



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 09:32 AM UTC

PDB ID : 6G5I / pdb_00006g5i
EMDB ID : EMD-4353
Title : Cryo-EM structure of a late human pre-40S ribosomal subunit - State R
Authors : Ameismeier, M.; Cheng, J.; Berninghausen, O.; Beckmann, R.
Deposited on : 2018-03-29
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

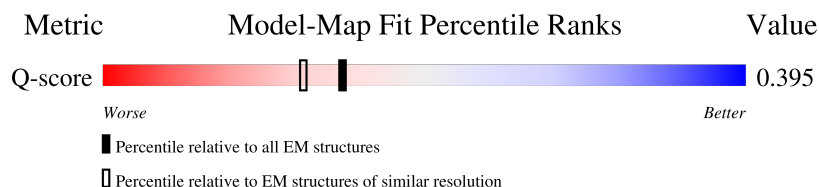
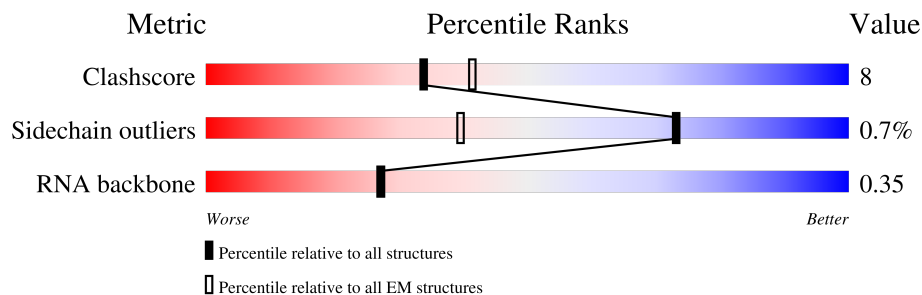
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	1882	
2	A	295	
3	B	264	
4	C	293	

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Mol	Chain	Length	Quality of chain
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	133	
27	Z	125	
28	b	84	
29	c	69	

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Mol	Chain	Length	Quality of chain
30	d	56	
31	e	59	
32	f	156	
33	g	317	
34	x	252	
35	y	412	
36	z	568	

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 77185 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	1657	Total	C	N	O	P	0	0
			35380	15792	6352	11579	1657		

- Molecule 2 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	216	Total	C	N	O	S	0	0
			1705	1083	299	315	8		

- Molecule 3 is a protein called 40S ribosomal protein S3a.

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 40S ribosomal protein S2.

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 40S ribosomal protein S3.

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 40S ribosomal protein S4, 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 40S ribosomal protein S5.

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 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	230	Total	C	N	O	S	0	0
			1862	1164	371	320	7		

- Molecule 9 is a protein called 40S ribosomal protein S7.

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 40S ribosomal protein S8.

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 40S ribosomal protein S9.

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 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	95	Total	C	N	O	S	0	0
			800	522	142	131	5		

- Molecule 13 is a protein called 40S ribosomal protein S11.

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 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	123	Total	C	N	O	S	0	0
			953	598	169	177	9		

- Molecule 15 is a protein called 40S ribosomal protein S13.

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 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	135	Total	C	N	O	S	0	0
			1009	618	198	187	6		

- Molecule 17 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	120	Total	C	N	O	S	0	0
			984	625	184	168	7		

- Molecule 18 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

- Molecule 19 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	122	Total	C	N	O	S	0	0
			990	621	184	182	3		

- Molecule 20 is a protein called 40S ribosomal protein S18.

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 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	144	Total	C	N	O	S	0	0
			1122	703	217	199	3		

- Molecule 22 is a protein called 40S ribosomal protein S20.

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 40S ribosomal protein S21.

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 40S ribosomal protein S15a.

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 40S ribosomal protein S23.

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 40S ribosomal protein S24.

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 40S ribosomal protein S25.

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 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 29 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	61	Total	C	N	O	S	0	0
			479	292	95	90	2		

- Molecule 30 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	55	Total	C	N	O	S	0	0
			458	286	94	73	5		

- Molecule 31 is a protein called 40S ribosomal protein S30.

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

- Molecule 32 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	63	Total	C	N	O	S	0	0
			510	320	97	86	7		

- Molecule 33 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

- Molecule 34 is a protein called RNA-binding protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	x	175	Total	C	N	O	S	0	0
			1365	878	249	234	4		

- Molecule 35 is a protein called RNA-binding protein NOB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	y	317	Total	C	N	O	S	0	0
			2490	1576	456	448	10		

- Molecule 36 is a protein called Serine/threonine-protein kinase RIO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	z	29	Total	C	N	O	S	0	0
			257	160	57	39	1		

