102:ILE:HG23	6:E:182:MET:HE1	1.85	0.57
7:F:157:GLY:HA2	7:F:160:GLU:HG2	1.86	0.57
5:D:177:LEU:HD12	5:D:178:ARG:N	2.20	0.57
25:X:63:ASN:O	25:X:63:ASN:ND2	2.36	0.57
1:2:98:C:OP2	1:2:426:A:O2'	2.21	0.56
1:2:1286:G:O2'	33:f:94:LYS:NZ	2.38	0.56
1:2:1856:C:H2'	1:2:1857:G:H8	1.69	0.56
1:2:1865:C:OP2	28:a:5:ARG:NH1	2.37	0.56
7:F:59:LYS:HE3	7:F:60:ARG:O	2.05	0.56
1:2:388:U:H2'	1:2:389:A:C8	2.39	0.56
1:2:1204:A:O2'	1:2:1700:C:OP2	2.19	0.56
34:g:31:ILE:H	34:g:42:MET:HE2	1.70	0.56
1:2:124:U:H3	1:2:216:C:H42	1.51	0.56
1:2:916:A:C5	15:N:73:ARG:HD3	2.39	0.56
1:2:1083:A:N7	1:2:1841:C:O2'	2.29	0.56
1:2:1542:C:H42	18:Q:44:PRO:HG3	1.69	0.56
4:C:191:VAL:HG11	4:C:236:PHE:HA	1.87	0.56
5:D:116:ARG:HH22	36:n:175:GLU:HB2	1.70	0.56
7:F:141:VAL:HG11	7:F:145:ARG:HB3	1.86	0.56
18:Q:42:ILE:HG22	18:Q:44:PRO:HD2	1.88	0.56
1:2:1605:G:N1	1:2:1635:C:O2	2.39	0.56
1:2:1647:A:OP1	18:Q:138:ARG:NH2	2.35	0.56
8:G:159:ARG:NH2	8:G:171:THR:O	2.39	0.56
1:2:84:A:H5'	26:Y:122:LYS:HD3	1.86	0.56
1:2:1292:C:H5'	1:2:1295:A:H61	1.70	0.56
10:I:103:LEU:HD13	10:I:172:LEU:HD23	1.87	0.56
1:2:373:G:N2	13:L:83:GLN:OE1	2.37	0.56
1:2:541:U:O2	1:2:543:C:N4	2.39	0.56
1:2:1445:U:O4	1:2:1446:A:N6	2.38	0.56
1:2:1863:A:OP2	28:a:4:LYS:NZ	2.29	0.56
7:F:144:LEU:O	7:F:148:ASN:ND2	2.39	0.56
12:K:53:LYS:HG3	12:K:69:TRP:CE2	2.40	0.56
1:2:1189:A:H2'	1:2:1190:A:C8	2.41	0.56
23:V:39:VAL:HG13	23:V:44:GLY:HA2	1.87	0.56
25:X:63:ASN:C	25:X:63:ASN:ND2	2.64	0.56
1:2:1327:G:H1	1:2:1502:C:H42	1.54	0.56
1:2:1538:C:O2	1:2:1539:U:O2'	2.22	0.56
1:2:74:G:C6	8:G:168:LYS:HD3	2.40	0.56
2:A:135:THR:O	2:A:138:SER:OG	2.22	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:175:PHE:HE1	6:E:198:ARG:HD2	1.71	0.56
7:F:122:ARG:HB3	30:c:59:LEU:HD13	1.87	0.56
1:2:434:G:OP2	10:I:25:ARG:NH2	2.39	0.56
1:2:942:G:H2'	1:2:943:U:C6	2.40	0.56
9:H:165:ASN:O	9:H:168:HIS:NE2	2.38	0.56
1:2:118:C:H1'	1:2:445:A:C5	2.40	0.55
13:L:126:VAL:HG12	13:L:145:VAL:HG22	1.88	0.55
17:P:89:MET:HB3	17:P:92:SER:HB2	1.89	0.55
34:g:96:THR:OG1	34:g:97:THR:N	2.39	0.55
1:2:1260:A:OP1	1:2:1261:C:N4	2.39	0.55
7:F:19:LEU:HD22	7:F:41:VAL:HG11	1.87	0.55
12:K:11:ILE:HD13	12:K:45:VAL:HG13	1.87	0.55
1:2:528:A:N1	1:2:554:A:N6	2.53	0.55
1:2:597:G:H4'	1:2:646:G:H4'	1.87	0.55
2:A:147:LEU:O	2:A:165:ASN:ND2	2.38	0.55
3:B:92:GLN:HE22	3:B:229:MET:HE1	1.71	0.55
7:F:121:PRO:O	7:F:146:ARG:NH1	2.39	0.55
7:F:123:GLU:HB2	7:F:197:GLU:OE2	2.05	0.55
23:V:22:ARG:NH1	24:W:67:GLY:O	2.40	0.55
7:F:113:VAL:HB	7:F:182:LYS:C	2.30	0.55
28:a:36:ILE:HD13	28:a:78:VAL:HG11	1.88	0.55
31:d:19:ARG:HB2	31:d:19:ARG:HH11	1.71	0.55
1:2:1231:C:H4'	1:2:1665:G:C8	2.42	0.55
1:2:1287:A:H2'	33:f:95:ARG:HH12	1.70	0.55
1:2:1569:A:H61	1:2:1613:G:N2	2.04	0.55
9:H:147:LYS:HA	24:W:49:GLU:HG2	1.87	0.55
26:Y:42:GLU:O	26:Y:46:LYS:HG2	2.07	0.55
27:Z:47:LEU:H	27:Z:47:LEU:HD12	1.70	0.55
6:E:100:ARG:HG2	6:E:102:ILE:HG12	1.89	0.55
15:N:83:ASP:N	15:N:83:ASP:OD1	2.37	0.55
8:G:70:HIS:O	8:G:98:ARG:NH2	2.40	0.55
10:I:119:LEU:HA	10:I:153:LYS:HG3	1.88	0.55
19:R:100:PRO:O	19:R:103:LYS:HG3	2.07	0.55
7:F:117:ILE:HB	7:F:183:GLY:N	2.21	0.55
20:S:72:GLN:O	20:S:72:GLN:NE2	2.39	0.55
1:2:1210:G:OP1	28:a:82:LYS:NZ	2.38	0.55
1:2:533:A:H2'	1:2:534:G:O4'	2.06	0.55
1:2:1313:A:C8	14:M:33:ARG:HD3	2.42	0.55
5:D:123:LEU:HD11	5:D:154:ASP:HB2	1.88	0.55
11:J:136:ARG:NH2	11:J:158:ASP:OD2	2.40	0.55
7:F:187:SER:HB3	7:F:190:ILE:HB	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:45:TRP:HA	8:G:48:TYR:HD2	1.72	0.54
12:K:65:ARG:HH11	31:d:25:SER:HB2	1.72	0.54
33:f:133:ALA:O	33:f:139:HIS:ND1	2.39	0.54
1:2:165:G:OP2	1:2:165:G:N2	2.34	0.54
1:2:1245:G:O2'	1:2:1492:U:OP1	2.24	0.54
1:2:1660:C:OP2	31:d:32:ARG:NH1	2.41	0.54
10:I:3:ILE:O	10:I:30:GLY:N	2.41	0.54
14:M:61:TYR:O	14:M:65:VAL:HG13	2.08	0.54
20:S:131:VAL:HG12	20:S:132:ARG:HD2	1.89	0.54
23:V:51:LYS:HD2	23:V:76:ASP:OD2	2.07	0.54
26:Y:57:VAL:HB	26:Y:60:PHE:CE2	2.42	0.54
1:2:379:C:O2	10:I:5:ARG:NE	2.33	0.54
1:2:682:U:O2'	24:W:4:MET:SD	2.63	0.54
3:B:136:ARG:HB2	3:B:218:LEU:HD11	1.88	0.54
1:2:963:A:N3	1:2:1055:A:O2'	2.40	0.54
1:2:1189:A:H2'	1:2:1190:A:H8	1.72	0.54
9:H:148:LEU:HD12	24:W:49:GLU:HG3	1.89	0.54
14:M:53:ALA:HB3	14:M:103:VAL:HG23	1.89	0.54
18:Q:82:TYR:HD2	18:Q:85:ARG:NH2	2.06	0.54
1:2:106:C:H2'	1:2:107:A:C8	2.42	0.54
1:2:1677:U:O4	1:2:1678:A:N6	2.40	0.54
20:S:129:LEU:HD21	20:S:144:ARG:HH21	1.73	0.54
1:2:912:C:H2'	1:2:914:U:H1'	1.90	0.54
1:2:991:G:C6	1:2:1134:G:H5''	2.43	0.54
3:B:30:TRP:CE2	16:O:19:PRO:HD3	2.43	0.54
8:G:57:ASP:HA	8:G:106:LEU:HA	1.89	0.54
18:Q:22:VAL:O	18:Q:70:VAL:HA	2.08	0.54
24:W:111:MET:HG3	24:W:115:GLU:HB3	1.90	0.54
1:2:177:G:H2'	1:2:178:C:H4'	1.88	0.54
1:2:1497:G:O2'	12:K:62:PHE:O	2.25	0.54
7:F:127:ARG:NH2	7:F:132:GLY:O	2.41	0.54
7:F:22:LYS:HD2	7:F:101:HIS:CE1	2.42	0.54
17:P:26:LEU:HD13	17:P:88:GLU:HB2	1.90	0.54
1:2:625:G:N1	25:X:64:SER:O	2.38	0.54
1:2:801:U:O4	9:H:106:ARG:NH1	2.38	0.54
1:2:1020:A:OP2	15:N:70:LYS:NZ	2.30	0.54
3:B:32:ASP:OD1	3:B:46:LYS:NZ	2.37	0.54
20:S:114:LEU:HD12	20:S:122:GLY:HA2	1.90	0.54
34:g:192:THR:OG1	34:g:213:ASP:OD2	2.22	0.54
1:2:1614:A:C8	17:P:43:ARG:HD3	2.43	0.53
2:A:5:LEU:HD13	23:V:41:LYS:HA	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:70:GLU:HA	7:F:73:THR:HG22	1.90	0.53
18:Q:71:ARG:HB3	18:Q:73:LYS:HE3	1.90	0.53
19:R:71:ILE:HG13	19:R:74:GLN:HB2	1.90	0.53
1:2:1101:U:H2'	1:2:1102:G:H8	1.73	0.53
1:2:1232:U:H5	1:2:1526:G:H1	1.56	0.53
1:2:1290:G:H21	1:2:1302:G:HO2'	1.55	0.53
4:C:172:ASN:ND2	11:J:95:ASP:OD2	2.41	0.53
17:P:113:GLY:O	17:P:114:HIS:ND1	2.39	0.53
21:T:82:ARG:O	21:T:82:ARG:NH1	2.41	0.53
1:2:17:C:H2'	1:2:18:C:C6	2.43	0.53
1:2:1446:A:H5''	22:U:58:THR:HG23	1.91	0.53
1:2:1454:A:H2	1:2:1476:A:H1'	1.73	0.53
1:2:24:C:H2'	1:2:25:A:C8	2.44	0.53
1:2:1259:A:OP2	1:2:1623:A:N6	2.41	0.53
1:2:677:G:N1	1:2:1027:A:OP2	2.34	0.53
1:2:906:U:O2'	1:2:907:G:N7	2.37	0.53
1:2:1452:A:H4'	1:2:1453:C:O5'	2.07	0.53
1:2:1497:G:H2'	12:K:62:PHE:HD2	1.72	0.53
7:F:109:LEU:HA	7:F:112:LEU:HD22	1.91	0.53
7:F:144:LEU:HG	7:F:148:ASN:HD21	1.73	0.53
26:Y:114:MET:HG3	26:Y:125:VAL:HG21	1.90	0.53
1:2:102:A:H4'	1:2:104:A:C8	2.43	0.53
1:2:980:A:H2'	1:2:981:A:C8	2.43	0.53
1:2:1101:U:H2'	1:2:1102:G:C8	2.44	0.53
5:D:119:CYS:SG	5:D:136:VAL:HG21	2.48	0.53
11:J:30:LYS:HG3	32:e:42:PHE:CE2	2.44	0.53
1:2:28:U:H2'	1:2:29:G:C8	2.44	0.53
1:2:1109:C:N3	19:R:126:MET:HG3	2.24	0.53
1:2:1267:C:OP2	33:f:82:LYS:NZ	2.41	0.53
4:C:209:VAL:HB	4:C:210:PRO:HD3	1.91	0.53
5:D:205:PRO:HA	19:R:42:PRO:HG2	1.90	0.53
21:T:64:LEU:HD23	21:T:70:ALA:HB3	1.90	0.53
1:2:1563:G:O3'	21:T:101:ARG:NH2	2.42	0.53
14:M:36:ARG:NH1	33:f:105:TYR:OH	2.42	0.53
22:U:94:PRO:HD2	22:U:97:ILE:HD13	1.91	0.53
24:W:23:ARG:NH1	24:W:65:LEU:O	2.41	0.53
34:g:68:ASP:N	34:g:68:ASP:OD1	2.40	0.53
1:2:659:G:O2'	1:2:662:G:O2'	2.25	0.53
1:2:1174:U:H2'	1:2:1175:G:H8	1.73	0.53
8:G:135:PRO:HB2	8:G:141:ILE:HD13	1.90	0.53
1:2:528:A:H2'	1:2:529:A:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:581:U:OP1	11:J:133:ARG:NH2	2.42	0.53
1:2:1452:A:H62	1:2:1473:G:H21	1.56	0.53
1:2:1535:U:H6	7:F:88:MET:HE2	1.73	0.53
1:2:1660:C:H5''	31:d:32:ARG:HH12	1.74	0.53
1:2:1735:A:H2	1:2:1799:G:N2	2.00	0.53
5:D:27:ARG:CZ	12:K:63:ALA:HB3	2.39	0.53
10:I:106:SER:HB3	10:I:171:LEU:HG	1.90	0.53
24:W:30:CYS:SG	24:W:31:SER:N	2.81	0.53
1:2:1550:G:H3'	1:2:1579:A:H61	1.75	0.52
1:2:1648:G:C8	18:Q:125:ARG:HB3	2.44	0.52
25:X:57:VAL:HG22	25:X:67:ARG:HB2	1.90	0.52
28:a:36:ILE:HG21	28:a:78:VAL:HG21	1.91	0.52
1:2:1453:C:H2'	1:2:1454:A:H4'	1.91	0.52
1:2:1456:G:H2'	1:2:1457:U:C6	2.43	0.52
2:A:121:LEU:HD12	2:A:143:PRO:HG2	1.92	0.52
6:E:72:ILE:HB	6:E:77:ARG:HG3	1.91	0.52
7:F:26:ASP:OD1	7:F:26:ASP:N	2.42	0.52
32:e:11:LYS:O	32:e:15:GLN:HG2	2.09	0.52
1:2:1532:C:H42	1:2:1637:A:N6	2.06	0.52
18:Q:43:GLU:OE2	21:T:10:ASN:ND2	2.43	0.52
34:g:121:VAL:HG21	34:g:154:VAL:HB	1.90	0.52
1:2:467:G:H5'	8:G:72:ARG:HH12	1.74	0.52
1:2:1652:G:H1	1:2:1672:U:H3	1.57	0.52
1:2:1802:C:H2'	1:2:1803:U:C6	2.45	0.52
4:C:81:ILE:HG21	4:C:88:ILE:HD11	1.92	0.52
8:G:6:SER:HB3	8:G:13:GLN:HG3	1.91	0.52
13:L:80:MET:HE1	13:L:120:VAL:O	2.09	0.52
23:V:32:ILE:HD12	23:V:34:MET:HG3	1.91	0.52
1:2:683:G:H4'	24:W:4:MET:HB3	1.91	0.52
1:2:864:A:N3	25:X:8:ARG:NH2	2.58	0.52
1:2:1723:G:H2'	1:2:1724:A:C4	2.45	0.52
2:A:106:GLY:N	2:A:136:GLU:OE2	2.42	0.52
11:J:131:ARG:NH2	11:J:143:ASN:OD1	2.42	0.52
31:d:31:ILE:O	31:d:37:ASN:N	2.42	0.52
2:A:173:LEU:HD11	2:A:177:MET:HE3	1.91	0.52
6:E:160:ILE:HD12	6:E:169:ILE:HG12	1.92	0.52
16:O:101:GLY:HA3	16:O:134:PRO:HG2	1.92	0.52
26:Y:18:LEU:O	26:Y:85:ASN:ND2	2.42	0.52
34:g:33:SER:HB3	34:g:43:TRP:NE1	2.21	0.52
1:2:595:U:H2'	1:2:596:U:C6	2.45	0.52
1:2:1004:U:H2'	1:2:1005:G:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:84:GLN:O	2:A:88:LEU:HD22	2.10	0.52
7:F:114:ASN:HA	7:F:184:SER:HB3	1.92	0.52
11:J:53:ILE:HD13	11:J:81:LEU:HD21	1.91	0.52
14:M:91:LEU:HD22	14:M:100:PRO:HD2	1.92	0.52
4:C:125:LYS:HG3	4:C:143:CYS:HB2	1.91	0.52
5:D:16:ILE:HD11	31:d:38:MET:HE2	1.91	0.52
1:2:17:C:O2'	1:2:1194:A:N1	2.37	0.52
1:2:1402:A:H5'	22:U:51:LYS:HD2	1.91	0.52
1:2:1690:U:H2'	1:2:1691:U:C6	2.45	0.52
2:A:198:MET:HG3	2:A:200:ASP:H	1.74	0.52
6:E:151:ASP:HB3	6:E:154:ILE:HG13	1.92	0.52
10:I:165:GLN:HE22	10:I:172:LEU:HB2	1.74	0.52
2:A:24:HIS:HB3	2:A:51:LEU:HD21	1.92	0.52
15:N:13:GLN:NE2	29:b:21:LYS:HE3	2.24	0.52
24:W:39:THR:O	24:W:43:LYS:HG2	2.10	0.52
28:a:45:VAL:HG11	28:a:53:ILE:HD12	1.92	0.52
30:c:32:VAL:HG11	30:c:56:LEU:HD12	1.92	0.52
1:2:1250:A:N1	1:2:1340:U:H5'	2.26	0.51
20:S:109:GLU:HB3	20:S:111:LEU:HD21	1.91	0.51
5:D:126:ILE:O	5:D:129:SER:OG	2.27	0.51
5:D:132:LYS:HE3	5:D:189:MET:SD	2.51	0.51
6:E:44:LEU:HD13	6:E:72:ILE:HD11	1.93	0.51
22:U:78:ASP:OD1	31:d:54:LYS:HD2	2.10	0.51
34:g:79:LEU:HD22	34:g:113:PHE:HB2	1.91	0.51
16:O:65:ASP:OD1	16:O:66:ARG:N	2.43	0.51
17:P:42:ARG:HD2	17:P:43:ARG:H	1.74	0.51
22:U:38:ASP:OD1	22:U:41:ARG:NH2	2.44	0.51
26:Y:111:LYS:HA	26:Y:114:MET:HE2	1.93	0.51
1:2:1627:C:H2'	1:2:1628:C:C6	2.45	0.51
6:E:175:PHE:HE2	6:E:225:ILE:HG21	1.74	0.51
1:2:472:C:O2	1:2:475:C:N4	2.37	0.51
1:2:672:A:N6	1:2:1161:U:O2'	2.44	0.51
1:2:1144:A:H2'	1:2:1145:A:C8	2.45	0.51
1:2:16:G:H2'	1:2:17:C:C6	2.46	0.51
1:2:74:G:H5'	1:2:75:G:H21	1.76	0.51
1:2:1265:A:H8	33:f:78:LYS:HE2	1.76	0.51
6:E:138:HIS:CD2	6:E:148:ARG:HG2	2.46	0.51
1:2:297:A:H5'	6:E:132:GLY:HA2	1.93	0.51
17:P:50:ARG:H	17:P:53:GLN:HE22	1.59	0.51
23:V:33:GLN:OE1	23:V:52:THR:OG1	2.24	0.51
28:a:40:VAL:HG22	28:a:69:VAL:HB	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1203:G:H2'	1:2:1204:A:C8	2.46	0.51
4:C:98:LEU:O	4:C:101:SER:OG	2.28	0.51
10:I:101:ILE:HD12	10:I:190:LEU:HD11	1.92	0.51
10:I:144:LYS:HE3	10:I:145:ILE:HB	1.93	0.51
29:b:67:THR:HG22	29:b:69:GLY:H	1.76	0.51
34:g:284:PRO:HB2	34:g:302:TYR:HB3	1.92	0.51
1:2:141:A:C6	1:2:177:G:C4	2.99	0.51
1:2:169:U:H5''	8:G:135:PRO:HA	1.92	0.51
1:2:1598:G:H2'	27:Z:80:ARG:HH11	1.76	0.51
6:E:143:ASP:HB3	6:E:145:ARG:HG3	1.93	0.51
1:2:25:A:H2'	1:2:26:U:C6	2.46	0.51
1:2:302:A:O2'	10:I:64:ASN:OD1	2.18	0.51
1:2:1374:C:H2'	1:2:1375:G:O4'	2.11	0.51
1:2:1668:U:OP2	18:Q:141:TYR:OH	2.18	0.51
1:2:1798:C:H2'	1:2:1799:G:O4'	2.11	0.51
5:D:99:ILE:HG23	5:D:173:ARG:HH12	1.76	0.51
13:L:148:ALA:O	13:L:151:THR:OG1	2.28	0.51
6:E:126:VAL:HG22	6:E:158:ASP:O	2.10	0.50
7:F:112:LEU:HG	7:F:181:ALA:HB2	1.93	0.50
7:F:140:ASP:O	30:c:46:VAL:HG23	2.11	0.50
12:K:6:LYS:HD3	14:M:29:ASP:HB3	1.92	0.50
18:Q:31:LEU:HG	18:Q:33:LYS:HZ1	1.75	0.50
21:T:9:VAL:HG12	21:T:14:PHE:HB2	1.93	0.50
26:Y:20:ARG:HE	26:Y:22:GLN:HE21	1.57	0.50
29:b:65:GLN:HG2	29:b:72:ARG:HB3	1.93	0.50
1:2:67:C:C5	8:G:162:LEU:HB3	2.47	0.50
1:2:122:G:C6	1:2:123:G:H1'	2.46	0.50
1:2:1566:G:OP2	21:T:98:SER:OG	2.19	0.50
10:I:87:ASN:HB3	10:I:90:LEU:HD13	1.92	0.50
19:R:24:LEU:HB2	19:R:58:MET:HE1	1.91	0.50
34:g:291:TRP:CE3	34:g:295:GLY:HA2	2.46	0.50
4:C:167:ARG:NH1	4:C:218:GLY:O	2.43	0.50
7:F:108:PRO:HB2	7:F:112:LEU:HD13	1.92	0.50
12:K:49:MET:HA	12:K:52:LEU:HD12	1.92	0.50
18:Q:96:TYR:CD2	18:Q:108:ILE:HG21	2.46	0.50
24:W:86:LEU:HD21	24:W:113:HIS:HB2	1.92	0.50
1:2:487:U:O2'	1:2:488:U:O5'	2.27	0.50
1:2:508:A:H3'	1:2:509:G:H8	1.76	0.50
1:2:681:U:O2'	1:2:1160:U:OP1	2.28	0.50
7:F:116:ILE:HG13	7:F:179:ASN:HA	1.92	0.50
16:O:46:ASP:OD1	16:O:47:LEU:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:14:HIS:NE2	34:g:41:ILE:HG12	2.27	0.50
1:2:528:A:H2'	1:2:529:A:H8	1.76	0.50
1:2:1517:G:H3'	1:2:1518:C:C6	2.47	0.50
1:2:1616:U:H2'	17:P:47:ARG:NH1	2.27	0.50
19:R:10:LYS:HD3	19:R:53:TYR:CZ	2.47	0.50
34:g:42:MET:HB2	34:g:57:ARG:HB3	1.93	0.50
1:2:962:A:N6	7:F:134:VAL:HG11	2.26	0.50
1:2:1004:U:H2'	1:2:1005:G:C8	2.46	0.50
1:2:1033:G:N1	1:2:1080:A:O2'	2.30	0.50
1:2:1567:G:H1	1:2:1612:G:H21	1.59	0.50
1:2:1611:G:C8	1:2:1611:G:O5'	2.65	0.50
1:2:1819:A:H2'	1:2:1820:G:H8	1.76	0.50
1:2:1517:G:H3'	1:2:1518:C:H6	1.77	0.50
5:D:45:ARG:NH2	5:D:82:GLY:O	2.45	0.50
5:D:99:ILE:H	5:D:99:ILE:HD12	1.76	0.50
24:W:37:PHE:HE1	24:W:41:MET:HE3	1.77	0.50
1:2:159:A:N1	1:2:467:G:O2'	2.39	0.50
1:2:893:U:OP2	1:2:894:G:N2	2.45	0.50
1:2:945:U:H2'	1:2:946:U:C6	2.47	0.50
5:D:104:SER:OG	5:D:108:LYS:NZ	2.38	0.50
10:I:174:CYS:O	10:I:187:GLY:HA3	2.12	0.50
1:2:81:U:H2'	1:2:82:G:O4'	2.11	0.49
1:2:418:A:H2'	1:2:419:G:C8	2.47	0.49
1:2:1327:G:H1	1:2:1502:C:N4	2.09	0.49
1:2:1607:A:H62	1:2:1632:G:H4'	1.76	0.49
2:A:207:PRO:HA	2:A:210:ILE:HG13	1.92	0.49
7:F:81:ARG:O	7:F:85:LYS:NZ	2.35	0.49
25:X:26:GLN:HA	25:X:29:LYS:HG2	1.93	0.49
29:b:56:CYS:HB2	29:b:63:LEU:HD13	1.93	0.49
34:g:313:THR:O	34:g:315:GLY:N	2.41	0.49
1:2:948:C:H2'	1:2:949:G:H8	1.76	0.49
1:2:1540:G:OP2	21:T:43:LYS:HE3	2.12	0.49
2:A:76:VAL:HG12	2:A:87:VAL:HG22	1.94	0.49
7:F:116:ILE:O	7:F:119:SER:N	2.44	0.49
21:T:35:ASP:HB2	21:T:46:ALA:HB1	1.95	0.49
8:G:130:PRO:HB2	8:G:132:ARG:HD3	1.93	0.49
9:H:84:GLU:OE2	9:H:91:HIS:ND1	2.37	0.49
9:H:107:LYS:HD2	9:H:107:LYS:O	2.11	0.49
1:2:1030:A:H2'	1:2:1031:A:H8	1.77	0.49
1:2:1092:G:OP1	15:N:2:GLY:N	2.45	0.49
1:2:1174:U:H2'	1:2:1175:G:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1561:A:H4'	21:T:72:VAL:HG11	1.93	0.49
1:2:1616:U:O2'	1:2:1617:G:N7	2.36	0.49
4:C:183:LYS:HA	4:C:195:LEU:O	2.12	0.49
5:D:67:ARG:HH12	12:K:94:LEU:HD23	1.77	0.49
28:a:78:VAL:HG13	28:a:84:VAL:HG22	1.94	0.49
2:A:85:ARG:NH2	19:R:82:ASP:O	2.27	0.49
6:E:253:ASP:OD1	6:E:254:LYS:N	2.46	0.49
7:F:97:PHE:HB2	7:F:173:LEU:HD11	1.95	0.49
7:F:116:ILE:HD13	7:F:187:SER:HB2	1.93	0.49
6:E:124:CYS:HB3	6:E:141:THR:HB	1.93	0.49
18:Q:97:GLN:HB2	18:Q:105:LYS:HD2	1.94	0.49
1:2:495:U:H2'	1:2:496:C:O4'	2.13	0.49
1:2:531:A:H2'	1:2:532:C:O4'	2.12	0.49
1:2:1531:A:N6	7:F:80:GLY:O	2.45	0.49
8:G:78:SER:HB2	8:G:92:ARG:HG2	1.94	0.49
13:L:59:LYS:HD3	13:L:134:LEU:HB3	1.95	0.49
24:W:62:VAL:HG11	29:b:8:LEU:HG	1.94	0.49
34:g:87:LEU:HD13	34:g:111:VAL:HG21	1.94	0.49
3:B:231:LEU:HD12	3:B:231:LEU:O	2.13	0.49
5:D:20:GLU:OE2	5:D:76:ARG:NH2	2.42	0.49
9:H:121:THR:OG1	9:H:122:LEU:N	2.46	0.49
28:a:44:ILE:HD12	28:a:65:PRO:HG2	1.95	0.49
34:g:298:LEU:HB3	34:g:310:TRP:HD1	1.74	0.49
1:2:600:G:H2'	1:2:601:G:C8	2.48	0.49
1:2:943:U:C2	1:2:944:A:C8	3.01	0.49
1:2:1127:C:H5''	29:b:17:ARG:NH1	2.28	0.49
1:2:1235:G:N2	1:2:1525:C:O2	2.46	0.49
5:D:59:LEU:HA	5:D:66:ILE:HG12	1.94	0.49
7:F:114:ASN:CA	7:F:184:SER:HB3	2.43	0.49
17:P:40:ARG:HD3	17:P:42:ARG:NH2	2.26	0.49
24:W:87:GLU:HA	24:W:90:GLN:HE21	1.78	0.49
25:X:84:PHE:CE2	25:X:86:PRO:HA	2.48	0.49
30:c:42:ILE:HD11	30:c:58:LEU:HD21	1.94	0.49
1:2:189:U:OP1	10:I:148:LYS:NZ	2.30	0.49
1:2:398:A:H4'	1:2:399:C:H5''	1.95	0.49
1:2:944:A:H1'	16:O:136:PRO:HB3	1.95	0.49
1:2:1243:U:N3	1:2:1517:G:O6	2.43	0.49
3:B:142:PHE:O	3:B:208:HIS:N	2.44	0.49
21:T:33:TRP:HE1	21:T:102:ARG:NH2	2.10	0.49
1:2:991:G:N1	1:2:1134:G:H4'	2.28	0.48
1:2:1701:C:O2'	1:2:1702:G:OP1	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:124:HIS:HA	3:B:137:LEU:O	2.12	0.48
10:I:12:ARG:NH1	10:I:17:LYS:O	2.46	0.48
24:W:86:LEU:O	24:W:90:GLN:HG2	2.13	0.48
26:Y:102:THR:OG1	26:Y:103:SER:N	2.41	0.48
1:2:1025:U:OP1	1:2:1090:C:O2'	2.31	0.48
1:2:1202:U:O2'	4:C:115:GLN:O	2.27	0.48
1:2:1453:C:N3	1:2:1455:A:H1'	2.27	0.48
4:C:84:PHE:HE1	23:V:33:GLN:HE21	1.62	0.48
4:C:152:ARG:O	4:C:156:ILE:HG12	2.13	0.48
9:H:27:LEU:HD23	9:H:30:LEU:HD12	1.95	0.48
34:g:292:SER:OG	34:g:293:ALA:N	2.45	0.48
1:2:641:A:H2'	1:2:642:U:O4'	2.13	0.48
9:H:46:THR:OG1	9:H:63:PHE:O	2.31	0.48
18:Q:84:ILE:O	18:Q:88:ILE:HG22	2.13	0.48
20:S:26:ILE:HG13	20:S:27:ALA:H	1.78	0.48
1:2:962:A:P	1:2:963:A:H62	2.37	0.48
1:2:1339:U:H2'	1:2:1340:U:C6	2.48	0.48
6:E:62:LYS:HE2	6:E:62:LYS:HB3	1.69	0.48
8:G:98:ARG:NH2	8:G:103:ASP:OD2	2.44	0.48
12:K:5:LYS:HB3	14:M:29:ASP:CG	2.39	0.48
18:Q:13:PHE:HB3	18:Q:22:VAL:HA	1.94	0.48
35:h:6:ARG:HH11	35:h:6:ARG:HG3	1.77	0.48
1:2:158:A:H2'	1:2:159:A:O4'	2.13	0.48
1:2:217:A:H3'	1:2:218:U:H5''	1.94	0.48
1:2:441:C:H2'	1:2:442:C:C6	2.48	0.48
1:2:795:A:H3'	1:2:796:G:H5''	1.95	0.48
1:2:1036:A:H4'	1:2:1855:G:H21	1.77	0.48
1:2:1486:A:H2'	1:2:1487:A:O4'	2.13	0.48
4:C:169:TYR:OH	4:C:175:GLY:O	2.31	0.48
6:E:122:LYS:NZ	6:E:143:ASP:OD2	2.35	0.48
8:G:57:ASP:HB3	8:G:98:ARG:HD2	1.94	0.48
8:G:176:ILE:HG22	8:G:179:LEU:HB2	1.95	0.48
21:T:61:ALA:HA	21:T:64:LEU:HD12	1.95	0.48
34:g:91:ASP:HB2	34:g:98:THR:HG21	1.96	0.48
1:2:659:G:HO2'	1:2:662:G:HO2'	1.57	0.48
1:2:1648:G:O2'	1:2:1674:G:O6	2.32	0.48
5:D:116:ARG:NH2	36:n:175:GLU:HB2	2.29	0.48
29:b:31:TYR:HE2	29:b:33:MET:HE3	1.78	0.48
1:2:544:G:H2'	1:2:544:G:N3	2.27	0.48
1:2:568:C:H2'	1:2:569:A:H8	1.79	0.48
1:2:942:G:OP1	3:B:136:ARG:NH1	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1224:G:H5''	1:2:1531:A:H2	1.78	0.48
7:F:118:ASN:HB2	7:F:184:SER:N	2.28	0.48
11:J:149:VAL:HG11	11:J:157:ILE:HD11	1.96	0.48
17:P:26:LEU:HD21	17:P:87:PRO:HD2	1.94	0.48
27:Z:88:LEU:HD11	27:Z:107:VAL:HG21	1.95	0.48
30:c:33:GLU:HG2	30:c:41:SER:HB3	1.94	0.48
31:d:22:ARG:NH1	31:d:36:LEU:O	2.47	0.48
1:2:77:A:H2'	1:2:78:C:C6	2.48	0.48
1:2:115:U:H2'	1:2:116:U:C6	2.49	0.48
1:2:122:G:C5	1:2:123:G:H1'	2.48	0.48
1:2:141:A:C6	1:2:177:G:N3	2.82	0.48
1:2:600:G:H2'	1:2:601:G:H8	1.79	0.48
1:2:958:G:H2'	1:2:959:G:O4'	2.14	0.48
1:2:1673:U:H2'	1:2:1674:G:O4'	2.13	0.48
1:2:1866:A:N6	28:a:84:VAL:HB	2.29	0.48
5:D:55:THR:O	5:D:59:LEU:HD12	2.14	0.48
5:D:163:PRO:O	5:D:167:TYR:HB2	2.14	0.48
6:E:54:TYR:OH	6:E:97:GLU:OE2	2.26	0.48
22:U:23:THR:OG1	22:U:113:GLU:HB3	2.14	0.48
36:n:174:LEU:HD22	36:n:190:LEU:HD11	1.95	0.48
1:2:929:G:H2'	1:2:930:C:O4'	2.14	0.48
1:2:1255:G:H5'	1:2:1256:G:H4'	1.95	0.48
1:2:1456:G:H2'	1:2:1457:U:H6	1.79	0.48
4:C:64:THR:OG1	4:C:90:GLU:OE2	2.26	0.48
4:C:106:VAL:HA	4:C:128:VAL:HG22	1.96	0.48
5:D:8:LYS:HB3	22:U:61:LEU:HD21	1.96	0.48
5:D:157:MET:HA	5:D:189:MET:HE3	1.94	0.48
7:F:118:ASN:HB2	7:F:183:GLY:C	2.39	0.48
10:I:42:ARG:HH21	10:I:59:ARG:HH21	1.62	0.48
22:U:32:LEU:HD12	22:U:110:VAL:HG13	1.94	0.48
22:U:78:ASP:OD2	31:d:44:ARG:NH1	2.47	0.48
31:d:16:GLN:HA	31:d:19:ARG:HH22	1.79	0.48
34:g:191:HIS:NE2	34:g:217:MET:SD	2.79	0.48
7:F:51:HIS:CD2	7:F:90:VAL:HG11	2.49	0.47
20:S:9:PHE:H	27:Z:49:LEU:HD23	1.79	0.47
28:a:41:ILE:HG12	28:a:68:TYR:CD2	2.49	0.47
34:g:217:MET:HE3	34:g:219:TRP:NE1	2.24	0.47
1:2:5:U:H2'	1:2:6:G:H8	1.80	0.47
1:2:588:G:OP2	1:2:588:G:N2	2.40	0.47
1:2:868:G:H2'	9:H:114:GLN:HA	1.95	0.47
1:2:1058:A:H2'	1:2:1059:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1814:G:H2'	1:2:1815:A:C8	2.48	0.47
6:E:107:GLY:HA2	6:E:189:LEU:HG	1.97	0.47
11:J:111:GLN:NE2	11:J:127:ARG:HB2	2.29	0.47
18:Q:42:ILE:CG2	18:Q:44:PRO:HD2	2.44	0.47
20:S:55:ARG:NH1	20:S:55:ARG:HB3	2.30	0.47
20:S:104:ASP:O	20:S:108:ARG:HG2	2.15	0.47
1:2:85:A:H2'	1:2:86:C:C6	2.49	0.47
1:2:1199:A:H2'	1:2:1200:A:C8	2.50	0.47
1:2:1521:C:H42	20:S:137:LYS:HD2	1.78	0.47
1:2:1736:G:H2'	1:2:1737:G:C8	2.48	0.47
4:C:199:PRO:O	4:C:202:THR:OG1	2.24	0.47
5:D:17:PHE:HD2	5:D:77:PHE:CE1	2.31	0.47
13:L:77:VAL:O	13:L:123:GLY:N	2.46	0.47
19:R:51:ALA:O	19:R:54:VAL:HG12	2.14	0.47
1:2:416:U:N3	1:2:417:C:O2'	2.47	0.47
1:2:1533:A:N3	1:2:1533:A:H2'	2.27	0.47
17:P:83:MET:SD	17:P:83:MET:N	2.87	0.47
19:R:76:GLU:O	19:R:79:GLU:HG3	2.15	0.47
20:S:45:LEU:HD22	20:S:50:ILE:HD11	1.95	0.47
1:2:65:C:OP1	8:G:136:LYS:NZ	2.33	0.47
1:2:212:C:H2'	1:2:213:G:C8	2.48	0.47
1:2:687:C:H1'	9:H:116:ARG:NH2	2.30	0.47
7:F:95:HIS:C	7:F:97:PHE:H	2.23	0.47
21:T:27:LYS:HD3	21:T:27:LYS:H	1.79	0.47
1:2:5:U:H2'	1:2:6:G:C8	2.50	0.47
1:2:1236:G:H22	1:2:1522:A:H61	1.62	0.47
1:2:1598:G:H2'	27:Z:80:ARG:NH1	2.30	0.47
2:A:158:ASP:OD1	2:A:158:ASP:N	2.46	0.47
1:2:217:A:H3'	1:2:218:U:C5'	2.45	0.47
1:2:389:A:H2'	1:2:390:C:C6	2.50	0.47
1:2:582:U:H1'	26:Y:33:ALA:HB2	1.97	0.47
1:2:819:G:O2'	1:2:820:U:OP1	2.30	0.47
1:2:1304:U:H5	1:2:1306:U:H1'	1.79	0.47
1:2:1327:G:H22	1:2:1502:C:N4	2.11	0.47
1:2:1758:G:N2	1:2:1759:G:O6	2.47	0.47
2:A:5:LEU:HD12	2:A:8:LEU:HD12	1.97	0.47
5:D:104:SER:O	5:D:108:LYS:HD3	2.15	0.47
17:P:98:ASN:HB2	17:P:103:ASN:OD1	2.15	0.47
17:P:132:GLY:O	17:P:134:GLY:N	2.41	0.47
18:Q:51:LEU:HD13	18:Q:84:ILE:HD12	1.97	0.47
19:R:34:VAL:O	19:R:38:ILE:HG13	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:98:VAL:HG11	22:U:114:VAL:HG11	1.96	0.47
26:Y:20:ARG:HH21	26:Y:22:GLN:NE2	2.11	0.47
26:Y:105:LYS:O	26:Y:109:GLU:HG3	2.15	0.47
34:g:153:CYS:SG	34:g:154:VAL:N	2.88	0.47
1:2:224:A:N3	1:2:224:A:H2'	2.29	0.47
1:2:973:C:H42	16:O:55:ARG:HH22	1.61	0.47
1:2:980:A:H2'	1:2:981:A:H8	1.79	0.47
1:2:1730:U:H3	1:2:1805:G:N2	2.12	0.47
2:A:111:GLN:CD	2:A:111:GLN:H	2.23	0.47
20:S:16:LEU:HD22	20:S:33:ILE:HG12	1.97	0.47
21:T:83:GLN:O	21:T:90:SER:HB2	2.15	0.47
4:C:187:ARG:HH22	4:C:190:SER:HA	1.80	0.47
10:I:194:GLU:HG2	13:L:10:TYR:CE2	2.50	0.47
15:N:63:VAL:HG11	15:N:71:ILE:HG12	1.96	0.47
15:N:84:LEU:HD21	15:N:89:TYR:HB2	1.97	0.47
1:2:634:A:H2'	1:2:635:G:H8	1.80	0.47
1:2:1513:C:O2	31:d:10:HIS:ND1	2.36	0.47
1:2:1745:A:H8	1:2:1745:A:OP1	1.97	0.47
2:A:191:ARG:NH1	23:V:44:GLY:O	2.48	0.47
5:D:172:VAL:HG22	5:D:185:LYS:HG3	1.96	0.47
33:f:126:CYS:HB3	33:f:130:VAL:HG21	1.97	0.47
1:2:1025:U:H2'	1:2:1026:C:O4'	2.15	0.46
7:F:114:ASN:O	7:F:186:ASN:ND2	2.48	0.46
8:G:132:ARG:HH21	8:G:161:PRO:HD2	1.80	0.46
25:X:52:LEU:N	25:X:71:ARG:O	2.49	0.46
26:Y:117:VAL:HG23	26:Y:122:LYS:HG2	1.97	0.46
1:2:1016:U:O2	29:b:30:SER:OG	2.33	0.46
1:2:1485:U:H5'	5:D:151:LYS:HZ2	1.80	0.46
5:D:81:GLU:OE2	5:D:81:GLU:HA	2.16	0.46
6:E:104:ASP:OD1	6:E:105:THR:N	2.48	0.46
9:H:111:LYS:HA	9:H:111:LYS:HD3	1.60	0.46
10:I:147:LYS:HD2	10:I:147:LYS:C	2.40	0.46
16:O:99:ALA:H	16:O:133:THR:HB	1.80	0.46
3:B:173:THR:O	3:B:177:GLN:HG2	2.15	0.46
5:D:194:PRO:O	5:D:195:THR:OG1	2.26	0.46
7:F:117:ILE:HB	7:F:182:LYS:HA	1.97	0.46
15:N:92:ILE:HD11	15:N:139:TRP:HH2	1.81	0.46
1:2:29:G:H2'	1:2:30:C:C6	2.51	0.46
1:2:1516:G:C8	1:2:1517:G:H1'	2.50	0.46
7:F:74:ASN:C	7:F:77:MET:HE2	2.40	0.46
19:R:38:ILE:C	19:R:38:ILE:HD12	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:30:CYS:HB2	24:W:61:ILE:HG13	1.97	0.46
34:g:271:LYS:HG3	34:g:272:GLN:H	1.80	0.46
1:2:302:A:H1'	10:I:73:THR:HG23	1.98	0.46
1:2:1009:A:H5'	15:N:98:VAL:HG12	1.98	0.46
1:2:1457:U:OP2	19:R:59:LYS:NZ	2.49	0.46
4:C:61:MET:SD	4:C:61:MET:N	2.88	0.46
4:C:163:VAL:HG11	4:C:245:SER:HB3	1.96	0.46
1:2:870:A:H62	1:2:916:A:H5'	1.80	0.46
5:D:67:ARG:HA	5:D:70:THR:HG22	1.98	0.46
8:G:159:ARG:HG2	8:G:173:ALA:HB2	1.96	0.46
8:G:223:LYS:HD3	8:G:223:LYS:N	2.30	0.46
20:S:46:ARG:HH21	21:T:50:GLU:HA	1.80	0.46
23:V:43:THR:OG1	23:V:45:ARG:NH2	2.48	0.46
25:X:52:LEU:HD21	25:X:73:GLN:HB2	1.98	0.46
1:2:549:C:H2'	1:2:550:C:O4'	2.16	0.46
1:2:647:U:H2'	1:2:648:A:H8	1.81	0.46
1:2:1234:C:O5'	1:2:1254:C:N4	2.49	0.46
5:D:25:LEU:HA	5:D:28:GLU:HB2	1.98	0.46
5:D:105:LEU:HB3	5:D:184:ILE:HD12	1.97	0.46
6:E:72:ILE:HG12	6:E:90:ILE:HG12	1.98	0.46
7:F:74:ASN:O	7:F:77:MET:HE2	2.15	0.46
17:P:42:ARG:HD2	17:P:43:ARG:N	2.30	0.46
17:P:50:ARG:H	17:P:53:GLN:NE2	2.12	0.46
34:g:89:LEU:HB3	34:g:99:ARG:HB2	1.98	0.46
1:2:25:A:H2'	1:2:26:U:H6	1.81	0.46
1:2:685:A:H2'	1:2:686:U:O4'	2.15	0.46
1:2:823:U:C5	11:J:143:ASN:HB3	2.51	0.46
1:2:1521:C:N4	20:S:137:LYS:HB3	2.30	0.46
1:2:1554:C:H4'	12:K:33:PRO:HG3	1.98	0.46
1:2:1599:U:C5	7:F:166:ILE:HA	2.50	0.46
1:2:1667:U:H2'	1:2:1668:U:C6	2.50	0.46
4:C:105:GLU:HG2	4:C:216:MET:HE1	1.98	0.46
4:C:124:PHE:CZ	36:n:175:GLU:HG2	2.51	0.46
5:D:124:ARG:O	5:D:127:MET:N	2.49	0.46
8:G:32:MET:HG3	8:G:100:CYS:HB2	1.98	0.46
29:b:11:SER:O	29:b:14:GLU:HG2	2.16	0.46
34:g:89:LEU:O	34:g:98:THR:OG1	2.31	0.46
1:2:53:C:P	26:Y:112:ASN:HD22	2.39	0.46
1:2:582:U:H2'	1:2:583:A:O4'	2.15	0.46
1:2:912:C:H3'	1:2:913:A:H5'	1.98	0.46
1:2:1251:A:H2'	1:2:1252:C:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1513:C:H2'	1:2:1618:C:C5	2.51	0.46
5:D:23:GLU:O	5:D:27:ARG:HG2	2.15	0.46
5:D:157:MET:HA	5:D:189:MET:CE	2.46	0.46
29:b:2:PRO:HB2	29:b:3:LEU:H	1.58	0.46
1:2:511:U:H2'	1:2:512:A:C8	2.51	0.46
7:F:116:ILE:HB	7:F:178:ILE:O	2.16	0.46
24:W:18:GLU:HG2	24:W:65:LEU:HD13	1.98	0.46
34:g:40:ILE:HB	34:g:59:LEU:HB2	1.97	0.46
1:2:1571:G:H4'	1:2:1616:U:C4	2.52	0.45
1:2:1653:U:O2'	21:T:82:ARG:HB3	2.16	0.45
4:C:107:LEU:HD11	4:C:129:ALA:HB2	1.97	0.45
5:D:202:LYS:H	5:D:202:LYS:HG2	1.55	0.45
7:F:59:LYS:HD2	7:F:60:ARG:N	2.31	0.45
15:N:27:LYS:HA	15:N:27:LYS:HD3	1.65	0.45
15:N:87:ASP:N	15:N:87:ASP:OD1	2.48	0.45
18:Q:103:ALA:HA	18:Q:106:LYS:HE3	1.97	0.45
21:T:133:ARG:HD2	21:T:133:ARG:HA	1.76	0.45
21:T:142:ASN:HA	21:T:145:HIS:CE1	2.51	0.45
23:V:68:SER:O	23:V:72:LEU:HG	2.16	0.45
34:g:194:TYR:HE1	34:g:235:ILE:HG22	1.79	0.45
1:2:310:C:H2'	1:2:311:C:C6	2.52	0.45
1:2:581:U:H4'	26:Y:66:GLY:HA2	1.98	0.45
1:2:1007:C:H2'	1:2:1008:A:C8	2.51	0.45
1:2:1262:C:H2'	31:d:27:ARG:HH12	1.81	0.45
1:2:1703:C:H2'	1:2:1704:C:O4'	2.17	0.45
9:H:96:ALA:HB3	9:H:98:ARG:NH1	2.32	0.45
19:R:107:LYS:HE2	19:R:107:LYS:HB2	1.67	0.45
35:h:21:ARG:HE	35:h:21:ARG:HB3	1.64	0.45
1:2:146:G:H5'	1:2:147:A:OP2	2.16	0.45
1:2:443:U:H2'	1:2:444:G:O4'	2.16	0.45
1:2:501:C:H2'	1:2:502:C:H5''	1.98	0.45
1:2:1220:A:OP2	1:2:1221:G:H5''	2.16	0.45
5:D:204:LEU:HD12	5:D:204:LEU:HA	1.78	0.45
7:F:197:GLU:HG3	7:F:201:LYS:HD2	1.98	0.45
20:S:14:ARG:HD3	20:S:15:VAL:N	2.32	0.45
22:U:19:ARG:HG2	22:U:92:HIS:CE1	2.52	0.45
22:U:46:LYS:HB2	22:U:46:LYS:HE2	1.61	0.45
23:V:45:ARG:HG2	23:V:45:ARG:HH11	1.81	0.45
34:g:67:SER:OG	34:g:68:ASP:OD1	2.34	0.45
1:2:116:U:H3	1:2:347:G:H1	1.65	0.45
1:2:617:G:N7	25:X:67:ARG:NH1	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:822:U:H2'	1:2:824:C:OP2	2.16	0.45
1:2:1212:G:H1'	1:2:1689:C:H42	1.81	0.45
1:2:1740:C:H2'	1:2:1741:U:C6	2.51	0.45
7:F:187:SER:OG	7:F:188:TYR:N	2.48	0.45
12:K:29:MET:HE1	12:K:42:ASN:HB3	1.96	0.45
24:W:42:MET:HE2	24:W:42:MET:HB3	1.73	0.45
6:E:79:ASP:HB3	6:E:82:TYR:HB2	1.97	0.45
10:I:116:HIS:O	10:I:116:HIS:CD2	2.70	0.45
14:M:91:LEU:HD23	14:M:91:LEU:HA	1.78	0.45
16:O:31:CYS:HB3	16:O:44:VAL:HG22	1.99	0.45
16:O:84:ARG:O	16:O:87:GLU:HG3	2.16	0.45
1:2:17:C:H2'	1:2:18:C:H6	1.79	0.45
1:2:594:A:H61	1:2:643:A:H5''	1.82	0.45
1:2:1819:A:H2'	1:2:1820:G:C8	2.52	0.45
7:F:116:ILE:HG22	7:F:117:ILE:HD13	1.99	0.45
8:G:217:MET:HE3	8:G:218:LYS:N	2.32	0.45
9:H:47:ALA:HB1	9:H:49:LYS:HZ1	1.82	0.45
18:Q:58:LEU:HD22	18:Q:108:ILE:HD11	1.98	0.45
18:Q:100:VAL:HG13	18:Q:101:ASP:H	1.81	0.45
21:T:34:VAL:HG23	21:T:52:TRP:NE1	2.31	0.45
22:U:87:ARG:HG3	22:U:87:ARG:HH11	1.81	0.45
1:2:527:C:P	32:e:35:ARG:HH22	2.39	0.45
1:2:1603:G:OP1	20:S:31:THR:OG1	2.34	0.45
16:O:136:PRO:HG3	16:O:139:SER:HB3	1.98	0.45
21:T:134:ILE:O	21:T:138:VAL:HG22	2.17	0.45
24:W:24:GLN:HB3	29:b:7:LEU:HD12	1.99	0.45
26:Y:40:ILE:H	26:Y:40:ILE:HG13	1.60	0.45
1:2:1233:G:N2	1:2:1235:G:H22	2.15	0.45
1:2:1748:G:H1	1:2:1786:U:H3	1.65	0.45
3:B:48:LEU:O	16:O:51:GLU:HG3	2.17	0.45
6:E:240:ARG:HG3	6:E:241:GLY:N	2.32	0.45
20:S:63:GLU:O	20:S:67:VAL:HG23	2.17	0.45
21:T:33:TRP:CD1	21:T:33:TRP:N	2.84	0.45
21:T:123:LEU:HD21	21:T:128:GLN:HG3	1.99	0.45
24:W:115:GLU:CD	24:W:118:ARG:HH21	2.25	0.45
1:2:91:A:H61	8:G:89:THR:HG22	1.82	0.45
1:2:925:G:H1	1:2:1017:U:H3	1.64	0.45
1:2:1535:U:OP1	7:F:88:MET:HE1	2.16	0.45
6:E:192:ILE:HB	6:E:243:GLY:HA3	1.99	0.45
9:H:69:LEU:HG	9:H:96:ALA:HB2	1.99	0.45
9:H:80:VAL:HG23	9:H:92:VAL:HG13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:30:C:O2'	1:2:596:U:OP1	2.35	0.45
1:2:677:G:OP1	15:N:124:ARG:NH1	2.42	0.45
1:2:793:G:C5	1:2:794:A:H1'	2.52	0.45
1:2:941:C:H2'	1:2:942:G:C8	2.52	0.45
1:2:1084:A:OP1	1:2:1858:G:O2'	2.29	0.45
1:2:1134:G:OP1	28:a:6:ARG:HD3	2.16	0.45
1:2:1183:A:H2'	1:2:1184:G:H8	1.82	0.45
1:2:1262:C:N3	31:d:16:GLN:HB3	2.32	0.45
3:B:27:LYS:HA	3:B:51:ARG:NH1	2.32	0.45
3:B:171:ILE:HD12	3:B:197:ILE:HA	1.99	0.45
4:C:81:ILE:HG23	4:C:86:LEU:HB2	1.99	0.45
6:E:104:ASP:HB2	6:E:110:ALA:HB2	1.98	0.45
9:H:48:ALA:C	9:H:49:LYS:HZ2	2.25	0.45
12:K:32:HIS:HB2	12:K:42:ASN:ND2	2.32	0.45
1:2:49:C:N4	1:2:473:A:OP2	2.44	0.44
1:2:310:C:H4'	1:2:340:C:H1'	1.99	0.44
1:2:414:A:OP1	1:2:814:U:O2'	2.30	0.44
6:E:115:THR:HG23	6:E:118:GLU:H	1.82	0.44
6:E:139:LEU:HB2	6:E:150:PRO:HG3	1.98	0.44
8:G:1:MET:HE2	8:G:1:MET:HB3	1.85	0.44
1:2:900:C:O2'	1:2:901:G:OP1	2.34	0.44
1:2:921:G:C2	29:b:22:LYS:HD3	2.52	0.44
1:2:1338:G:H4'	22:U:74:SER:H	1.82	0.44
5:D:130:GLY:O	5:D:191:PRO:HG3	2.18	0.44
17:P:18:ARG:HD3	20:S:90:VAL:HA	1.99	0.44
17:P:84:ILE:HB	17:P:111:MET:HE3	1.99	0.44
20:S:28:PHE:HE1	20:S:38:ARG:H	1.65	0.44
29:b:26:GLN:HE21	29:b:26:GLN:HB2	1.61	0.44
30:c:29:GLN:HE22	30:c:43:ILE:HB	1.81	0.44
34:g:291:TRP:CE3	34:g:298:LEU:HD13	2.53	0.44
1:2:604:A:H2'	1:2:605:A:C8	2.52	0.44
1:2:1105:G:O3'	29:b:69:GLY:HA3	2.16	0.44
1:2:1443:C:O5'	18:Q:15:ARG:NH2	2.50	0.44
1:2:1650:A:H2'	1:2:1651:A:O4'	2.17	0.44
2:A:59:LEU:HD12	2:A:185:MET:CE	2.48	0.44
3:B:51:ARG:O	3:B:53:GLN:HG3	2.17	0.44
3:B:76:ASN:OD1	3:B:76:ASN:N	2.50	0.44
5:D:143:ARG:HH22	36:n:173:ASP:CG	2.25	0.44
6:E:37:LYS:HB2	6:E:40:GLU:HG2	2.00	0.44
7:F:145:ARG:NH1	7:F:149:GLN:HB2	2.32	0.44
9:H:145:ARG:NH1	24:W:49:GLU:OE2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:73:ASN:HA	12:K:76:ILE:HD12	1.99	0.44
24:W:111:MET:HE3	24:W:116:ALA:HA	1.98	0.44
1:2:17:C:H4'	1:2:1166:G:C8	2.52	0.44
1:2:820:U:OP1	6:E:259:LYS:NZ	2.49	0.44
1:2:929:G:N2	1:2:1104:G:H4'	2.33	0.44
1:2:1217:A:H2'	1:2:1218:C:C6	2.52	0.44
1:2:1405:A:H2'	1:2:1443:C:N4	2.33	0.44
1:2:1529:C:O2'	1:2:1530:U:OP1	2.34	0.44
1:2:1611:G:O2'	20:S:87:GLN:HB2	2.18	0.44
1:2:1677:U:OP1	7:F:71:ARG:NH2	2.50	0.44
4:C:187:ARG:HH11	4:C:187:ARG:HB3	1.83	0.44
5:D:117:ARG:CZ	36:n:168:SER:HB3	2.47	0.44
8:G:215:LYS:O	8:G:219:GLU:HG3	2.18	0.44
9:H:170:VAL:C	9:H:172:THR:H	2.25	0.44
25:X:40:PRO:O	25:X:77:ASN:ND2	2.42	0.44
34:g:18:VAL:HG22	34:g:33:SER:HB2	2.00	0.44
1:2:588:G:H4'	1:2:589:G:H5'	1.98	0.44
1:2:1485:U:H5'	5:D:151:LYS:HZ1	1.81	0.44
1:2:1741:U:H2'	1:2:1742:C:O4'	2.17	0.44
2:A:12:GLU:OE1	2:A:12:GLU:N	2.39	0.44
2:A:77:ILE:HB	2:A:124:VAL:HG12	2.00	0.44
7:F:71:ARG:NH1	7:F:75:SER:OG	2.49	0.44
7:F:127:ARG:HD2	7:F:136:ARG:HH11	1.81	0.44
12:K:11:ILE:HD12	12:K:11:ILE:HA	1.87	0.44
34:g:99:ARG:HB3	34:g:101:PHE:CZ	2.52	0.44
34:g:131:LEU:HD12	34:g:140:TYR:HB3	1.98	0.44
1:2:85:A:H2'	1:2:86:C:H6	1.82	0.44
1:2:625:G:O6	25:X:64:SER:N	2.51	0.44
1:2:1135:C:H2'	1:2:1136:U:O4'	2.17	0.44
1:2:1653:U:H2'	1:2:1654:G:C8	2.52	0.44
7:F:77:MET:O	7:F:77:MET:HG2	2.17	0.44
28:a:39:PHE:CE2	28:a:41:ILE:HD11	2.53	0.44
28:a:73:TYR:HB3	28:a:78:VAL:HB	2.00	0.44
34:g:85:GLY:HA2	34:g:108:VAL:HB	2.00	0.44
1:2:13:C:O2'	1:2:1355:C:N3	2.45	0.44
1:2:160:U:O2'	1:2:162:C:OP2	2.24	0.44
1:2:446:G:P	10:I:47:ARG:HH12	2.40	0.44
1:2:1745:A:H1'	8:G:31:ARG:NH2	2.33	0.44
5:D:158:ILE:HG23	5:D:189:MET:HE1	1.99	0.44
10:I:76:THR:HG23	10:I:108:PRO:HG2	1.99	0.44
15:N:13:GLN:NE2	29:b:21:LYS:HG3	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:60:ARG:HB3	19:R:66:VAL:HG11	1.99	0.44
1:2:385:G:H3'	13:L:136:LYS:HB2	2.00	0.44
1:2:563:G:O2'	1:2:564:A:H8	2.00	0.44
1:2:967:C:H2'	1:2:968:U:O4'	2.18	0.44
1:2:983:A:OP1	1:2:1073:U:O2'	2.33	0.44
3:B:122:GLU:HG2	3:B:140:VAL:HG23	1.98	0.44
3:B:217:MET:HE2	3:B:217:MET:HB2	1.75	0.44
4:C:108:LYS:HB2	4:C:233:LEU:HD22	2.00	0.44
6:E:44:LEU:HD11	6:E:70:ILE:HG21	1.99	0.44
6:E:159:THR:HG23	6:E:227:VAL:HG23	1.99	0.44
8:G:142:ARG:HB2	8:G:147:LEU:HB2	2.00	0.44
10:I:42:ARG:HB3	10:I:59:ARG:HB2	2.00	0.44
12:K:48:ALA:O	12:K:52:LEU:HG	2.17	0.44
26:Y:13:MET:HE3	26:Y:13:MET:HB2	1.71	0.44
1:2:96:C:H1'	1:2:474:G:H5'	1.99	0.44
1:2:822:U:H3	1:2:826:A:H62	1.66	0.44
4:C:72:ASP:OD2	4:C:272:HIS:NE2	2.44	0.44
10:I:66:SER:HA	10:I:73:THR:HA	2.00	0.44
10:I:101:ILE:HG22	10:I:172:LEU:HD22	2.00	0.44
11:J:151:LEU:HD12	11:J:151:LEU:HA	1.87	0.44
13:L:33:LEU:HD12	13:L:34:PRO:HD2	2.00	0.44
17:P:85:ILE:HB	17:P:86:LEU:HD22	2.00	0.44
18:Q:80:GLN:O	18:Q:84:ILE:HG23	2.18	0.44
26:Y:18:LEU:HD23	26:Y:18:LEU:HA	1.88	0.44
29:b:19:HIS:HB3	29:b:22:LYS:HG3	2.00	0.44
1:2:352:U:H5''	1:2:353:C:OP1	2.17	0.43
1:2:1244:U:OP1	33:f:78:LYS:HB2	2.18	0.43
1:2:1634:A:N1	20:S:142:ARG:NH2	2.66	0.43
5:D:185:LYS:HE3	5:D:185:LYS:HB2	1.79	0.43
7:F:142:SER:O	7:F:144:LEU:N	2.50	0.43
7:F:149:GLN:HG3	7:F:152:TRP:CE3	2.53	0.43
8:G:121:ILE:HB	8:G:124:LEU:HB3	2.00	0.43
9:H:17:ASP:O	9:H:21:SER:OG	2.30	0.43
9:H:142:LYS:HB2	9:H:142:LYS:HE3	1.71	0.43
17:P:41:GLN:HE22	17:P:83:MET:HB2	1.83	0.43
18:Q:38:PRO:HB2	18:Q:41:MET:HG2	1.99	0.43
20:S:14:ARG:HD2	20:S:17:ASN:N	2.29	0.43
20:S:14:ARG:HD3	20:S:15:VAL:H	1.83	0.43
1:2:1542:C:N4	18:Q:44:PRO:HG3	2.32	0.43
1:2:1611:G:C2	1:2:1612:G:C5	3.06	0.43
2:A:19:LEU:HD11	19:R:106:LEU:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:37:ALA:HB2	3:B:233:GLY:H	1.84	0.43
8:G:31:ARG:O	8:G:34:THR:OG1	2.32	0.43
30:c:32:VAL:HG21	30:c:58:LEU:HD11	2.00	0.43
34:g:238:ALA:O	34:g:239:LEU:HD13	2.18	0.43
1:2:37:C:H2'	1:2:38:A:O4'	2.18	0.43
1:2:96:C:H2'	1:2:97:U:C6	2.53	0.43
7:F:33:ILE:HD13	7:F:33:ILE:H	1.83	0.43
21:T:13:GLU:HA	21:T:16:ARG:HB3	2.00	0.43
1:2:616:A:N3	32:e:12:VAL:HG21	2.32	0.43
1:2:909:G:H2'	1:2:910:G:C8	2.53	0.43
4:C:108:LYS:HD2	4:C:233:LEU:HB3	1.99	0.43
7:F:147:VAL:O	7:F:151:ILE:HG12	2.17	0.43
9:H:97:GLN:OE1	9:H:97:GLN:HA	2.18	0.43
11:J:165:TYR:N	11:J:165:TYR:CD1	2.87	0.43
12:K:12:TYR:O	12:K:15:LEU:HG	2.18	0.43
12:K:53:LYS:HG3	12:K:69:TRP:CZ2	2.53	0.43
17:P:39:ALA:HA	17:P:42:ARG:HB3	2.00	0.43