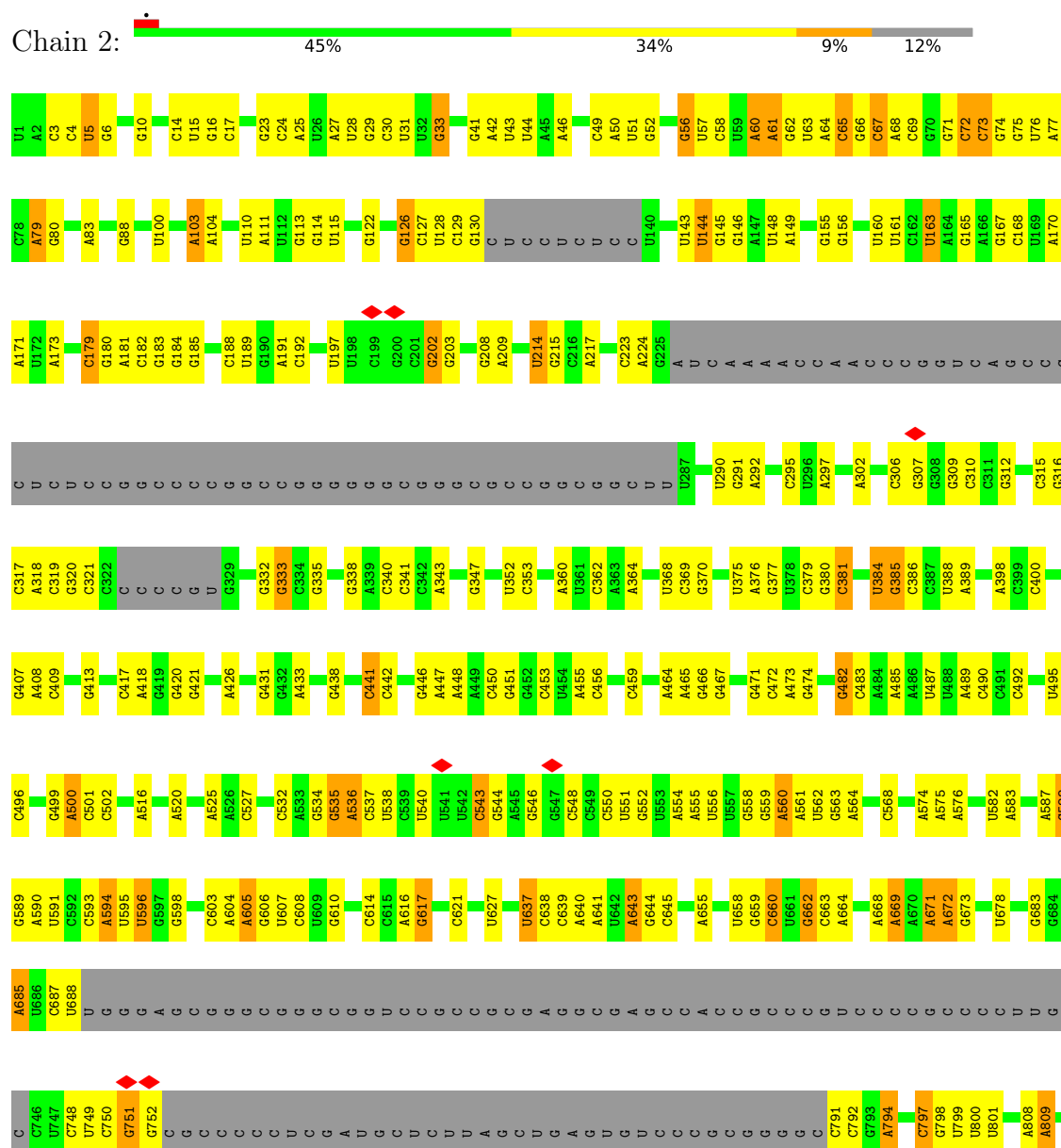
- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn).

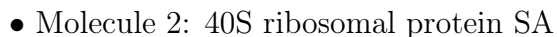
Mol	Chain	Residues	Atoms		AltConf
37	d	1	Total	Zn	0
			1	1	
37	f	1	Total	Zn	0
			1	1	
37	y	1	Total	Zn	0
			1	1	

3 Residue-property plots

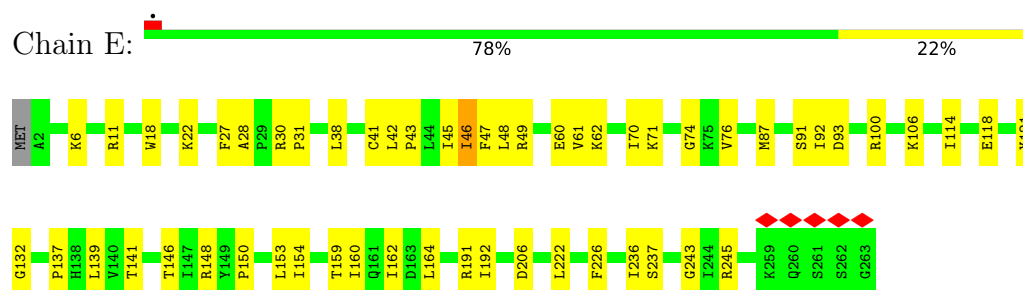
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

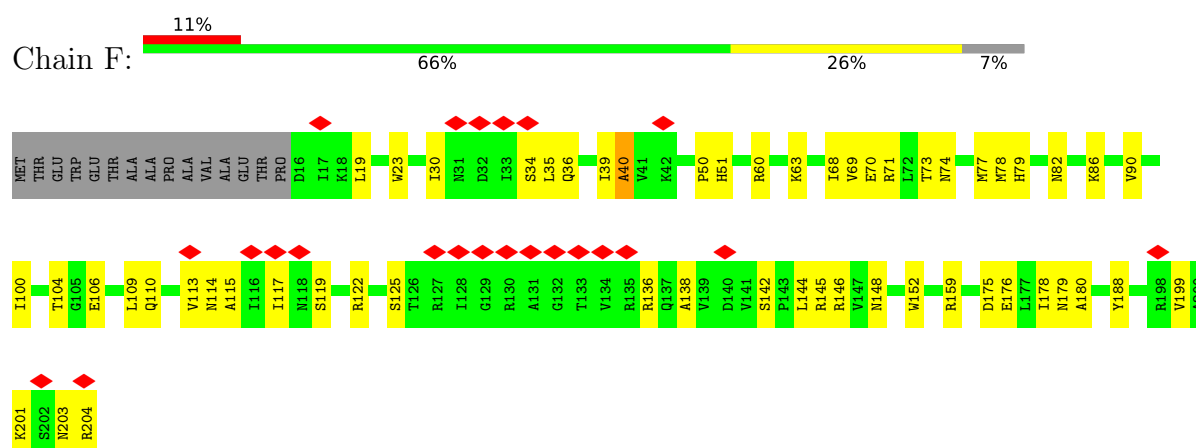




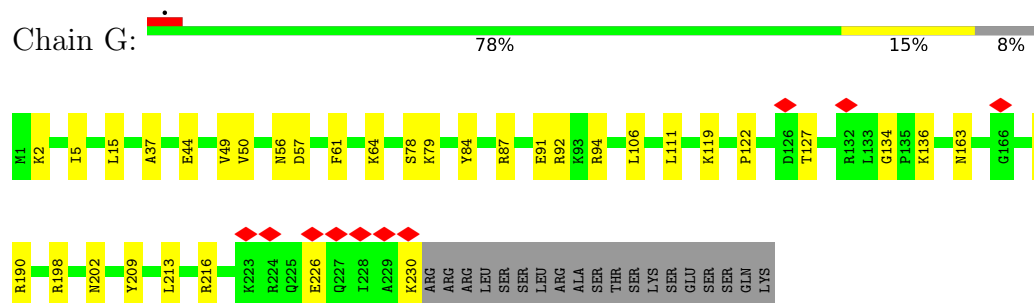
- Molecule 6: 40S ribosomal protein S4, X isoform