18:Q:109:LYS:O	18:Q:113:ILE:HG13	2.19	0.43
1:2:520:A:O2'	1:2:825:A:N3	2.46	0.43
1:2:808:A:HO2'	1:2:809:A:P	2.40	0.43
1:2:1745:A:C6	1:2:1746:U:H1'	2.52	0.43
1:2:1867:U:O2'	28:a:38:LYS:HG2	2.18	0.43
5:D:71:ALA:O	5:D:75:LYS:HG2	2.19	0.43
9:H:80:VAL:HG23	9:H:92:VAL:CG1	2.49	0.43
11:J:22:LYS:HA	11:J:22:LYS:HD2	1.79	0.43
16:O:69:SER:O	16:O:69:SER:OG	2.35	0.43
17:P:50:ARG:N	17:P:53:GLN:HE22	2.16	0.43
1:2:880:G:HO2'	1:2:881:G:P	2.38	0.43
1:2:1606:G:O2'	1:2:1607:A:O5'	2.34	0.43
1:2:1718:G:H21	1:2:1813:A:N6	2.17	0.43
4:C:271:ASP:HA	4:C:274:VAL:HG22	2.00	0.43
6:E:122:LYS:HD2	6:E:164:LEU:HD21	2.01	0.43
11:J:134:HIS:ND1	11:J:163:SER:HB2	2.33	0.43
17:P:55:SER:O	17:P:59:ARG:NE	2.51	0.43
25:X:80:LYS:O	25:X:81:ILE:HD13	2.18	0.43
1:2:142:C:OP1	1:2:179:C:N4	2.52	0.43
1:2:417:C:H3'	1:2:418:A:H5''	1.99	0.43
1:2:1850:A:H2'	1:2:1851:A:C8	2.53	0.43
5:D:107:TYR:CD1	5:D:110:LEU:HD12	2.53	0.43
9:H:30:LEU:O	9:H:37:LYS:HG2	2.19	0.43
14:M:93:LYS:HA	14:M:93:LYS:HD3	1.75	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:46:LYS:NZ	22:U:97:ILE:HG12	2.34	0.43
23:V:1:MET:HE1	23:V:13:VAL:HG22	2.01	0.43
1:2:154:U:H2'	1:2:155:G:O4'	2.19	0.43
1:2:913:A:C8	9:H:66:VAL:HG11	2.53	0.43
1:2:1019:C:H2'	1:2:1020:A:O4'	2.19	0.43
1:2:1030:A:H2'	1:2:1031:A:C8	2.53	0.43
1:2:1303:C:H2'	1:2:1304:U:H4'	2.01	0.43
1:2:1484:A:H2'	1:2:1485:U:C5	2.53	0.43
1:2:1487:A:H4'	1:2:1488:C:OP1	2.18	0.43
1:2:1784:G:N3	1:2:1784:G:H2'	2.34	0.43
5:D:10:LYS:HE3	22:U:111:GLU:HG2	2.01	0.43
6:E:60:GLU:HB3	26:Y:18:LEU:HD11	2.01	0.43
7:F:188:TYR:HA	7:F:191:LYS:HG2	2.01	0.43
10:I:172:LEU:HD23	10:I:172:LEU:HA	1.90	0.43
19:R:11:LYS:HB3	19:R:11:LYS:HE2	1.67	0.43
19:R:28:PHE:HE1	19:R:51:ALA:HB3	1.84	0.43
29:b:12:PRO:HD2	29:b:13:GLU:N	2.28	0.43
32:e:28:LYS:O	32:e:33:LYS:HB2	2.19	0.43
1:2:84:A:N3	1:2:150:A:O2'	2.45	0.43
1:2:107:A:H2'	1:2:108:G:H8	1.81	0.43
1:2:156:G:H2'	1:2:157:U:C6	2.54	0.43
1:2:860:G:OP2	9:H:107:LYS:HE2	2.19	0.43
1:2:1120:U:H5'	29:b:72:ARG:NH1	2.17	0.43
2:A:52:LYS:O	2:A:56:GLU:HG2	2.19	0.43
9:H:49:LYS:HA	9:H:49:LYS:HD3	1.80	0.43
9:H:163:GLN:HG2	9:H:189:PHE:CG	2.53	0.43
20:S:30:ILE:O	20:S:33:ILE:N	2.42	0.43
1:2:1035:A:H2'	1:2:1036:A:O4'	2.19	0.43
1:2:1324:G:O2'	1:2:1325:G:H5'	2.19	0.43
2:A:58:LEU:HD21	2:A:177:MET:HB3	2.00	0.43
4:C:165:VAL:HG13	4:C:244:ILE:HG23	2.01	0.43
6:E:175:PHE:CE1	6:E:198:ARG:HD2	2.51	0.43
7:F:59:LYS:HD2	7:F:60:ARG:H	1.83	0.43
12:K:8:ARG:O	12:K:11:ILE:HG22	2.19	0.43
16:O:44:VAL:HG11	16:O:85:CYS:SG	2.59	0.43
30:c:29:GLN:NE2	30:c:43:ILE:HB	2.33	0.43
32:e:33:LYS:O	32:e:37:GLN:HG3	2.19	0.43
1:2:1013:U:OP1	1:2:1129:G:O2'	2.35	0.42
1:2:1229:G:P	1:2:1530:U:H1'	2.58	0.42
1:2:1290:G:N2	1:2:1302:G:HO2'	2.12	0.42
3:B:107:ARG:HG3	3:B:107:ARG:NH1	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:18:LYS:HB3	5:D:18:LYS:HE3	1.83	0.42
5:D:161:GLY:O	5:D:164:VAL:HG12	2.18	0.42
18:Q:26:LYS:O	18:Q:67:ASP:HB2	2.19	0.42
20:S:36:VAL:HG23	20:S:67:VAL:HG11	2.01	0.42
25:X:94:ILE:HG12	25:X:125:VAL:HG21	2.02	0.42
31:d:49:ASP:OD1	31:d:49:ASP:N	2.52	0.42
1:2:57:U:OP1	1:2:504:G:O2'	2.34	0.42
1:2:1550:G:O2'	1:2:1558:C:O2	2.27	0.42
1:2:1785:C:H2'	1:2:1786:U:C6	2.54	0.42
5:D:105:LEU:HD12	5:D:184:ILE:HG21	2.00	0.42
6:E:45:ILE:HA	6:E:61:VAL:HG11	2.01	0.42
8:G:230:LYS:HB3	8:G:230:LYS:HE2	1.76	0.42
21:T:51:ASN:HB2	21:T:54:TYR:HD2	1.84	0.42
31:d:31:ILE:N	31:d:38:MET:O	2.51	0.42
34:g:130:LYS:HG2	34:g:141:THR:HG22	2.00	0.42
1:2:43:U:OP2	1:2:485:A:N6	2.47	0.42
1:2:389:A:H2'	1:2:390:C:H6	1.83	0.42
1:2:656:G:H5'	1:2:662:G:N2	2.33	0.42
1:2:875:A:OP2	1:2:875:A:H4'	2.18	0.42
1:2:1274:G:OP1	1:2:1274:G:N2	2.52	0.42
1:2:1655:C:OP1	21:T:89:PRO:HB2	2.19	0.42
5:D:45:ARG:CZ	5:D:83:SER:HA	2.50	0.42
7:F:80:GLY:N	7:F:83:ASN:OD1	2.38	0.42
9:H:112:ASN:OD1	9:H:114:GLN:HG2	2.18	0.42
12:K:62:PHE:HE1	12:K:65:ARG:HA	1.84	0.42
34:g:165:ILE:HD11	34:g:179:LEU:HD13	2.02	0.42
1:2:420:G:O2'	1:2:660:C:N3	2.44	0.42
1:2:433:A:H2'	1:2:434:G:C8	2.55	0.42
1:2:1681:U:H2'	1:2:1682:C:C6	2.54	0.42
5:D:95:GLY:O	5:D:126:ILE:HA	2.20	0.42
7:F:92:ILE:HG23	7:F:170:ALA:HA	2.01	0.42
8:G:38:ALA:HB1	8:G:41:LEU:HD12	2.00	0.42
8:G:103:ASP:OD1	8:G:105:ASN:N	2.40	0.42
13:L:80:MET:HA	13:L:86:ILE:HG22	2.01	0.42
22:U:23:THR:HA	22:U:87:ARG:O	2.20	0.42
22:U:50:VAL:HG23	22:U:91:LEU:HB3	2.02	0.42
23:V:41:LYS:HB2	23:V:41:LYS:HE3	1.80	0.42
1:2:491:C:OP2	26:Y:104:ARG:HB2	2.19	0.42
1:2:1018:U:H2'	1:2:1019:C:H6	1.85	0.42
1:2:1277:C:O2'	1:2:1278:A:O4'	2.36	0.42
1:2:1687:C:H2'	1:2:1688:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:74:LEU:HD13	3:B:74:LEU:HA	1.85	0.42
10:I:203:LYS:HE3	10:I:203:LYS:HB3	1.87	0.42
15:N:103:GLU:H	15:N:103:GLU:HG3	1.64	0.42
17:P:65:LYS:HE3	17:P:65:LYS:HB3	1.86	0.42
18:Q:85:ARG:HA	18:Q:88:ILE:HG22	2.01	0.42
22:U:30:LYS:HA	22:U:30:LYS:HD3	1.81	0.42
22:U:111:GLU:OE2	22:U:111:GLU:HA	2.19	0.42
27:Z:99:LEU:HB2	27:Z:109:TYR:CE2	2.54	0.42
33:f:107:LYS:HG3	33:f:110:GLU:H	1.85	0.42
1:2:1202:U:H2'	1:2:1203:G:O4'	2.20	0.42
1:2:1266:C:OP1	1:2:1267:C:H5''	2.19	0.42
1:2:1347:U:H2'	1:2:1348:G:N3	2.35	0.42
1:2:1520:G:C2	17:P:126:VAL:HG13	2.54	0.42
2:A:37:TYR:OH	2:A:57:LYS:NZ	2.47	0.42
2:A:59:LEU:HD13	2:A:59:LEU:HA	1.77	0.42
3:B:89:GLU:HB2	3:B:228:LEU:HD22	2.02	0.42
5:D:65:ARG:O	5:D:69:LEU:HD13	2.20	0.42
7:F:71:ARG:O	7:F:75:SER:HB2	2.20	0.42
10:I:61:ASP:OD1	10:I:62:VAL:HG23	2.20	0.42
16:O:74:ALA:HB1	16:O:115:ALA:HB2	2.00	0.42
29:b:34:ASP:HB2	29:b:82:LYS:HE2	2.02	0.42
32:e:27:LYS:HE2	32:e:27:LYS:HB3	1.80	0.42
34:g:152:SER:HB3	34:g:170:TRP:HD1	1.84	0.42
1:2:150:A:H5''	1:2:151:C:H5	1.85	0.42
1:2:482:G:OP1	25:X:76:LYS:HA	2.19	0.42
1:2:526:A:OP1	32:e:35:ARG:NH1	2.53	0.42
1:2:1392:U:H2'	1:2:1393:G:C8	2.55	0.42
1:2:1745:A:H2	8:G:33:ALA:HB3	1.83	0.42
2:A:170:SER:O	2:A:174:MET:HG2	2.20	0.42
3:B:138:PHE:O	3:B:213:ARG:N	2.53	0.42
16:O:131:ASP:OD1	16:O:131:ASP:C	2.63	0.42
18:Q:112:LEU:HD23	18:Q:112:LEU:HA	1.73	0.42
19:R:31:ASN:O	19:R:35:CYS:HB2	2.19	0.42
20:S:18:THR:HG22	20:S:101:ASN:HB3	2.00	0.42
28:a:87:ARG:NH2	28:a:92:ARG:O	2.52	0.42
1:2:609:U:H2'	1:2:610:G:H8	1.85	0.42
1:2:1013:U:C2	1:2:1014:G:C8	3.07	0.42
1:2:1045:U:H2'	1:2:1046:U:C6	2.54	0.42
1:2:1310:U:OP1	14:M:36:ARG:NE	2.50	0.42
1:2:1484:A:C8	1:2:1485:U:H5	2.38	0.42
1:2:1714:U:C4	1:2:1715:A:C8	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1728:U:O2'	1:2:1729:U:OP2	2.35	0.42
5:D:45:ARG:HD2	5:D:45:ARG:HA	1.80	0.42
11:J:48:PHE:CE2	11:J:52:LYS:HE3	2.54	0.42
16:O:61:LYS:HA	16:O:61:LYS:HD2	1.76	0.42
17:P:23:ASP:HA	17:P:26:LEU:HD12	2.01	0.42
1:2:99:A:H61	1:2:433:A:H1'	1.84	0.42
1:2:340:C:C4	1:2:341:C:H1'	2.55	0.42
1:2:1283:C:H2'	14:M:100:PRO:HA	2.01	0.42
1:2:1654:G:H2'	1:2:1655:C:C6	2.55	0.42
3:B:30:TRP:HE3	3:B:46:LYS:HB3	1.85	0.42
3:B:228:LEU:O	3:B:231:LEU:HB3	2.20	0.42
4:C:166:ARG:HB3	4:C:247:THR:HB	2.02	0.42
9:H:47:ALA:HB1	9:H:49:LYS:NZ	2.34	0.42
10:I:103:LEU:HA	10:I:171:LEU:O	2.20	0.42
18:Q:81:ILE:C	18:Q:83:ALA:H	2.28	0.42
22:U:26:SER:HB3	22:U:110:VAL:HA	2.02	0.42
22:U:58:THR:O	22:U:58:THR:OG1	2.33	0.42
24:W:37:PHE:CE1	24:W:41:MET:HE3	2.54	0.42
25:X:40:PRO:HB3	25:X:81:ILE:HD11	2.02	0.42
1:2:1120:U:H2'	1:2:1121:G:H8	1.84	0.42
2:A:176:TRP:NE1	2:A:197:VAL:O	2.50	0.42
8:G:46:LYS:O	8:G:117:GLY:HA3	2.20	0.42
11:J:58:ARG:O	11:J:62:THR:HG23	2.20	0.42
15:N:94:LYS:HB2	15:N:94:LYS:HE3	1.81	0.42
18:Q:103:ALA:O	18:Q:106:LYS:HG2	2.20	0.42
28:a:45:VAL:CG1	28:a:53:ILE:HD12	2.50	0.42
1:2:583:A:OP1	11:J:162:ARG:NH2	2.46	0.41
1:2:1235:G:H1'	1:2:1524:G:H22	1.85	0.41
1:2:1274:G:HO2'	1:2:1275:G:N2	2.17	0.41
1:2:1377:U:O2	1:2:1379:A:H5'	2.20	0.41
4:C:260:VAL:O	4:C:260:VAL:HG23	2.20	0.41
5:D:210:ILE:HG21	19:R:19:LYS:HD2	2.01	0.41
1:2:1225:U:O2'	1:2:1226:G:H5'	2.19	0.41
1:2:1538:C:H1'	21:T:44:GLU:HB2	2.02	0.41
1:2:1608:U:H4'	20:S:130:ARG:NH1	2.35	0.41
1:2:1675:A:H5''	7:F:77:MET:SD	2.60	0.41
7:F:149:GLN:HG3	7:F:152:TRP:HE3	1.85	0.41
9:H:126:HIS:CE1	9:H:181:THR:HG23	2.55	0.41
9:H:155:LYS:HB3	9:H:188:GLU:OE1	2.20	0.41
10:I:26:LYS:O	10:I:29:LEU:HD23	2.20	0.41
10:I:143:LYS:HD2	10:I:143:LYS:HA	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:103:ASN:HB3	16:O:139:SER:HB2	2.01	0.41
17:P:40:ARG:HD3	17:P:40:ARG:HA	1.87	0.41
20:S:125:HIS:CE1	20:S:131:VAL:HG21	2.54	0.41
21:T:60:THR:O	21:T:64:LEU:HG	2.20	0.41
27:Z:79:ILE:HG21	27:Z:83:LEU:HD23	2.02	0.41
1:2:495:U:OP1	6:E:49:ARG:NH1	2.53	0.41
1:2:976:G:H2'	1:2:977:C:C6	2.56	0.41
1:2:1679:A:H5'	7:F:60:ARG:HD3	2.02	0.41
5:D:106:ARG:HG3	5:D:107:TYR:N	2.35	0.41
18:Q:100:VAL:HG13	18:Q:101:ASP:N	2.35	0.41
20:S:46:ARG:NH2	21:T:50:GLU:HA	2.35	0.41
24:W:3:ARG:HD3	24:W:6:VAL:HG12	2.01	0.41
1:2:15:U:O2'	1:2:669:A:N6	2.51	0.41
1:2:357:C:H2'	1:2:358:C:C6	2.55	0.41
1:2:455:A:O2'	1:2:1735:A:H8	2.03	0.41
1:2:1215:C:O2'	1:2:1645:C:OP2	2.32	0.41
1:2:1313:A:H4'	1:2:1314:U:O4'	2.20	0.41
1:2:1316:C:H2'	1:2:1317:C:H6	1.86	0.41
1:2:1728:U:C5	1:2:1808:U:H1'	2.55	0.41
2:A:73:ASP:O	2:A:120:ARG:N	2.43	0.41
3:B:99:ASN:OD1	3:B:100:PHE:N	2.54	0.41
6:E:126:VAL:HG23	6:E:156:VAL:HA	2.02	0.41
9:H:73:GLN:HB3	9:H:135:PHE:CE1	2.55	0.41
11:J:170:PRO:HB3	11:J:174:LYS:HG2	2.03	0.41
18:Q:40:GLU:C	18:Q:41:MET:HE2	2.45	0.41
22:U:56:MET:HE3	22:U:88:LEU:HD22	2.02	0.41
1:2:170:A:OP2	8:G:140:ARG:NH1	2.53	0.41
1:2:941:C:OP1	3:B:136:ARG:NH2	2.53	0.41
1:2:1172:U:H2'	1:2:1173:A:H8	1.86	0.41
1:2:1779:G:H5''	1:2:1780:G:N7	2.36	0.41
7:F:120:GLY:HA2	7:F:121:PRO:HD3	1.89	0.41
10:I:147:LYS:HD2	10:I:147:LYS:O	2.20	0.41
11:J:140:GLN:NE2	26:Y:64:PHE:O	2.52	0.41
23:V:65:SER:O	23:V:69:ILE:HG13	2.21	0.41
34:g:11:LEU:O	34:g:306:LEU:HD12	2.20	0.41
1:2:125:C:O2	1:2:339:A:H2	2.04	0.41
1:2:1047:C:H2'	1:2:1048:G:O4'	2.20	0.41
1:2:1240:A:O2'	1:2:1267:C:H4'	2.20	0.41
1:2:1685:U:H2'	1:2:1686:G:O4'	2.21	0.41
8:G:65:GLN:O	8:G:65:GLN:NE2	2.52	0.41
10:I:89:GLU:O	10:I:93:THR:OG1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y:91:LEU:O	26:Y:95:GLY:N	2.54	0.41
33:f:134:SER:HA	33:f:139:HIS:CE1	2.56	0.41
34:g:35:SER:HB3	34:g:39:THR:O	2.20	0.41
1:2:855:G:HO2'	13:L:71:ARG:NH1	2.18	0.41
1:2:1121:G:H22	3:B:146:ARG:HH21	1.69	0.41
1:2:1204:A:H2'	1:2:1205:C:C6	2.55	0.41
1:2:1266:C:H3'	1:2:1267:C:C5'	2.50	0.41
1:2:1516:G:H5'	1:2:1517:G:OP2	2.21	0.41
1:2:1658:G:H2'	1:2:1659:U:O4'	2.21	0.41
5:D:54:ARG:HG3	5:D:57:ASN:HB3	2.03	0.41
6:E:128:LYS:HG2	6:E:140:VAL:HB	2.03	0.41
11:J:136:ARG:HG2	11:J:160:SER:H	1.86	0.41
31:d:19:ARG:HB2	31:d:19:ARG:NH1	2.36	0.41
1:2:4:C:H4'	4:C:207:ALA:HB2	2.02	0.41
1:2:444:G:N2	1:2:446:G:H3'	2.36	0.41
1:2:574:A:H2'	1:2:575:A:H5''	2.02	0.41
1:2:916:A:C4	15:N:73:ARG:HD3	2.55	0.41
1:2:959:G:H1'	1:2:964:A:N6	2.36	0.41
1:2:1164:G:O2'	1:2:1165:G:H5'	2.20	0.41
1:2:1239:U:H3'	1:2:1241:A:OP2	2.20	0.41
1:2:1276:A:H61	1:2:1322:G:H4'	1.85	0.41
1:2:1316:C:H2'	1:2:1317:C:C6	2.56	0.41
1:2:1567:G:H1	1:2:1612:G:N2	2.19	0.41
1:2:1581:C:H5'	1:2:1582:C:C5	2.47	0.41
1:2:1612:G:O5'	1:2:1612:G:H8	2.04	0.41
6:E:159:THR:HG23	6:E:227:VAL:CG2	2.51	0.41
9:H:191:GLU:H	9:H:191:GLU:CD	2.28	0.41
11:J:126:ALA:O	11:J:130:ILE:HG13	2.20	0.41
11:J:163:SER:O	11:J:167:GLY:N	2.46	0.41
13:L:37:TYR:CE2	13:L:51:ILE:HG23	2.56	0.41
15:N:106:ARG:CZ	15:N:106:ARG:HB3	2.51	0.41
29:b:12:PRO:CD	29:b:13:GLU:H	2.30	0.41
32:e:36:MET:HB3	32:e:36:MET:HE3	1.75	0.41
1:2:445:A:H2'	1:2:446:G:O4'	2.21	0.41
1:2:651:U:H2'	1:2:652:U:C6	2.56	0.41
1:2:1683:C:H2'	1:2:1684:C:H6	1.86	0.41
3:B:110:MET:HE3	3:B:113:MET:HE3	2.03	0.41
4:C:106:VAL:H	36:n:191:THR:HG21	1.85	0.41
4:C:174:ILE:HD12	23:V:4:ASP:HB2	2.02	0.41
6:E:98:ASN:OD1	6:E:98:ASN:N	2.54	0.41
8:G:48:TYR:CE1	8:G:116:LYS:HA	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:120:ASP:N	8:G:120:ASP:OD1	2.52	0.41
8:G:150:GLU:O	8:G:151:ASP:HB3	2.21	0.41
8:G:213:LEU:HD23	8:G:213:LEU:HA	1.82	0.41
11:J:63:LEU:O	11:J:70:ARG:NH1	2.52	0.41
11:J:64:ASP:O	11:J:70:ARG:HD3	2.20	0.41
11:J:124:HIS:CE1	32:e:35:ARG:HB2	2.56	0.41
13:L:4:ILE:HD13	13:L:4:ILE:HA	1.79	0.41
14:M:40:LYS:H	14:M:40:LYS:HG2	1.72	0.41
16:O:39:ASP:OD1	16:O:39:ASP:C	2.63	0.41
19:R:10:LYS:HD3	19:R:53:TYR:CE2	2.56	0.41
21:T:38:LYS:O	21:T:38:LYS:HD3	2.21	0.41
21:T:130:ASP:O	21:T:134:ILE:HG12	2.20	0.41
25:X:33:GLY:O	25:X:37:LYS:HG2	2.20	0.41
28:a:32:LYS:O	28:a:37:LYS:NZ	2.50	0.41
34:g:207:CYS:H	34:g:218:LEU:HD13	1.85	0.41
1:2:291:G:N3	13:L:41:GLY:HA3	2.36	0.41
1:2:653:A:H2'	1:2:654:A:O4'	2.21	0.41
1:2:1120:U:C2	1:2:1121:G:C8	3.08	0.41
1:2:1144:A:H5'	1:2:1355:C:H5	1.84	0.41
1:2:1332:A:N3	5:D:141:LYS:HE3	2.36	0.41
1:2:1405:A:H2'	1:2:1443:C:H42	1.86	0.41
1:2:1484:A:H2'	1:2:1485:U:C6	2.56	0.41
3:B:150:ILE:O	19:R:132:ARG:HG3	2.21	0.41
8:G:24:LEU:HB3	8:G:28:TYR:CE1	2.56	0.41
10:I:74:ARG:HA	10:I:74:ARG:HD2	1.93	0.41
15:N:34:LYS:HE2	15:N:67:THR:HB	2.03	0.41
19:R:31:ASN:ND2	19:R:55:THR:OG1	2.54	0.41
24:W:106:THR:HG22	24:W:122:GLY:O	2.21	0.41
27:Z:80:ARG:HG3	27:Z:82:SER:H	1.86	0.41
30:c:10:LYS:NZ	30:c:37:ASP:OD2	2.36	0.41
1:2:845:G:H2'	1:2:846:G:O4'	2.21	0.40
1:2:1227:G:C6	1:2:1638:G:H1'	2.56	0.40
1:2:1240:A:H1'	1:2:1267:C:O2'	2.21	0.40
1:2:1391:C:H4'	31:d:55:LEU:HD22	2.01	0.40
1:2:1563:G:C5'	21:T:101:ARG:HH21	2.27	0.40
11:J:50:LEU:O	11:J:54:ARG:HG3	2.21	0.40
11:J:125:HIS:HA	11:J:128:VAL:HG22	2.03	0.40
11:J:175:ARG:O	11:J:179:LYS:HG2	2.21	0.40
16:O:113:GLN:CD	28:a:46:GLU:H	2.30	0.40
18:Q:47:LEU:HB2	18:Q:81:ILE:HD13	2.03	0.40
1:2:14:C:OP1	4:C:190:SER:OG	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:293:C:O2'	1:2:294:U:H3'	2.21	0.40
1:2:868:G:N7	9:H:115:LYS:HB3	2.36	0.40
1:2:1692:U:H2'	1:2:1693:G:C8	2.57	0.40
7:F:41:VAL:HG13	7:F:46:ALA:HB2	2.03	0.40
21:T:28:LEU:HD12	21:T:28:LEU:HA	1.97	0.40
25:X:100:VAL:HG12	25:X:125:VAL:HA	2.04	0.40
29:b:36:LYS:NZ	29:b:42:LYS:O	2.54	0.40
34:g:30:MET:HE1	34:g:71:ILE:HD13	2.03	0.40
1:2:92:A:N6	1:2:444:G:H1'	2.35	0.40
1:2:642:U:H4'	1:2:644:G:H4'	2.03	0.40
1:2:958:G:O2'	1:2:959:G:P	2.79	0.40
1:2:1293:A:OP2	1:2:1295:A:N6	2.54	0.40
1:2:1613:G:H8	1:2:1613:G:P	2.45	0.40
8:G:113:ILE:HD12	8:G:124:LEU:HD21	2.02	0.40
10:I:113:TYR:O	10:I:117:TYR:N	2.55	0.40
15:N:56:ASP:OD2	29:b:51:GLN:N	2.53	0.40
16:O:88:LEU:HD12	16:O:88:LEU:HA	1.79	0.40
18:Q:80:GLN:NE2	18:Q:81:ILE:HG13	2.36	0.40
18:Q:111:ILE:HD13	18:Q:111:ILE:HA	1.95	0.40
20:S:85:ASN:OD1	20:S:85:ASN:N	2.53	0.40
24:W:66:THR:C	24:W:68:ARG:H	2.29	0.40
25:X:7:LEU:HD12	25:X:7:LEU:HA	1.79	0.40
1:2:647:U:H2'	1:2:648:A:C8	2.56	0.40
5:D:206:ASP:OD1	5:D:206:ASP:N	2.54	0.40
6:E:126:VAL:HG11	6:E:139:LEU:HD11	2.04	0.40
8:G:49:VAL:HB	8:G:115:LYS:HB3	2.02	0.40
8:G:61:PHE:CD2	8:G:72:ARG:HD3	2.56	0.40
8:G:67:VAL:HG11	8:G:75:LEU:HD11	2.03	0.40
8:G:162:LEU:HD13	8:G:162:LEU:HA	1.93	0.40
10:I:107:THR:HB	10:I:108:PRO:HD3	2.03	0.40
1:2:637:U:H2'	1:2:638:C:H6	1.87	0.40
1:2:1044:G:H4'	1:2:1045:U:H5	1.86	0.40
1:2:1283:C:C2	14:M:100:PRO:HB3	2.57	0.40
1:2:1349:G:H2'	1:2:1350:U:C6	2.57	0.40
6:E:253:ASP:OD1	6:E:253:ASP:C	2.64	0.40
7:F:109:LEU:O	7:F:113:VAL:HG22	2.21	0.40
7:F:119:SER:C	7:F:190:ILE:HG21	2.46	0.40
12:K:55:ARG:HG3	12:K:57:TYR:HE2	1.85	0.40
18:Q:105:LYS:O	18:Q:109:LYS:HB3	2.22	0.40
22:U:67:LYS:HD2	22:U:76:THR:HB	2.04	0.40
25:X:88:ASP:OD1	25:X:88:ASP:N	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:c:59:LEU:H	30:c:59:LEU:HD23	1.87	0.40
34:g:288:SER:O	34:g:289:LEU:HD13	2.21	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	
2	A	211/295 (72%)	206 (98%)	4 (2%)	1 (0%)	24	54
3	B	211/264 (80%)	205 (97%)	6 (3%)	0	100	100
4	C	216/293 (74%)	212 (98%)	4 (2%)	0	100	100
5	D	223/243 (92%)	220 (99%)	3 (1%)	0	100	100
6	E	260/263 (99%)	251 (96%)	9 (4%)	0	100	100
7	F	187/204 (92%)	160 (86%)	26 (14%)	1 (0%)	24	54
8	G	228/249 (92%)	221 (97%)	7 (3%)	0	100	100
9	H	184/194 (95%)	172 (94%)	12 (6%)	0	100	100
10	I	203/208 (98%)	193 (95%)	10 (5%)	0	100	100
11	J	178/194 (92%)	172 (97%)	6 (3%)	0	100	100
12	K	95/165 (58%)	91 (96%)	4 (4%)	0	100	100
13	L	149/158 (94%)	145 (97%)	4 (3%)	0	100	100
14	M	119/132 (90%)	107 (90%)	9 (8%)	3 (2%)	4	17
15	N	147/151 (97%)	142 (97%)	5 (3%)	0	100	100
16	O	133/151 (88%)	127 (96%)	6 (4%)	0	100	100
17	P	124/145 (86%)	112 (90%)	12 (10%)	0	100	100
18	Q	136/146 (93%)	121 (89%)	14 (10%)	1 (1%)	18	48
19	R	130/135 (96%)	127 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	S	141/152 (93%)	125 (89%)	16 (11%)	0	100	100
21	T	142/145 (98%)	134 (94%)	7 (5%)	1 (1%)	18	48
22	U	99/119 (83%)	93 (94%)	6 (6%)	0	100	100
23	V	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
24	W	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
25	X	139/143 (97%)	137 (99%)	2 (1%)	0	100	100
26	Y	122/130 (94%)	116 (95%)	6 (5%)	0	100	100
27	Z	70/125 (56%)	66 (94%)	4 (6%)	0	100	100
28	a	97/101 (96%)	94 (97%)	2 (2%)	1 (1%)	12	39
29	b	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
30	c	60/62 (97%)	55 (92%)	5 (8%)	0	100	100
31	d	53/55 (96%)	50 (94%)	3 (6%)	0	100	100
32	e	54/56 (96%)	53 (98%)	1 (2%)	0	100	100
33	f	72/74 (97%)	65 (90%)	6 (8%)	1 (1%)	9	30
34	g	312/315 (99%)	290 (93%)	21 (7%)	1 (0%)	36	65
35	h	20/25 (80%)	20 (100%)	0	0	100	100
36	n	24/193 (12%)	21 (88%)	3 (12%)	0	100	100
All	All	4826/5580 (86%)	4581 (95%)	235 (5%)	10 (0%)	44	72