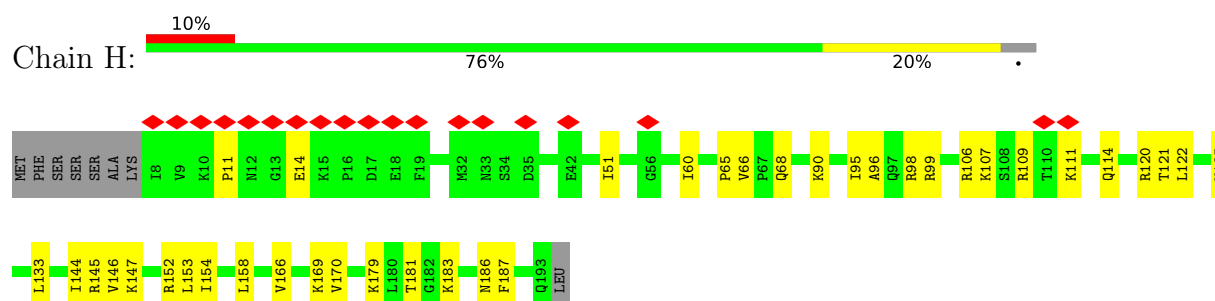
- Molecule 7: 40S ribosomal protein S5



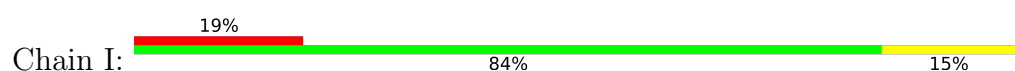
- Molecule 8: 40S ribosomal protein S6

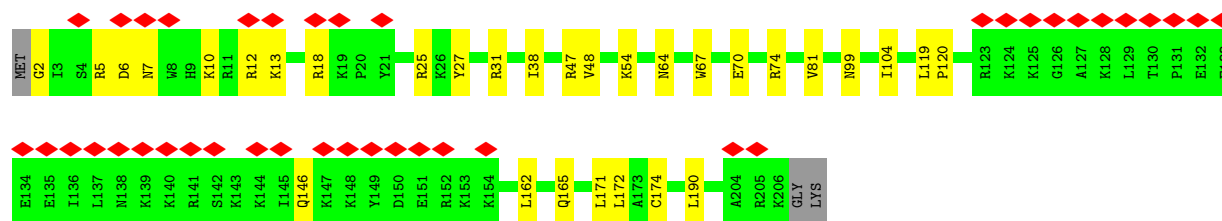


- Molecule 9: 40S ribosomal protein S7



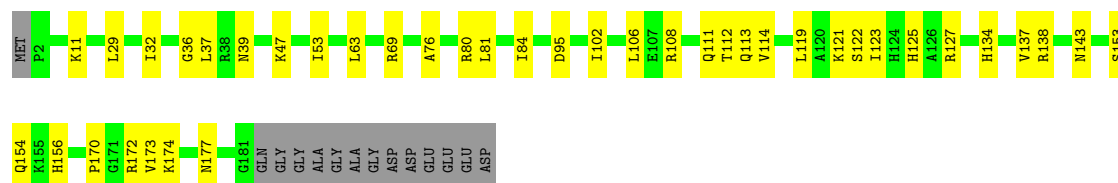
- Molecule 10: 40S ribosomal protein S8





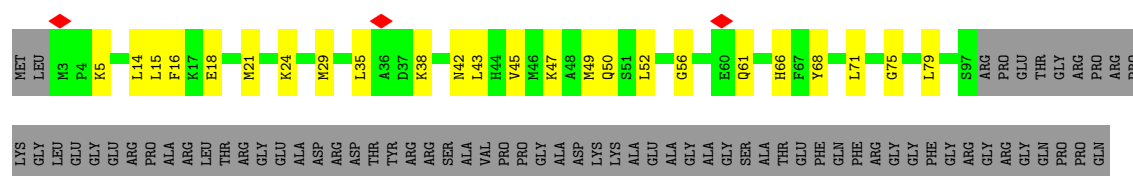
- Molecule 11: 40S ribosomal protein S9

Chain J: 72% 21% 7%



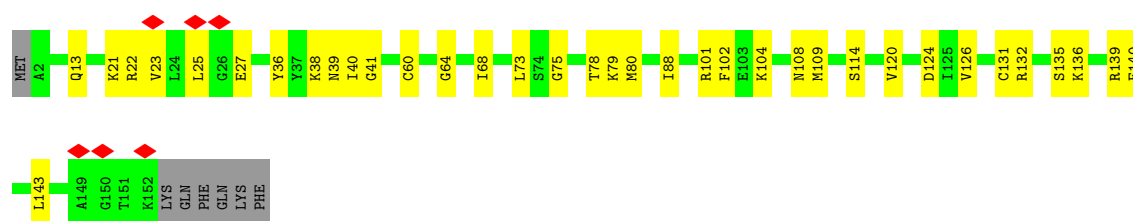
- Molecule 12: 40S ribosomal protein S10

Chain K: 43% 15% 42%



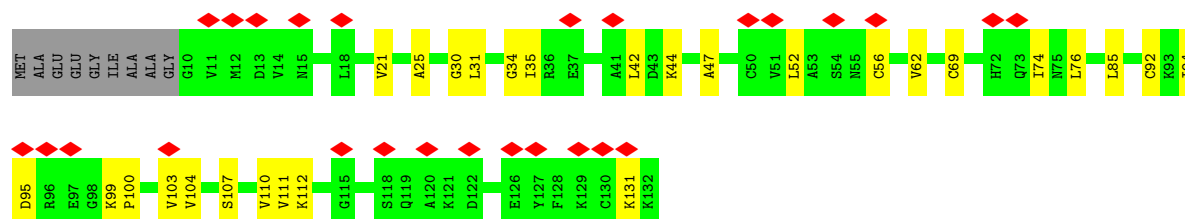
- Molecule 13: 40S ribosomal protein S11

Chain L: 73% 23% 4%



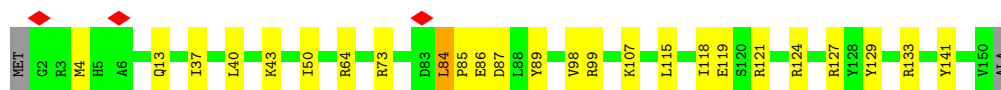
- Molecule 14: 40S ribosomal protein S12