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	M	109	VAL
18	Q	13	PHE
28	a	63	VAL
2	A	189	ILE
7	F	79	HIS
14	M	110	VAL
34	g	161	SER
14	M	31	LEU
21	T	70	ALA
33	f	108	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	
2	A	179/243 (74%)	175 (98%)	4 (2%)	45	77
3	B	194/231 (84%)	190 (98%)	4 (2%)	47	77
4	C	184/225 (82%)	182 (99%)	2 (1%)	65	88
5	D	189/202 (94%)	175 (93%)	14 (7%)	13	38
6	E	224/225 (100%)	221 (99%)	3 (1%)	61	86
7	F	159/170 (94%)	149 (94%)	10 (6%)	16	45
8	G	200/218 (92%)	192 (96%)	8 (4%)	28	62
9	H	167/174 (96%)	158 (95%)	9 (5%)	20	51
10	I	178/180 (99%)	170 (96%)	8 (4%)	24	58
11	J	160/168 (95%)	156 (98%)	4 (2%)	42	74
12	K	88/136 (65%)	87 (99%)	1 (1%)	65	88
13	L	135/142 (95%)	127 (94%)	8 (6%)	18	48
14	M	102/108 (94%)	101 (99%)	1 (1%)	68	89
15	N	130/131 (99%)	120 (92%)	10 (8%)	12	35
16	O	105/119 (88%)	100 (95%)	5 (5%)	23	55
17	P	112/130 (86%)	108 (96%)	4 (4%)	31	65
18	Q	114/121 (94%)	110 (96%)	4 (4%)	32	66
19	R	119/122 (98%)	109 (92%)	10 (8%)	10	31
20	S	124/132 (94%)	116 (94%)	8 (6%)	15	44
21	T	114/115 (99%)	103 (90%)	11 (10%)	8	26
22	U	93/107 (87%)	89 (96%)	4 (4%)	26	60
23	V	66/67 (98%)	63 (96%)	3 (4%)	24	58
24	W	112/113 (99%)	109 (97%)	3 (3%)	39	73
25	X	113/115 (98%)	106 (94%)	7 (6%)	16	46
26	Y	108/112 (96%)	103 (95%)	5 (5%)	24	57
27	Z	64/103 (62%)	64 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	a	87/89 (98%)	81 (93%)	6 (7%)	14	41
29	b	74/74 (100%)	67 (90%)	7 (10%)	8	26
30	c	55/55 (100%)	53 (96%)	2 (4%)	31	65
31	d	48/48 (100%)	45 (94%)	3 (6%)	16	45
32	e	45/45 (100%)	39 (87%)	6 (13%)	4	12
33	f	67/67 (100%)	66 (98%)	1 (2%)	57	84
34	g	272/273 (100%)	259 (95%)	13 (5%)	23	55
35	h	21/24 (88%)	21 (100%)	0	100	100
36	n	22/160 (14%)	22 (100%)	0	100	100
All	All	4224/4744 (89%)	4036 (96%)	188 (4%)	26	58