Chain M: 20% 72% 21% 7%



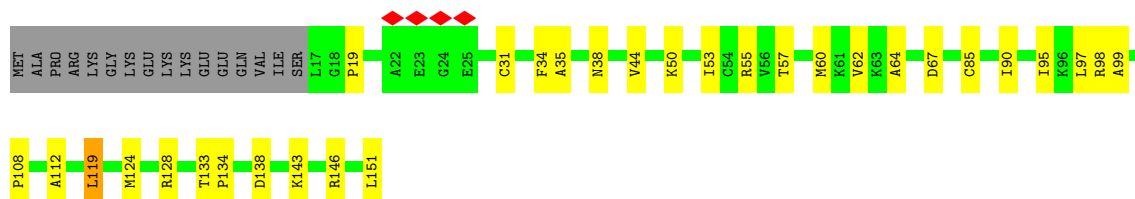
- Molecule 15: 40S ribosomal protein S13

Chain N:  82% 16% ..



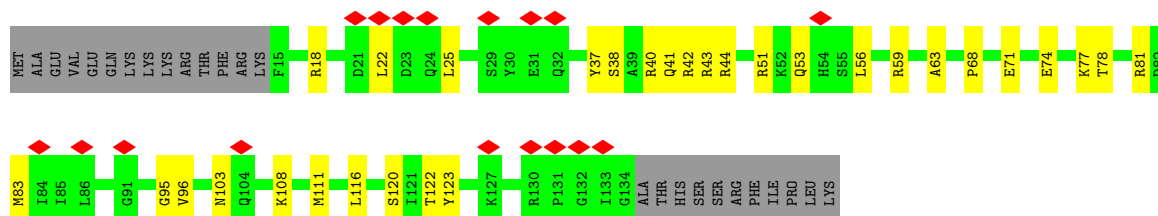
- Molecule 16: 40S ribosomal protein S14

Chain O:  69% 20% 11%



- Molecule 17: 40S ribosomal protein S15

Chain P:  12% 61% 21% 17%



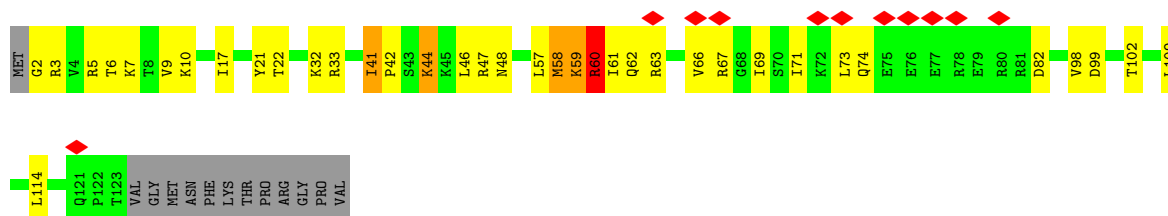
- Molecule 18: 40S ribosomal protein S16

Chain Q:  77% 18% 5%

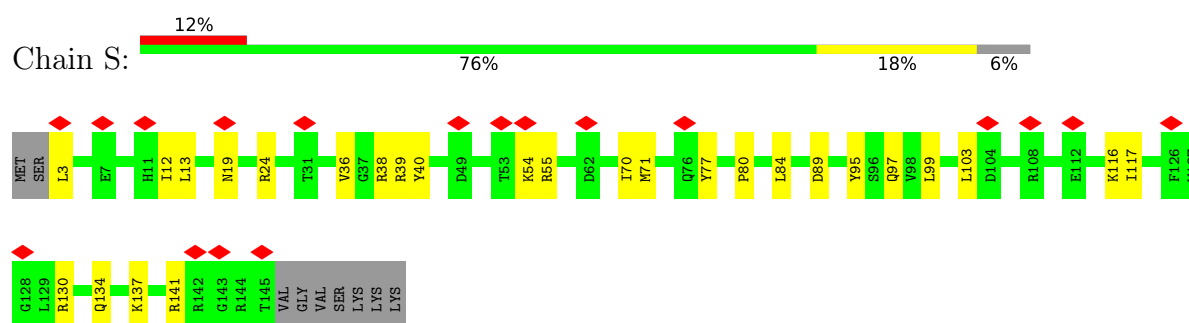


- Molecule 19: 40S ribosomal protein S17

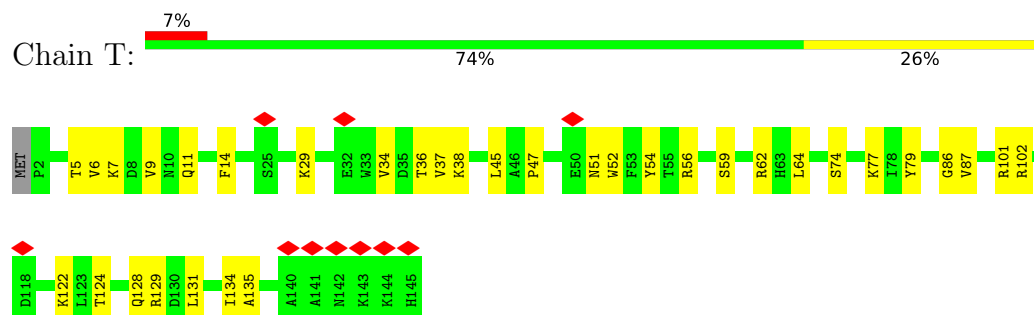
Chain R:  8% 63% 24% 10%



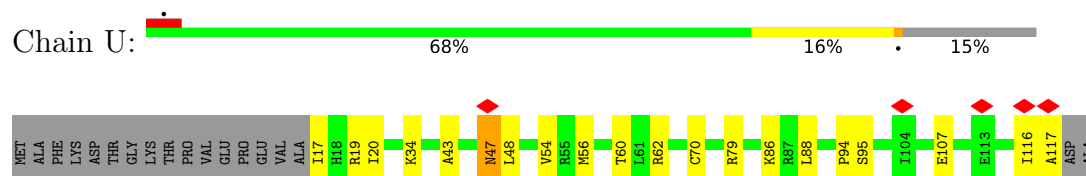
- Molecule 20: 40S ribosomal protein S18



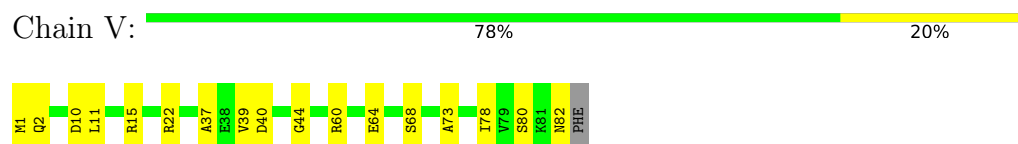
- Molecule 21: 40S ribosomal protein S19



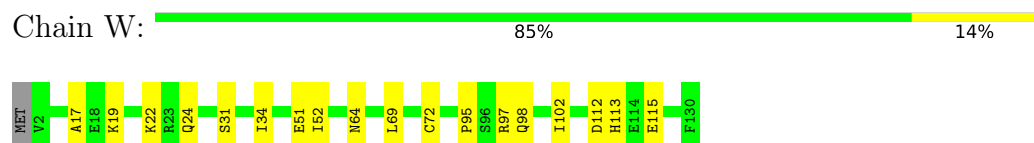
- Molecule 22: 40S ribosomal protein S20



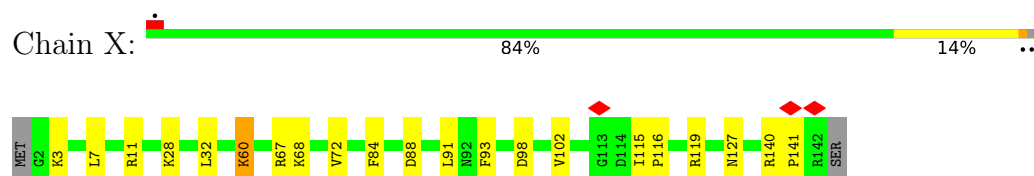
- Molecule 23: 40S ribosomal protein S21



- Molecule 24: 40S ribosomal protein S15a



- Molecule 25: 40S ribosomal protein S23

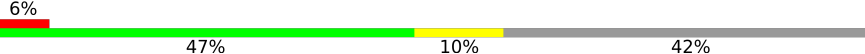


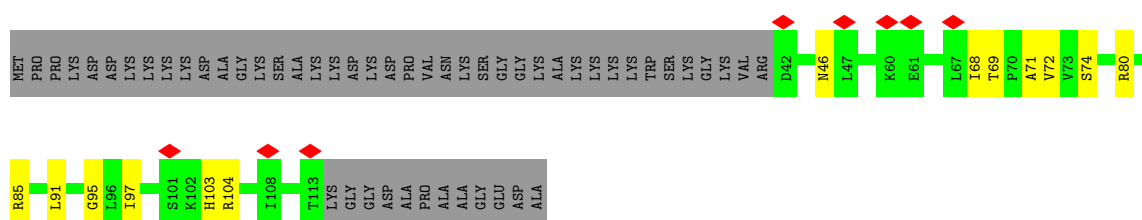
- Molecule 26: 40S ribosomal protein S24

Chain Y:  77% 14% 7%



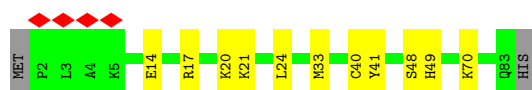
- Molecule 27: 40S ribosomal protein S25

Chain Z:  6% 47% 10% 42%



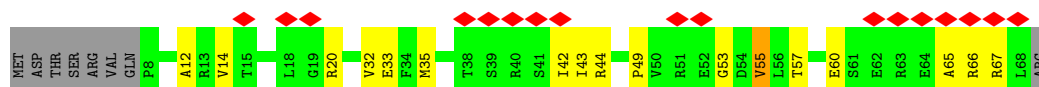
- Molecule 28: 40S ribosomal protein S27

Chain b:  5% 85% 13%



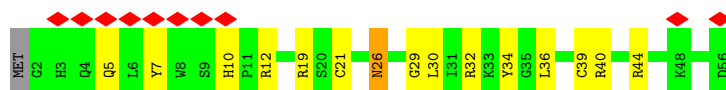
- Molecule 29: 40S ribosomal protein S28

Chain c:  25% 64% 23% 12%



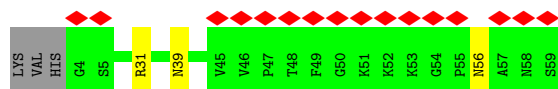
- Molecule 30: 40S ribosomal protein S29