All (188) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	15	VAL
2	A	59	LEU
2	A	104	THR
2	A	188	THR
3	B	91	VAL
3	B	108	ASP
3	B	143	THR
3	B	172	MET
4	C	63	VAL
4	C	184	VAL
5	D	25	LEU
5	D	41	VAL
5	D	55	THR
5	D	69	LEU
5	D	94	ARG
5	D	104	SER
5	D	105	LEU
5	D	128	GLU
5	D	134	CYS
5	D	137	VAL
5	D	154	ASP
5	D	175	VAL
5	D	185	LYS
5	D	204	LEU
6	E	23	LEU

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Mol	Chain	Res	Type
6	E	32	SER
6	E	104	ASP
7	F	26	ASP
7	F	33	ILE
7	F	79	HIS
7	F	89	THR
7	F	111	VAL
7	F	147	VAL
7	F	168	THR
7	F	169	ILE
7	F	173	LEU
7	F	178	ILE
8	G	10	THR
8	G	18	VAL
8	G	20	ASP
8	G	68	LEU
8	G	96	SER
8	G	139	SER
8	G	185	LEU
8	G	200	LYS
9	H	12	ASN
9	H	21	SER
9	H	77	VAL
9	H	121	THR
9	H	134	VAL
9	H	139	ILE
9	H	160	LYS
9	H	166	VAL
9	H	172	THR
10	I	14	THR
10	I	45	THR
10	I	76	THR
10	I	81	VAL
10	I	115	SER
10	I	130	THR
10	I	158	ILE
10	I	159	SER
11	J	93	LYS
11	J	114	VAL
11	J	155	LYS
11	J	173	VAL
12	K	16	PHE

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Mol	Chain	Res	Type
13	L	4	ILE
13	L	6	THR
13	L	16	ILE
13	L	45	LYS
13	L	46	THR
13	L	51	ILE
13	L	52	GLU
13	L	67	SER
14	M	127	TYR
15	N	9	LYS
15	N	14	SER
15	N	22	VAL
15	N	27	LYS
15	N	30	SER
15	N	63	VAL
15	N	66	VAL
15	N	72	LEU
15	N	80	LEU
15	N	143	SER
16	O	17	LEU
16	O	52	THR
16	O	88	LEU
16	O	91	THR
16	O	137	SER
17	P	45	LEU
17	P	79	HIS
17	P	90	VAL
17	P	123	TYR
18	Q	34	VAL
18	Q	41	MET
18	Q	72	VAL
18	Q	121	VAL
19	R	9	VAL
19	R	15	VAL
19	R	24	LEU
19	R	41	ILE
19	R	85	VAL
19	R	91	LEU
19	R	98	VAL
19	R	120	THR
19	R	124	VAL
19	R	130	THR

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Mol	Chain	Res	Type
20	S	4	VAL
20	S	55	ARG
20	S	70	ILE
20	S	85	ASN
20	S	98	VAL
20	S	99	LEU
20	S	114	LEU
20	S	131	VAL
21	T	4	VAL
21	T	6	VAL
21	T	9	VAL
21	T	33	TRP
21	T	34	VAL
21	T	36	THR
21	T	48	TYR
21	T	72	VAL
21	T	75	MET
21	T	79	TYR
21	T	103	VAL
22	U	20	ILE
22	U	25	THR
22	U	40	ILE
22	U	46	LYS
23	V	39	VAL
23	V	47	ASN
23	V	52	THR
24	W	27	ILE
24	W	57	ARG
24	W	80	ASP
25	X	63	ASN
25	X	72	VAL
25	X	81	ILE
25	X	105	PHE
25	X	115	ILE
25	X	119	ARG
25	X	128	VAL
26	Y	6	THR
26	Y	35	VAL
26	Y	51	THR
26	Y	68	LYS
26	Y	120	THR
28	a	29	CYS

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Mol	Chain	Res	Type
28	a	40	VAL
28	a	79	ILE
28	a	81	SER
28	a	90	GLU
28	a	100	ARG
29	b	7	LEU
29	b	35	VAL
29	b	45	THR
29	b	53	VAL
29	b	62	VAL
29	b	63	LEU
29	b	74	THR
30	c	38	THR
30	c	45	ASN
31	d	20	SER
31	d	30	LEU
31	d	49	ASP
32	e	15	GLN
32	e	27	LYS
32	e	29	THR
32	e	43	VAL
32	e	45	VAL
32	e	48	THR
33	f	108	VAL
34	g	45	LEU
34	g	68	ASP
34	g	98	THR
34	g	111	VAL
34	g	128	THR
34	g	137	VAL
34	g	194	TYR
34	g	198	VAL
34	g	199	THR
34	g	252	THR
34	g	277	THR
34	g	289	LEU
34	g	310	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (54) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	141	ASN

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Mol	Chain	Res	Type
3	B	159	GLN
4	C	134	ASN
6	E	161	GLN
7	F	65	GLN
7	F	82	ASN
7	F	110	GLN
7	F	114	ASN
7	F	148	ASN
7	F	186	ASN
8	G	186	GLN
9	H	39	GLN
9	H	68	GLN
9	H	76	GLN
9	H	112	ASN
9	H	126	HIS
10	I	155	ASN
11	J	140	GLN
12	K	61	GLN
13	L	18	GLN
13	L	19	ASN
13	L	100	ASN
14	M	75	ASN
15	N	13	GLN
15	N	69	ASN
15	N	138	ASN
16	O	26	ASN
17	P	41	GLN
17	P	79	HIS
18	Q	48	GLN
18	Q	86	GLN
18	Q	142	GLN
19	R	62	GLN
19	R	93	GLN
19	R	127	ASN
20	S	87	GLN
20	S	97	GLN
21	T	42	HIS
21	T	126	GLN
22	U	81	GLN
22	U	100	GLN
24	W	24	GLN
25	X	23	HIS

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Mol	Chain	Res	Type
25	X	31	HIS
26	Y	22	GLN
26	Y	112	ASN
27	Z	64	ASN
29	b	26	GLN
29	b	83	GLN
30	c	7	GLN
34	g	56	GLN
34	g	147	HIS
34	g	215	GLN
34	g	296	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1622/1869 (86%)	618 (38%)	19 (1%)

All (618) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	C
1	2	4	C
1	2	13	C
1	2	15	U
1	2	17	C
1	2	33	G
1	2	34	U
1	2	41	G
1	2	44	U
1	2	45	A
1	2	46	A
1	2	56	G
1	2	67	C
1	2	68	A
1	2	73	C
1	2	74	G
1	2	77	A
1	2	80	G
1	2	83	A
1	2	99	A

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Mol	Chain	Res	Type
1	2	102	A
1	2	103	A
1	2	113	G
1	2	115	U
1	2	124	U
1	2	125	C
1	2	126	G
1	2	127	C
1	2	128	U
1	2	129	C
1	2	130	G
1	2	141	A
1	2	142	C
1	2	143	U
1	2	145	G
1	2	147	A
1	2	148	U
1	2	150	A
1	2	155	G
1	2	160	U
1	2	163	U
1	2	168	C
1	2	170	A
1	2	173	A
1	2	174	C
1	2	175	A
1	2	176	U
1	2	177	G
1	2	178	C
1	2	179	C
1	2	180	G
1	2	181	A
1	2	182	C
1	2	183	G
1	2	184	G
1	2	189	U
1	2	190	G
1	2	191	A
1	2	192	C
1	2	194	C
1	2	197	U
1	2	199	C

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Mol	Chain	Res	Type
1	2	200	G
1	2	202	G
1	2	207	G
1	2	210	U
1	2	211	G
1	2	212	C
1	2	213	G
1	2	215	G
1	2	216	C
1	2	217	A
1	2	218	U
1	2	219	U
1	2	221	A
1	2	222	U
1	2	224	A
1	2	225	G
1	2	293	C
1	2	294	U
1	2	305	U
1	2	306	C
1	2	308	G
1	2	310	C
1	2	311	C
1	2	314	U
1	2	315	C
1	2	316	G
1	2	317	C
1	2	318	A
1	2	319	C
1	2	320	G
1	2	322	C
1	2	330	G
1	2	332	G
1	2	335	G
1	2	340	C
1	2	341	C
1	2	342	C
1	2	344	U
1	2	352	U
1	2	353	C
1	2	357	C
1	2	362	C

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Mol	Chain	Res	Type
1	2	364	A
1	2	368	U
1	2	369	C
1	2	370	G
1	2	385	G
1	2	386	C
1	2	398	A
1	2	400	C
1	2	407	G
1	2	409	C
1	2	413	G
1	2	415	A
1	2	417	C
1	2	418	A
1	2	436	G
1	2	448	A
1	2	449	A
1	2	450	C
1	2	464	A
1	2	466	G
1	2	467	G
1	2	470	G
1	2	471	G
1	2	472	C
1	2	473	A
1	2	474	G
1	2	476	A
1	2	478	G
1	2	482	G
1	2	487	U
1	2	488	U
1	2	492	C
1	2	496	C
1	2	512	A
1	2	515	G
1	2	516	A
1	2	517	C
1	2	525	A
1	2	532	C
1	2	533	A
1	2	534	G
1	2	537	C

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Mol	Chain	Res	Type
1	2	538	U
1	2	539	C
1	2	540	U
1	2	541	U
1	2	544	G
1	2	545	A
1	2	546	G
1	2	547	G
1	2	550	C
1	2	552	G
1	2	554	A
1	2	555	A
1	2	556	U
1	2	559	G
1	2	563	G
1	2	570	C
1	2	572	U
1	2	575	A
1	2	576	A
1	2	579	C
1	2	584	A
1	2	587	A
1	2	590	A
1	2	591	U
1	2	604	A
1	2	605	A
1	2	606	G
1	2	607	U
1	2	608	C
1	2	614	C
1	2	617	G
1	2	627	U
1	2	628	A
1	2	632	C
1	2	640	A
1	2	643	A
1	2	644	G
1	2	645	C
1	2	649	U
1	2	655	A
1	2	660	C
1	2	668	A

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Mol	Chain	Res	Type
1	2	669	A
1	2	671	A
1	2	672	A
1	2	673	G
1	2	678	U
1	2	688	U
1	2	747	U
1	2	748	C
1	2	752	G
1	2	793	G
1	2	794	A
1	2	795	A
1	2	797	C
1	2	798	G
1	2	799	U
1	2	800	U
1	2	803	C
1	2	804	U
1	2	809	A
1	2	810	A
1	2	811	A
1	2	813	A
1	2	820	U
1	2	821	G
1	2	822	U
1	2	823	U
1	2	824	C
1	2	827	A
1	2	832	G
1	2	834	C
1	2	842	C
1	2	844	U
1	2	847	A
1	2	853	C
1	2	856	C
1	2	857	U
1	2	859	G
1	2	862	A
1	2	863	U
1	2	864	A
1	2	865	A
1	2	869	A

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Mol	Chain	Res	Type
1	2	870	A
1	2	871	U
1	2	873	G
1	2	874	G
1	2	875	A
1	2	876	C
1	2	877	C
1	2	878	G
1	2	879	C
1	2	880	G
1	2	881	G
1	2	884	C
1	2	885	U
1	2	888	U
1	2	889	U
1	2	890	U
1	2	892	U
1	2	893	U
1	2	894	G
1	2	897	U
1	2	898	U
1	2	900	C
1	2	901	G
1	2	902	G
1	2	904	A
1	2	906	U
1	2	907	G
1	2	908	A
1	2	912	C
1	2	913	A
1	2	914	U
1	2	920	A
1	2	930	C
1	2	933	G
1	2	940	U
1	2	943	U
1	2	952	G
1	2	955	A
1	2	957	A
1	2	959	G
1	2	960	U
1	2	961	G

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Mol	Chain	Res	Type
1	2	964	A
1	2	965	U
1	2	966	U
1	2	967	C
1	2	970	G
1	2	971	G
1	2	973	C
1	2	976	G
1	2	978	G
1	2	982	G
1	2	990	A
1	2	991	G
1	2	992	A
1	2	999	G
1	2	1001	A
1	2	1002	U
1	2	1017	U
1	2	1021	U
1	2	1023	A
1	2	1026	C
1	2	1027	A
1	2	1045	U
1	2	1049	A
1	2	1057	C
1	2	1060	A
1	2	1061	U
1	2	1062	A
1	2	1080	A
1	2	1083	A
1	2	1085	C
1	2	1088	U
1	2	1096	G
1	2	1100	A
1	2	1109	C
1	2	1113	A
1	2	1114	U
1	2	1115	U
1	2	1116	C
1	2	1118	C
1	2	1120	U
1	2	1148	A
1	2	1154	U

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Mol	Chain	Res	Type
1	2	1155	U
1	2	1156	U
1	2	1157	G
1	2	1166	G
1	2	1171	G
1	2	1187	G
1	2	1195	A
1	2	1201	U
1	2	1203	G
1	2	1207	G
1	2	1209	A
1	2	1215	C
1	2	1216	C
1	2	1220	A
1	2	1221	G
1	2	1222	G
1	2	1225	U
1	2	1226	G
1	2	1227	G
1	2	1229	G
1	2	1230	C
1	2	1231	C
1	2	1234	C
1	2	1235	G
1	2	1237	C
1	2	1238	U
1	2	1240	A
1	2	1241	A
1	2	1242	U
1	2	1243	U
1	2	1244	U
1	2	1245	G
1	2	1247	C
1	2	1248	U
1	2	1251	A
1	2	1252	C
1	2	1253	A
1	2	1254	C
1	2	1256	G
1	2	1257	G
1	2	1259	A
1	2	1260	A

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Mol	Chain	Res	Type
1	2	1263	U
1	2	1264	C
1	2	1265	A
1	2	1267	C
1	2	1268	C
1	2	1269	G
1	2	1271	C
1	2	1274	G
1	2	1275	G
1	2	1276	A
1	2	1283	C
1	2	1284	A
1	2	1287	A
1	2	1288	U
1	2	1291	A
1	2	1293	A
1	2	1294	G
1	2	1295	A
1	2	1298	G
1	2	1299	A
1	2	1300	U
1	2	1302	G
1	2	1303	C
1	2	1304	U
1	2	1306	U
1	2	1308	U
1	2	1309	C
1	2	1311	C
1	2	1313	A
1	2	1314	U
1	2	1315	U
1	2	1319	U
1	2	1321	G
1	2	1322	G
1	2	1323	U
1	2	1324	G
1	2	1325	G
1	2	1326	U
1	2	1327	G
1	2	1330	G
1	2	1331	C
1	2	1336	C

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Mol	Chain	Res	Type
1	2	1340	U
1	2	1341	C
1	2	1348	G
1	2	1352	G
1	2	1358	U
1	2	1360	U
1	2	1362	U
1	2	1364	U
1	2	1371	U
1	2	1372	U
1	2	1378	A
1	2	1382	A
1	2	1384	C
1	2	1393	G
1	2	1396	A
1	2	1397	U
1	2	1398	G
1	2	1402	A
1	2	1403	C
1	2	1404	U
1	2	1405	A
1	2	1406	G
1	2	1443	C
1	2	1444	U
1	2	1447	G
1	2	1448	A
1	2	1449	G
1	2	1452	A
1	2	1453	C
1	2	1454	A
1	2	1458	G
1	2	1461	G
1	2	1462	U
1	2	1463	U
1	2	1466	G
1	2	1471	C
1	2	1475	G
1	2	1477	U
1	2	1478	U
1	2	1479	G
1	2	1483	A
1	2	1484	A

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Mol	Chain	Res	Type
1	2	1485	U
1	2	1486	A
1	2	1488	C
1	2	1489	A
1	2	1490	G
1	2	1494	U
1	2	1495	G
1	2	1497	G
1	2	1498	A
1	2	1500	G
1	2	1501	C
1	2	1506	A
1	2	1507	G
1	2	1508	A
1	2	1509	U
1	2	1510	G
1	2	1512	C
1	2	1513	C
1	2	1514	G
1	2	1517	G
1	2	1520	G
1	2	1522	A
1	2	1523	C
1	2	1528	G
1	2	1530	U
1	2	1531	A
1	2	1532	C
1	2	1533	A
1	2	1534	C
1	2	1535	U
1	2	1537	A
1	2	1539	U
1	2	1540	G
1	2	1541	G
1	2	1543	U
1	2	1544	C
1	2	1546	G
1	2	1547	C
1	2	1552	G
1	2	1555	U
1	2	1560	U
1	2	1561	A

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Mol	Chain	Res	Type
1	2	1562	C
1	2	1564	C
1	2	1565	C
1	2	1566	G
1	2	1568	C
1	2	1569	A
1	2	1571	G
1	2	1572	C
1	2	1573	G
1	2	1575	G
1	2	1578	U
1	2	1580	A
1	2	1581	C
1	2	1584	G
1	2	1586	U
1	2	1599	U
1	2	1600	G
1	2	1601	A
1	2	1603	G
1	2	1604	G
1	2	1606	G
1	2	1607	A
1	2	1608	U
1	2	1610	G
1	2	1612	G
1	2	1614	A
1	2	1615	U
1	2	1616	U
1	2	1617	G
1	2	1618	C
1	2	1619	A
1	2	1621	U
1	2	1622	U
1	2	1623	A
1	2	1624	U
1	2	1626	C
1	2	1627	C
1	2	1628	C
1	2	1630	A
1	2	1631	U
1	2	1632	G
1	2	1634	A

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Mol	Chain	Res	Type
1	2	1635	C
1	2	1636	G
1	2	1637	A
1	2	1638	G
1	2	1639	G
1	2	1642	U
1	2	1643	U
1	2	1647	A
1	2	1649	U
1	2	1655	C
1	2	1662	U
1	2	1663	A
1	2	1665	G
1	2	1671	G
1	2	1680	G
1	2	1689	C
1	2	1690	U
1	2	1698	C
1	2	1702	G
1	2	1707	U
1	2	1709	G
1	2	1710	C
1	2	1711	U
1	2	1712	A
1	2	1713	C
1	2	1714	U
1	2	1715	A
1	2	1719	A
1	2	1720	U
1	2	1721	U
1	2	1722	G
1	2	1723	G
1	2	1724	A
1	2	1725	U
1	2	1726	G
1	2	1728	U
1	2	1729	U
1	2	1735	A
1	2	1736	G
1	2	1742	C
1	2	1745	A
1	2	1746	U

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Mol	Chain	Res	Type
1	2	1750	C
1	2	1751	C
1	2	1752	C
1	2	1754	G
1	2	1755	C
1	2	1758	G
1	2	1760	G
1	2	1761	U
1	2	1773	C
1	2	1774	C
1	2	1775	U
1	2	1776	G
1	2	1777	G
1	2	1778	C
1	2	1779	G
1	2	1780	G
1	2	1783	C
1	2	1789	G
1	2	1790	A
1	2	1791	A
1	2	1794	C
1	2	1795	G
1	2	1796	G
1	2	1797	U
1	2	1800	A
1	2	1803	U
1	2	1806	A
1	2	1809	A
1	2	1811	C
1	2	1812	U
1	2	1813	A
1	2	1816	G
1	2	1823	A
1	2	1825	A
1	2	1826	G
1	2	1828	C
1	2	1829	G
1	2	1830	U
1	2	1835	A
1	2	1838	U
1	2	1840	U
1	2	1846	G

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Mol	Chain	Res	Type
1	2	1849	G
1	2	1850	A
1	2	1851	A
1	2	1861	G
1	2	1862	G
1	2	1863	A
1	2	1864	U
1	2	1865	C
1	2	1869	A

All (19) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	180	G
1	2	293	C
1	2	578	C
1	2	604	A
1	2	808	A
1	2	819	G
1	2	880	G
1	2	900	C
1	2	958	G
1	2	1200	A
1	2	1230	C
1	2	1339	U
1	2	1452	A
1	2	1487	A
1	2	1529	C
1	2	1546	G
1	2	1642	U
1	2	1712	A
1	2	1718	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

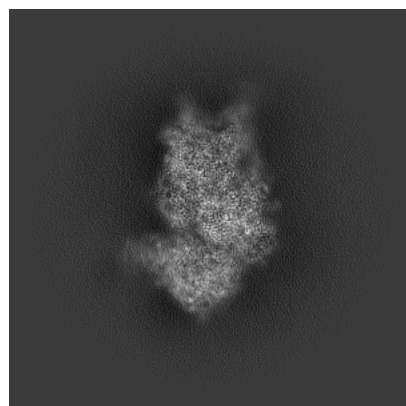
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62448. These allow visual inspection of the internal detail of the map and identification of artifacts.