Chain d:  18% 71% 25%

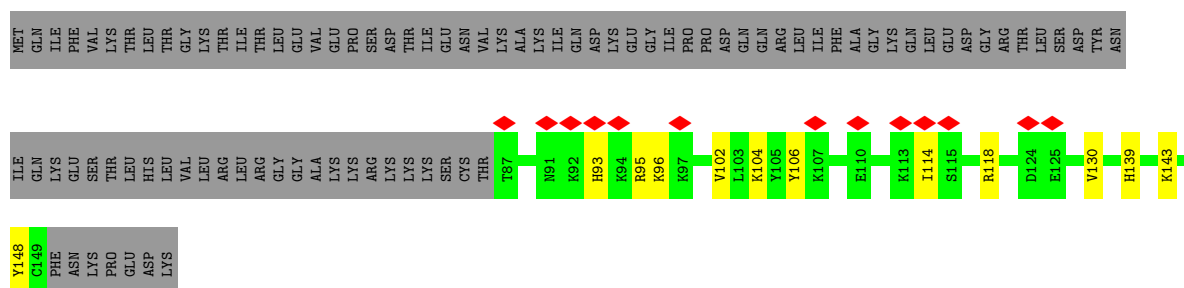


- Molecule 31: 40S ribosomal protein S30

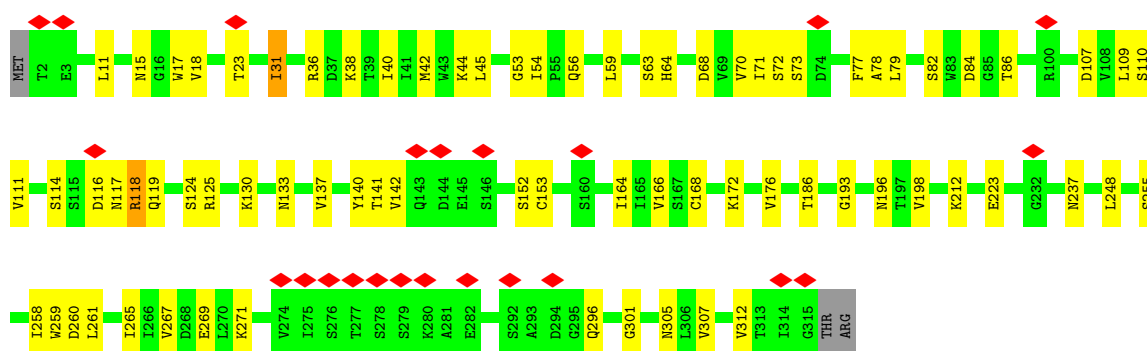
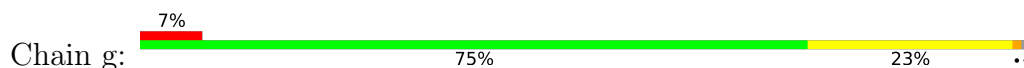
Chain e:  27% 90% 5% 5%



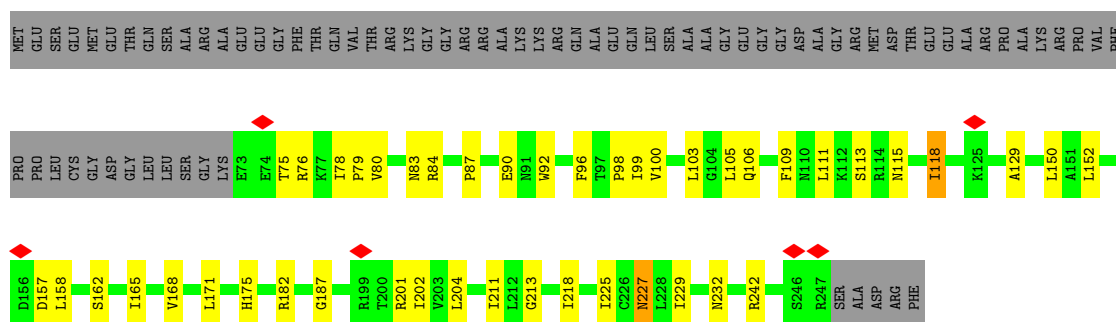
- Molecule 32: Ribosomal protein S27a



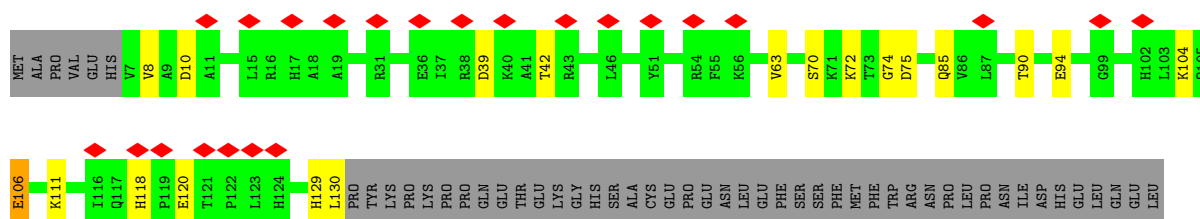
• Molecule 33: Receptor of activated protein C kinase 1