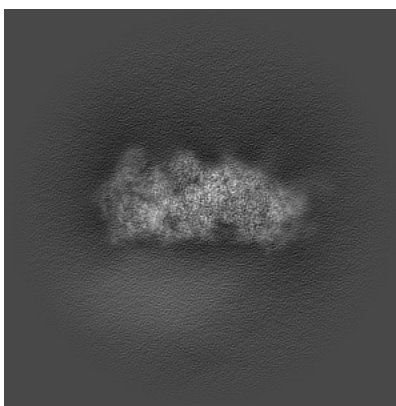
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

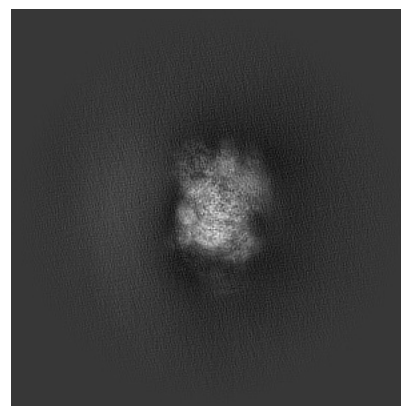
6.1.1 Primary map



X

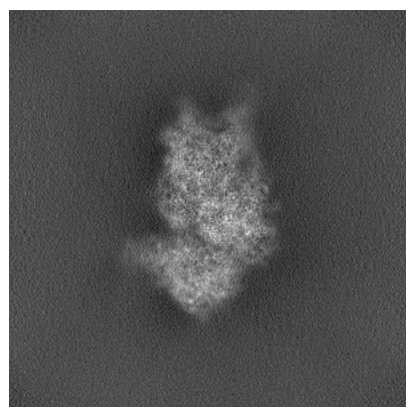


Y

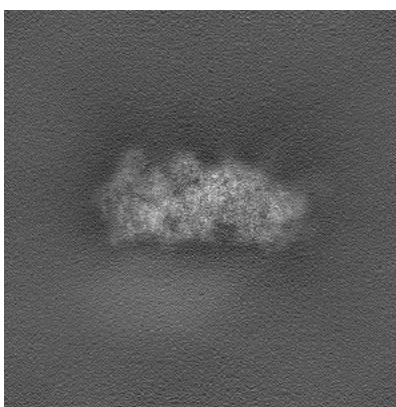


Z

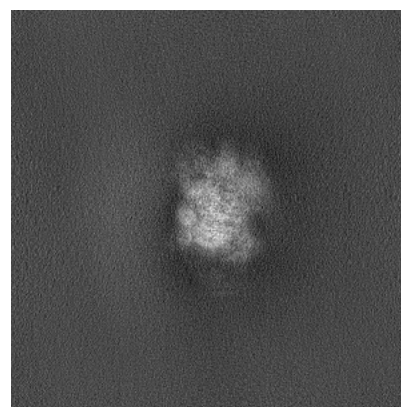
6.1.2 Raw map



X



Y

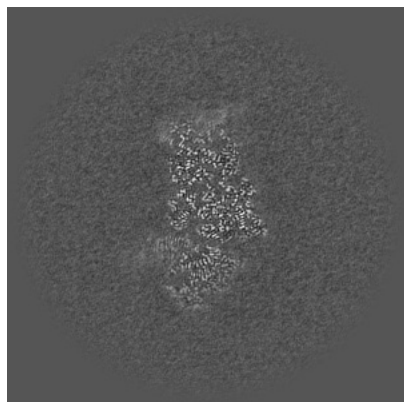


Z

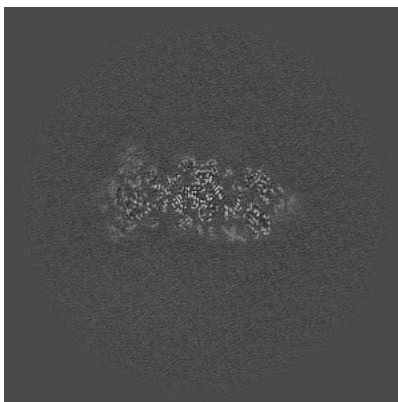
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

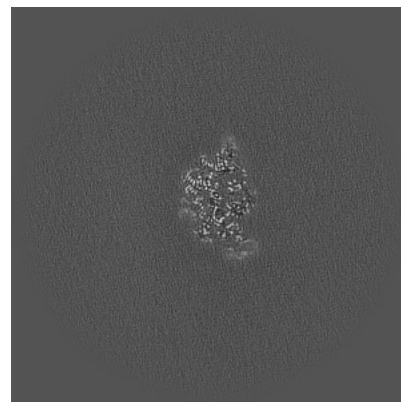
6.2.1 Primary map



X Index: 256

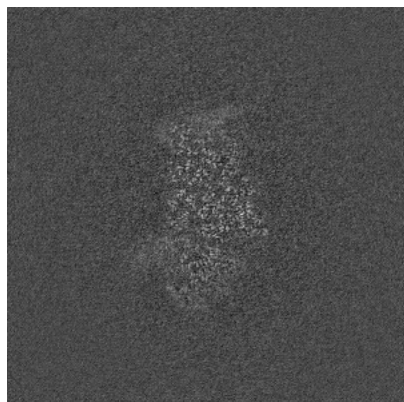


Y Index: 256

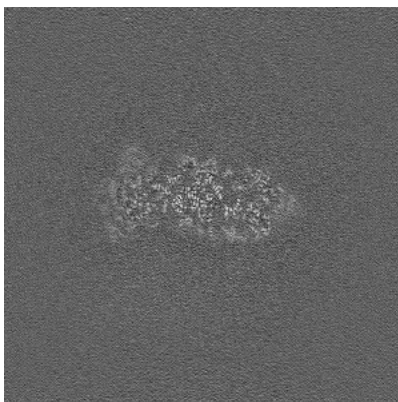


Z Index: 256

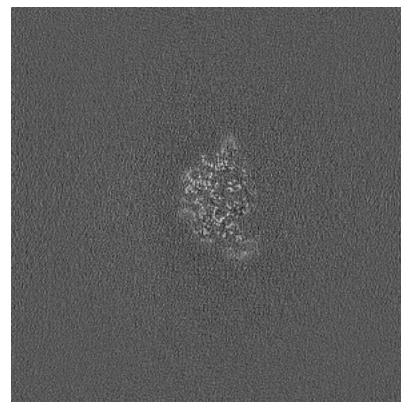
6.2.2 Raw map



X Index: 256



Y Index: 256

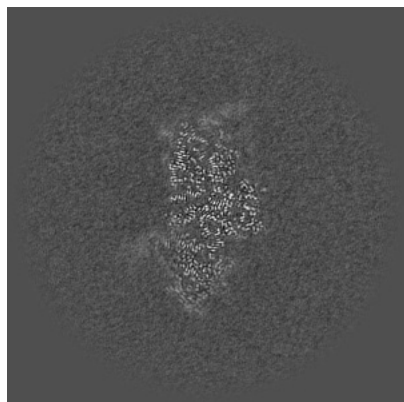


Z Index: 256

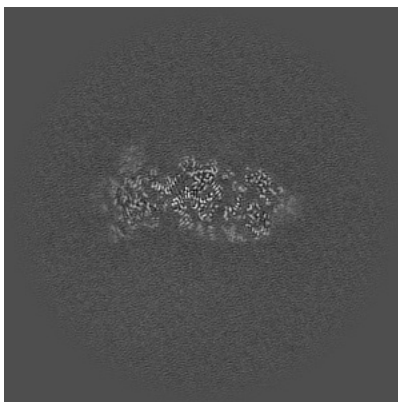
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

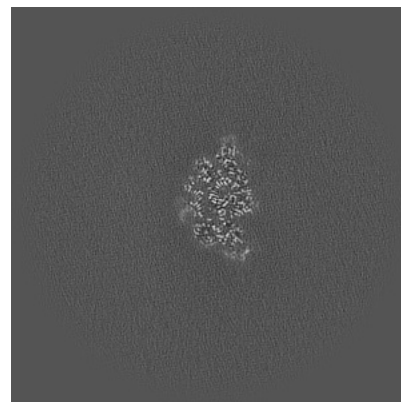
6.3.1 Primary map



X Index: 262

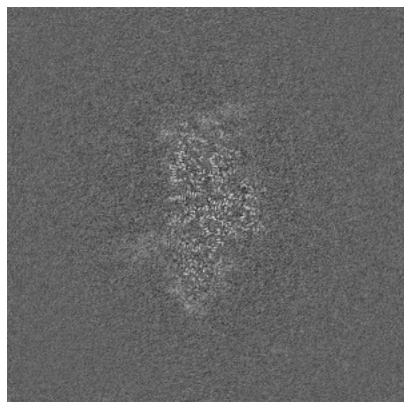


Y Index: 255

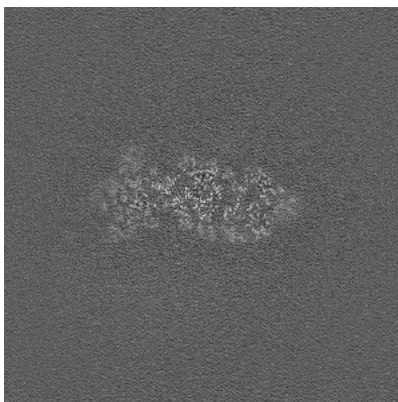


Z Index: 262

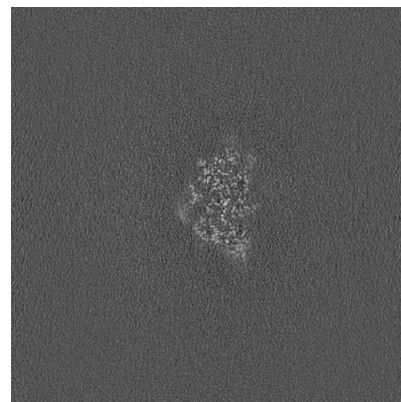
6.3.2 Raw map



X Index: 262



Y Index: 255

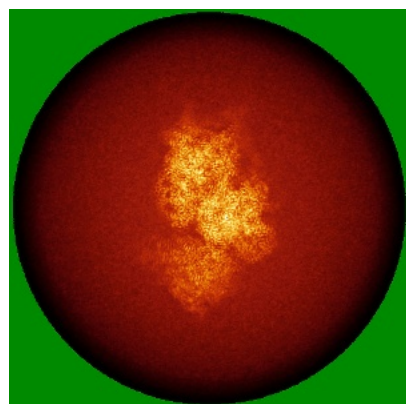


Z Index: 267

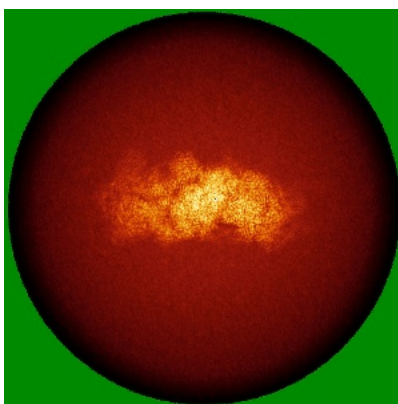
The images above show the largest variance slices of the map in three orthogonal directions.

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

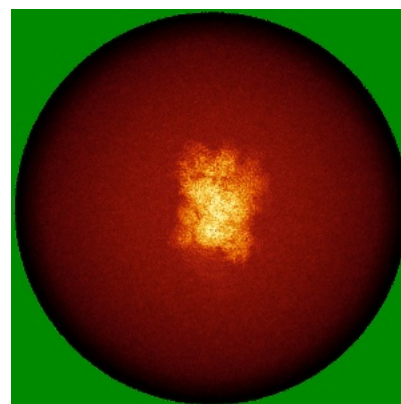
6.4.1 Primary map



X

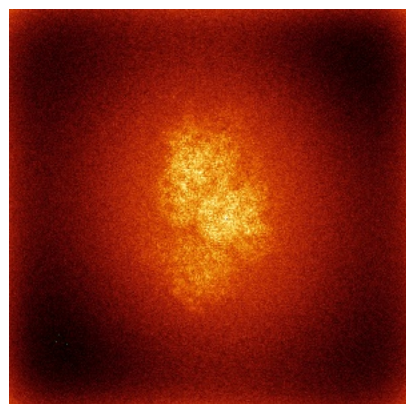


Y

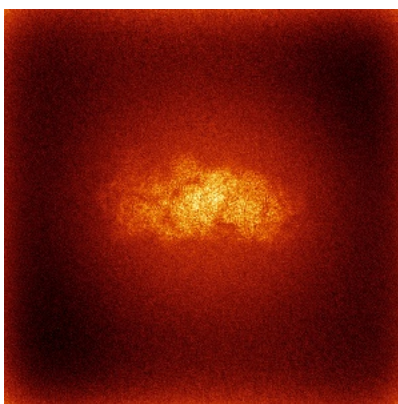


Z

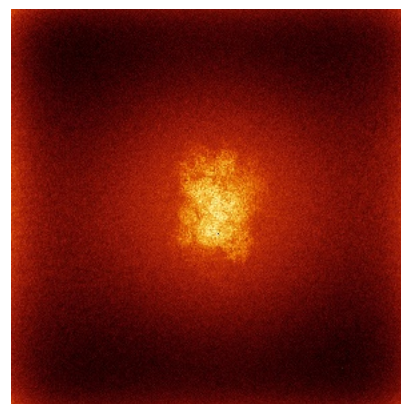
6.4.2 Raw map



X



Y

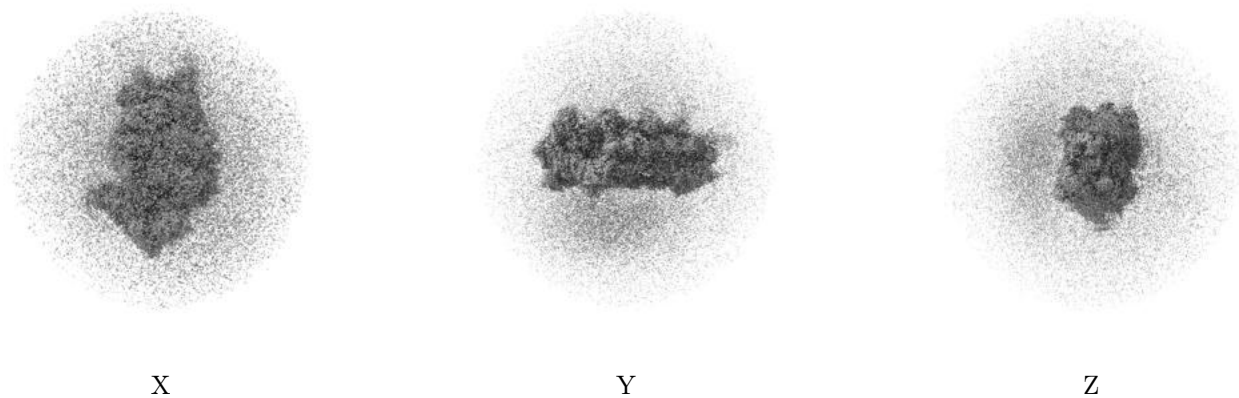


Z

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.

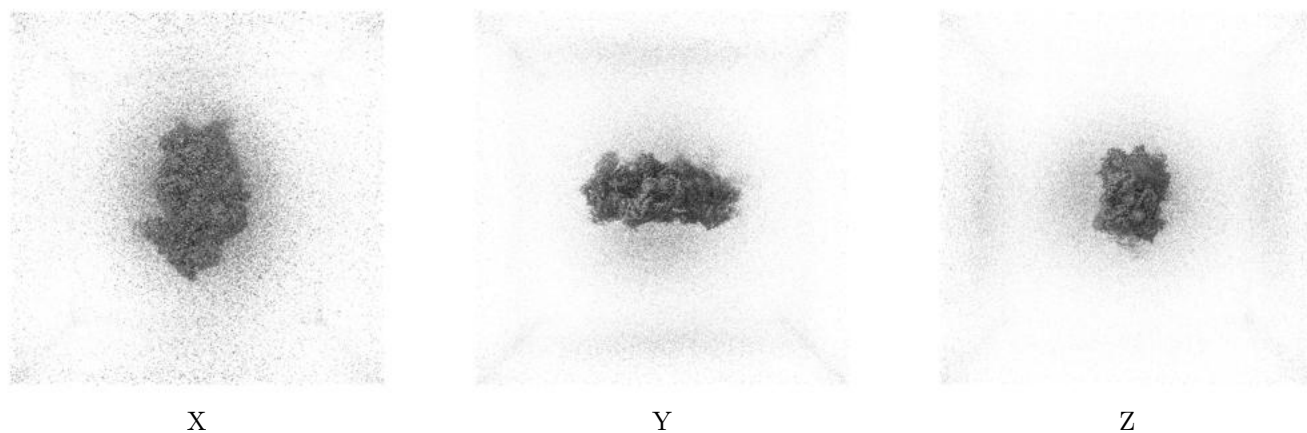
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.192. 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.

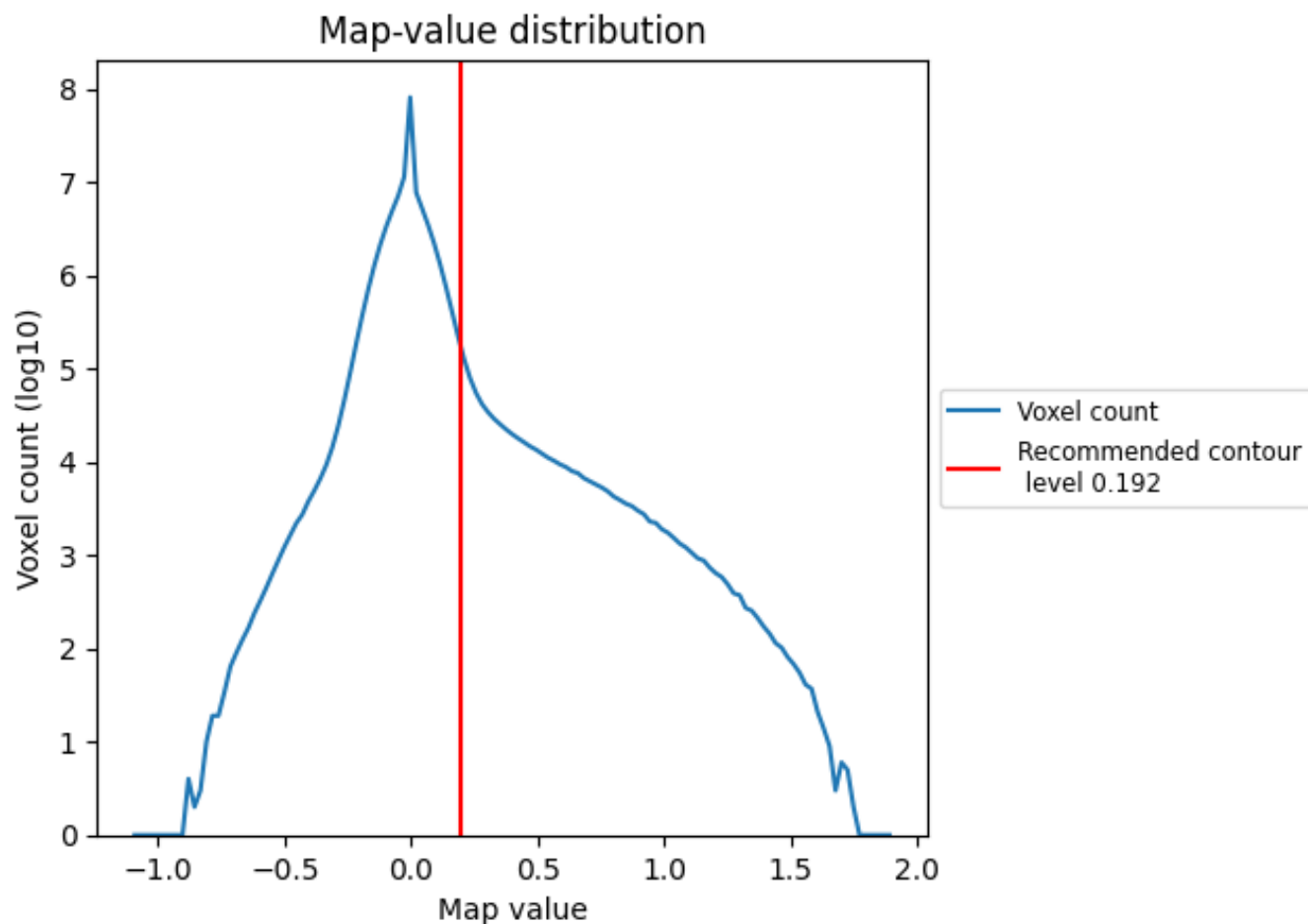
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

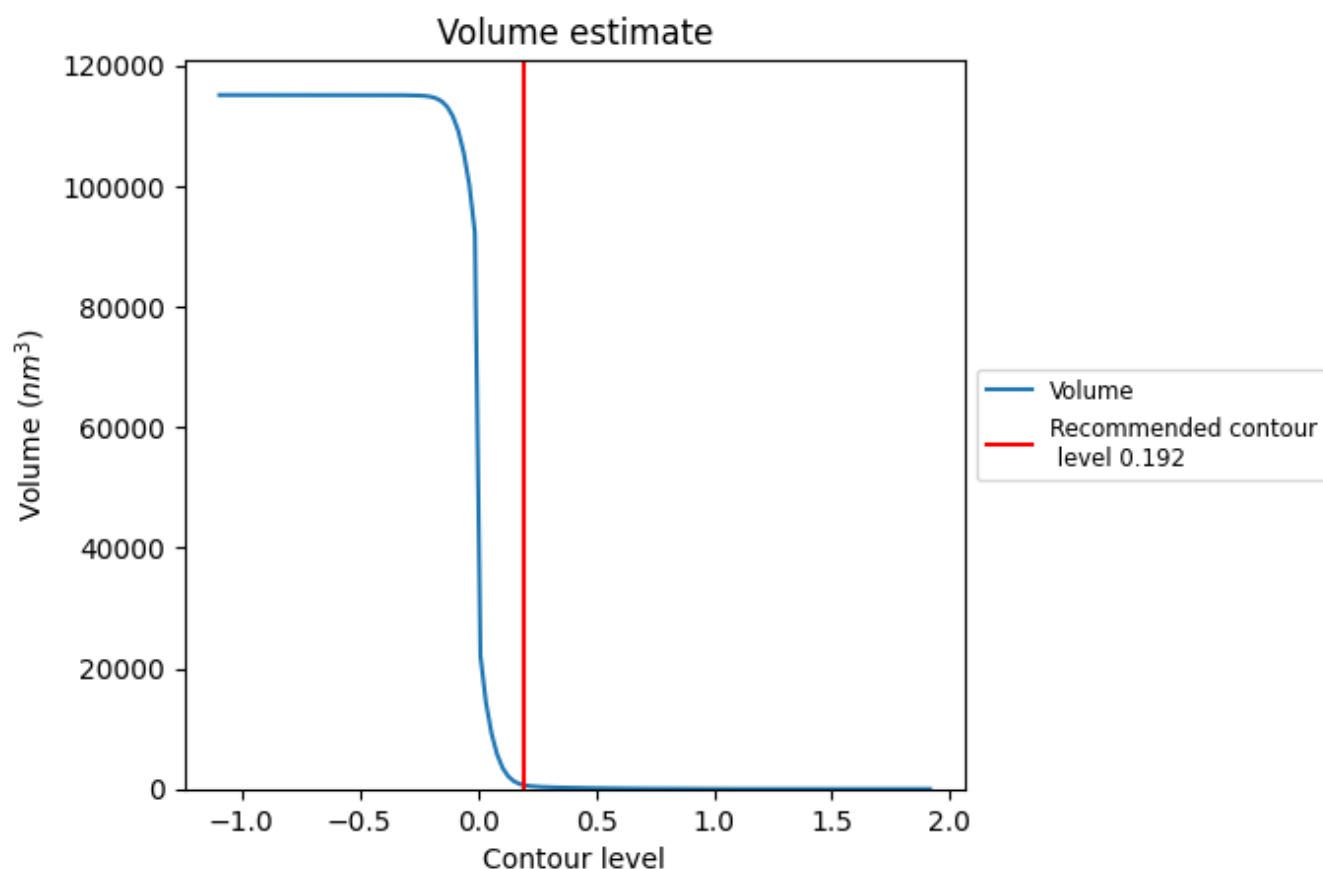
This section contains the results of statistical analysis of the map.

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.

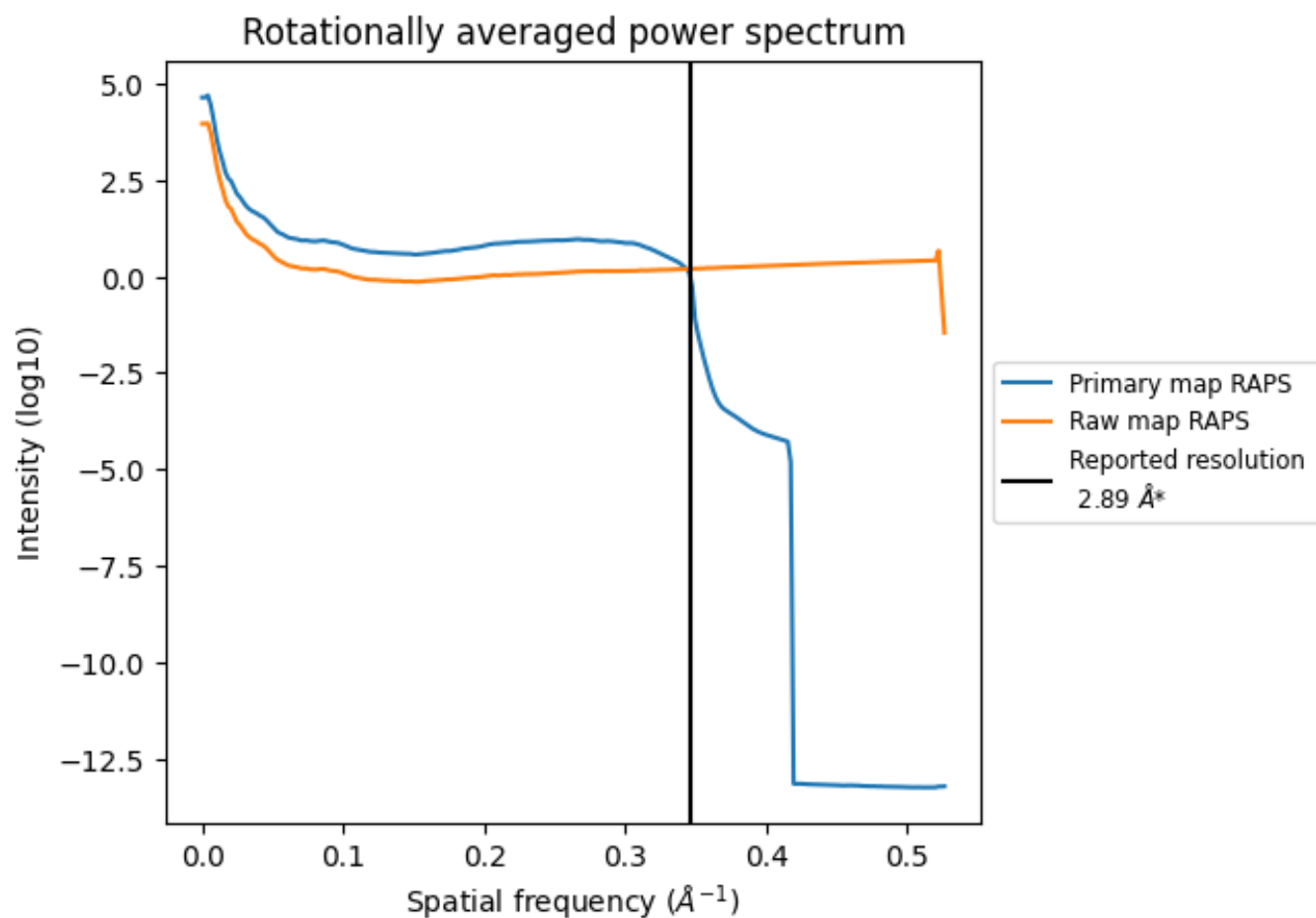
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 686 nm^3 ; this corresponds to an approximate mass of 619 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 ⓘ

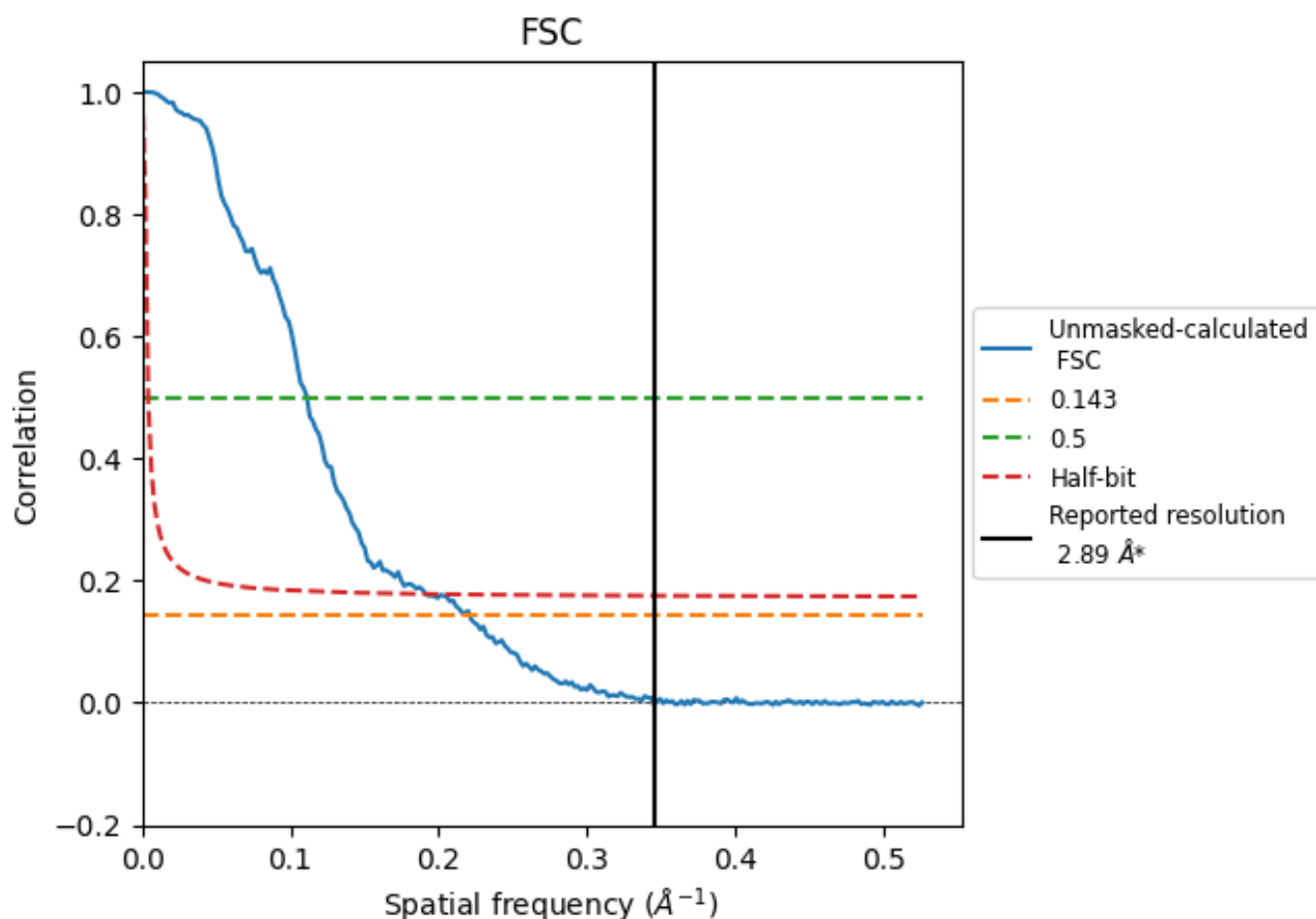


*Reported resolution corresponds to spatial frequency of 0.346 $\text{\AA}^{-1}$

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 0.346 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

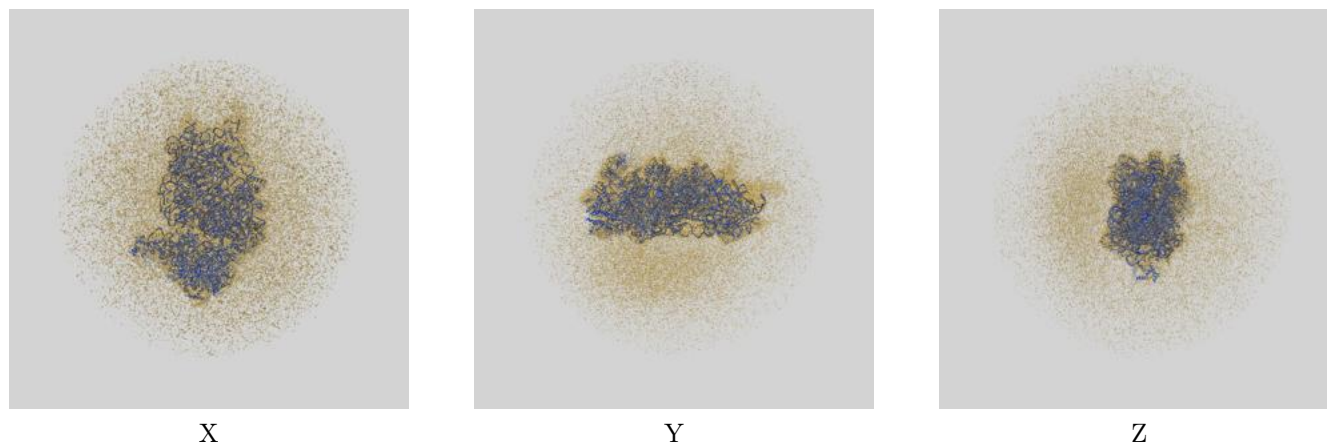
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.89	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.52	9.00	5.23

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.52 differs from the reported value 2.89 by more than 10 %

9 Map-model fit [i](#)

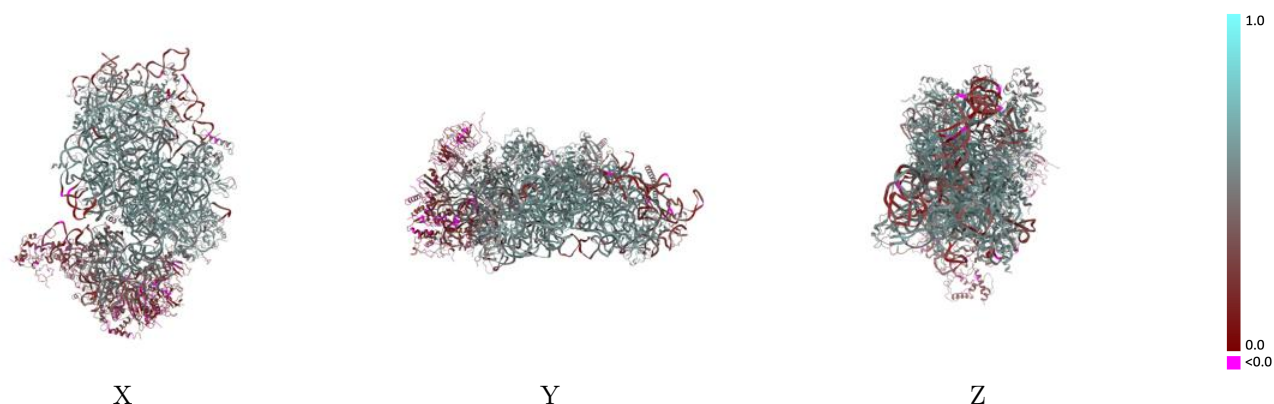
This section contains information regarding the fit between EMDB map EMD-62448 and PDB model 9KMX. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



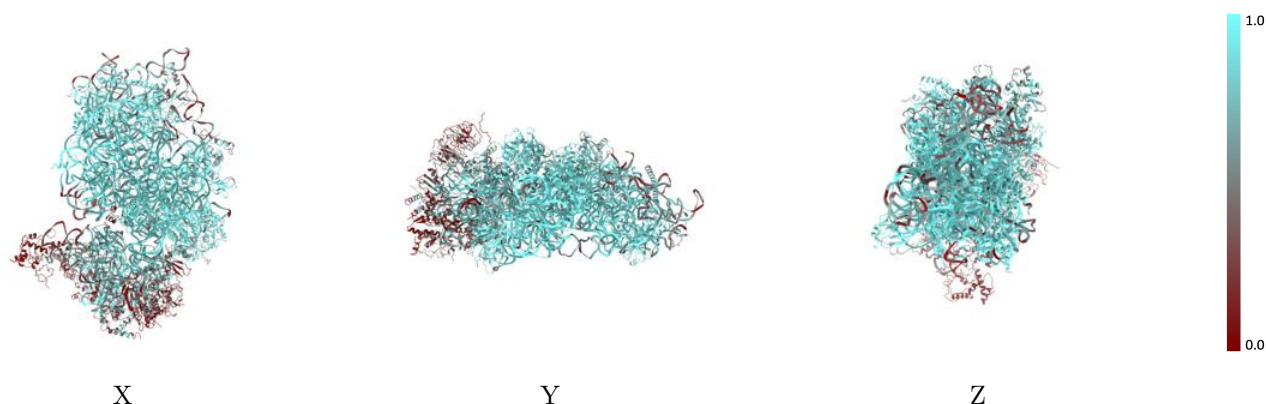
The images above show the 3D surface view of the map at the recommended contour level 0.192 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



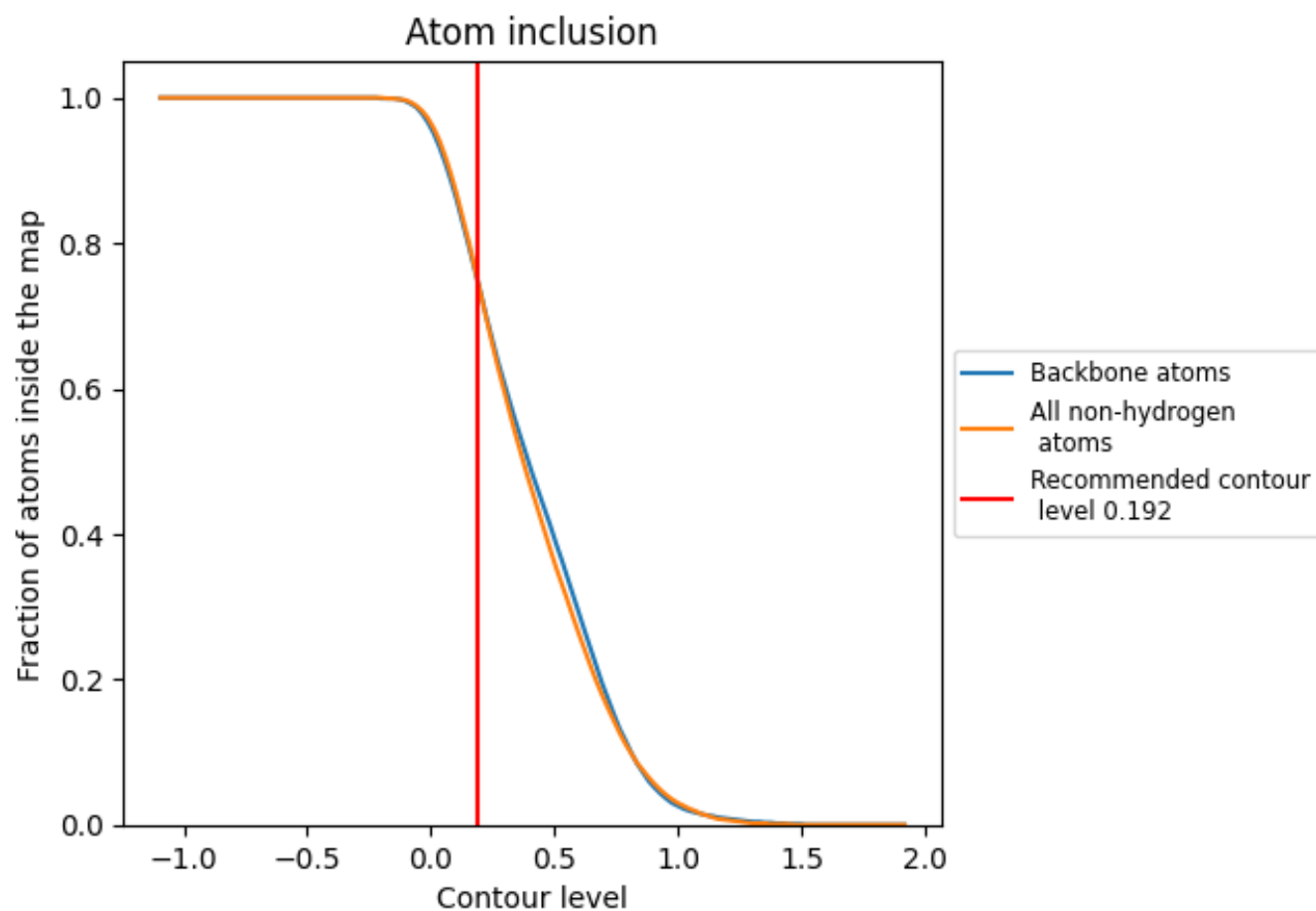
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.192).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 74% 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 (0.192) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7450	 0.4550
2	 0.8140	 0.4660
A	 0.9080	 0.5720
B	 0.8800	 0.5460
C	 0.9120	 0.5860
D	 0.6130	 0.4170
E	 0.9190	 0.5940
F	 0.3430	 0.2210
G	 0.8360	 0.5170
H	 0.7220	 0.4860
I	 0.8390	 0.5370
J	 0.9240	 0.5810
K	 0.3840	 0.2410
L	 0.8790	 0.5790
M	 0.1300	 0.2030
N	 0.9030	 0.5710
O	 0.8440	 0.5380
P	 0.2990	 0.2460
Q	 0.5260	 0.3220
R	 0.7370	 0.4870
S	 0.3410	 0.2170
T	 0.4570	 0.2110
U	 0.5900	 0.4230
V	 0.9120	 0.5780
W	 0.9380	 0.6030
X	 0.9210	 0.5910
Y	 0.9280	 0.5780
Z	 0.1930	 0.1680
a	 0.9130	 0.5770
b	 0.8430	 0.5350
c	 0.3670	 0.2510
d	 0.6920	 0.4500
e	 0.7730	 0.5360
f	 0.0740	 0.2130
g	 0.2620	 0.1920



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Chain	Atom inclusion	Q-score
h	 0.8510	 0.5620
n	 0.2690	 0.4310