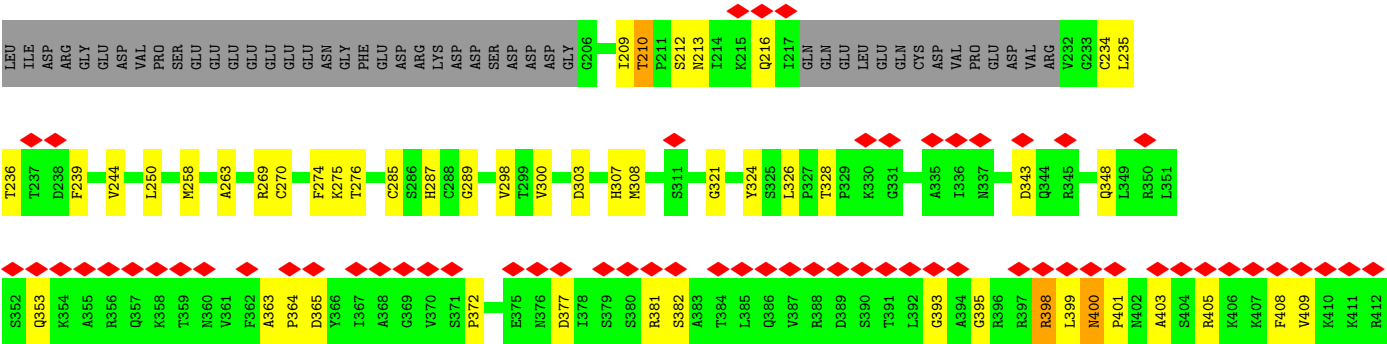


• Molecule 34: RNA-binding protein PNO1

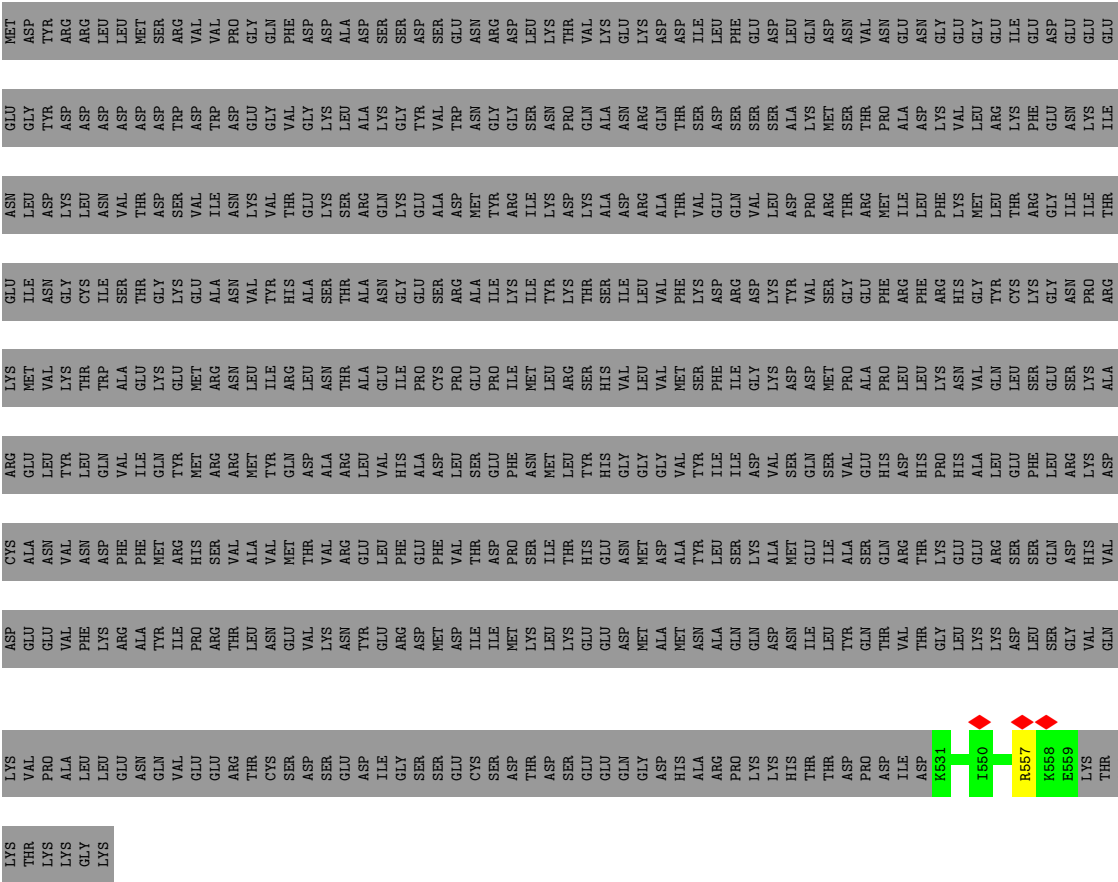


• Molecule 35: RNA-binding protein NOB1





● Molecule 36: Serine/threonine-protein kinase RIO1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83883	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.194	Depositor
Minimum map value	-0.068	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	390.24, 390.24, 390.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.45	0/39560	0.56	4/61645 (0.0%)
2	A	0.54	0/1742	0.83	2/2367 (0.1%)
3	B	0.44	0/1756	0.79	0/2350
4	C	0.53	0/1726	0.82	1/2332 (0.0%)
5	D	0.37	0/1780	0.82	0/2397
6	E	0.54	0/2118	0.81	0/2849
7	F	0.35	0/1516	0.86	1/2037 (0.0%)
8	G	0.39	0/1885	0.75	0/2510
9	H	0.36	0/1524	0.78	0/2042
10	I	0.41	0/1711	0.73	0/2282
11	J	0.54	0/1524	0.85	2/2035 (0.1%)
12	K	0.33	0/824	0.76	0/1112
13	L	0.54	0/1250	0.73	0/1673
14	M	0.32	0/963	0.78	2/1291 (0.2%)
15	N	0.47	0/1226	0.84	0/1649
16	O	0.41	0/1022	0.76	0/1372
17	P	0.32	0/1003	0.67	0/1341
18	Q	0.40	0/1126	0.85	0/1506
19	R	0.40	0/1002	0.89	3/1345 (0.2%)
20	S	0.30	0/1202	0.69	0/1610
21	T	0.33	0/1142	0.79	0/1530
22	U	0.39	0/813	0.83	0/1092
23	V	0.46	0/631	0.68	0/844
24	W	0.63	0/1051	0.85	0/1406
25	X	0.50	0/1116	0.83	0/1490
26	Y	0.47	0/1031	0.82	1/1370 (0.1%)
27	Z	0.32	0/580	0.76	0/780
28	b	0.40	0/653	0.78	0/876
29	c	0.33	0/481	0.79	0/643
30	d	0.38	0/469	0.69	0/623
31	e	0.38	0/447	0.72	0/587
32	f	0.29	0/520	0.67	0/690

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.32	0/2497	0.72	2/3399 (0.1%)
34	x	0.41	0/1387	0.85	0/1871
35	y	0.36	0/2539	0.74	0/3430
36	z	0.34	0/258	0.81	0/331
All	All	0.44	0/82075	0.68	18/118707 (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
2	A	0	1
5	D	0	1
7	F	0	2
13	L	0	1
20	S	0	1
25	X	0	2
26	Y	0	1
29	c	0	1
33	g	0	2
34	x	0	2
35	y	0	3
All	All	0	17

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	R	44	LYS	N-CA-C	11.07	124.72	111.33
26	Y	119	GLY	N-CA-C	8.18	122.54	112.73
19	R	60	ARG	CA-C-N	8.00	131.42	120.46
19	R	60	ARG	C-N-CA	8.00	131.42	120.46
11	J	137	VAL	CA-C-N	6.66	134.26	121.54
11	J	137	VAL	C-N-CA	6.66	134.26	121.54
2	A	184	ARG	CA-C-N	6.40	128.85	120.28
2	A	184	ARG	C-N-CA	6.40	128.85	120.28
14	M	44	LYS	CA-C-N	5.89	130.74	122.08
14	M	44	LYS	C-N-CA	5.89	130.74	122.08
7	F	122	ARG	N-CA-C	-5.66	106.25	114.12
1	2	1601	A	P-O3'-C3'	5.55	128.52	120.20
4	C	132	ASP	N-CA-C	-5.22	102.14	109.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	g	118	ARG	CA-C-N	5.16	131.39	121.54
33	g	118	ARG	C-N-CA	5.16	131.39	121.54
1	2	1403	C	P-O3'-C3'	5.10	127.85	120.20
1	2	1865	C	C1'-C2'-O2'	-5.09	100.77	108.40
1	2	1316	C	P-O3'-C3'	5.07	127.81	120.20

There are no chirality outliers.

All (17) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	189	ILE	Peptide
5	D	194	PRO	Peptide
7	F	138	ALA	Peptide
7	F	40	ALA	Peptide
13	L	41	GLY	Peptide
20	S	80	PRO	Peptide
25	X	127	ASN	Peptide
25	X	60	LYS	Peptide
26	Y	29	HIS	Peptide
29	c	35	MET	Peptide
33	g	259	TRP	Peptide
33	g	31	ILE	Peptide
34	x	113	SER	Peptide
34	x	162	SER	Peptide
35	y	106	GLU	Peptide
35	y	210	THR	Peptide
35	y	365	ASP	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	35380	0	17863	426	0
2	A	1705	0	1706	43	0
3	B	1729	0	1803	32	0
4	C	1690	0	1777	63	0
5	D	1752	0	1848	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	E	2076	0	2177	39	0
7	F	1495	0	1549	42	0
8	G	1862	0	2018	28	0
9	H	1501	0	1593	24	0
10	I	1682	0	1769	25	0
11	J	1499	0	1618	27	0
12	K	800	0	818	20	0
13	L	1229	0	1302	24	0
14	M	953	0	990	19	0
15	N	1202	0	1289	20	0
16	O	1009	0	1034	26	0
17	P	984	0	1028	28	0
18	Q	1109	0	1174	19	0
19	R	990	0	1037	80	0
20	S	1184	0	1244	22	0
21	T	1122	0	1153	29	0
22	U	803	0	873	13	0
23	V	625	0	628	14	0
24	W	1034	0	1080	13	0
25	X	1098	0	1167	16	0
26	Y	1014	0	1082	14	0
27	Z	574	0	627	12	0
28	b	640	0	665	7	0
29	c	479	0	507	16	0
30	d	458	0	448	12	0
31	e	442	0	487	3	0
32	f	510	0	521	9	0
33	g	2440	0	2396	46	0
34	x	1365	0	1447	43	0
35	y	2490	0	2543	66	0
36	z	257	0	302	1	0
37	d	1	0	0	0	0
37	f	1	0	0	0	0
37	y	1	0	0	0	0
All	All	77185	0	61563	1095	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 8.

All (1095) 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)
19:R:66:VAL:CG1	19:R:69:ILE:HG12	1.23	1.65
19:R:66:VAL:HG12	19:R:69:ILE:CG1	1.32	1.53
19:R:66:VAL:HG12	19:R:69:ILE:CD1	1.41	1.50
19:R:66:VAL:CG1	19:R:69:ILE:CG1	1.86	1.43
4:C:103:LYS:HD2	4:C:133:TYR:CE2	1.60	1.36
4:C:102:LEU:CD2	4:C:130:ILE:HD11	1.63	1.28
19:R:66:VAL:HG11	19:R:69:ILE:CG2	1.74	1.17
1:2:1867:U:OP1	35:y:393:GLY:N	1.82	1.10
19:R:66:VAL:CG1	19:R:69:ILE:CD1	2.22	1.10
4:C:103:LYS:CD	4:C:133:TYR:HE2	1.67	1.06
19:R:32:LYS:HG2	19:R:47:ARG:NH2	1.70	1.06
4:C:102:LEU:HD21	4:C:130:ILE:HD11	1.06	1.04
19:R:66:VAL:HG13	19:R:69:ILE:HG12	1.08	1.03
1:2:1709:G:N1	1:2:1824:A:C2	2.29	1.01
35:y:324:TYR:CG	35:y:401:PRO:HG2	1.96	1.01
1:2:1215:C:H42	1:2:1220:A:N6	1.59	1.01
4:C:103:LYS:HD2	4:C:133:TYR:HE2	0.93	1.01
4:C:102:LEU:HD21	4:C:130:ILE:CD1	1.90	1.00
1:2:1206:G:H1	1:2:1692:U:H3	1.10	1.00
1:2:1869:A:O2'	35:y:118:HIS:NE2	1.95	0.99
35:y:324:TYR:CB	35:y:401:PRO:HG2	1.91	0.99
19:R:58:MET:HE2	19:R:58:MET:HA	1.43	0.99
1:2:1260:A:H61	1:2:1617:G:H21	1.09	0.97
1:2:1606:G:N2	1:2:1633:A:N7	2.13	0.97
19:R:66:VAL:CG1	19:R:69:ILE:CG2	2.44	0.96
1:2:1260:A:N6	1:2:1617:G:H21	1.65	0.95
19:R:21:TYR:HE1	19:R:58:MET:HE1	1.30	0.95
1:2:1566:G:N2	1:2:1569:A:C5	2.36	0.93
1:2:185:G:H1	1:2:214:U:H3	1.05	0.93
1:2:885:U:H3	1:2:901:G:H1	1.18	0.92
19:R:66:VAL:CG1	19:R:69:ILE:HD13	2.00	0.91
19:R:66:VAL:HG11	19:R:69:ILE:HG23	1.50	0.91
1:2:1215:C:N4	1:2:1220:A:H61	1.68	0.91
1:2:1215:C:H42	1:2:1220:A:H61	0.90	0.90
35:y:72:LYS:NZ	35:y:106:GLU:OE2	2.04	0.90
1:2:925:G:H1	1:2:1017:U:H3	0.93	0.90
4:C:102:LEU:CG	4:C:130:ILE:HD11	2.01	0.89
1:2:1271:C:H42	1:2:1511:U:H3	1.18	0.89
19:R:66:VAL:HG12	19:R:69:ILE:HD13	1.53	0.89
19:R:66:VAL:HG11	19:R:69:ILE:HG21	1.55	0.89
1:2:1232:U:H3	1:2:1526:G:H1	1.19	0.88
19:R:59:LYS:HZ1	19:R:63:ARG:HG2	1.35	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:58:MET:HA	19:R:58:MET:CE	2.02	0.88
1:2:1656:G:H1	1:2:1668:U:H3	1.22	0.87
1:2:1865:C:N3	34:x:204:LEU:HB2	1.90	0.87
19:R:21:TYR:CE1	19:R:58:MET:HE1	2.11	0.85
19:R:66:VAL:CG1	19:R:69:ILE:HG23	2.06	0.85
19:R:60:ARG:CZ	19:R:60:ARG:HA	2.07	0.84
19:R:67:ARG:HG3	19:R:67:ARG:HH11	1.40	0.84
19:R:32:LYS:CD	19:R:47:ARG:HH22	1.91	0.84
19:R:66:VAL:HG12	19:R:69:ILE:HD11	1.59	0.83
19:R:32:LYS:CG	19:R:47:ARG:HH22	1.91	0.83
1:2:197:U:H3	1:2:202:G:H1	0.83	0.83
4:C:102:LEU:CD2	4:C:130:ILE:CD1	2.50	0.83
4:C:133:TYR:CD1	4:C:215:MET:O	2.32	0.82
19:R:32:LYS:HE3	19:R:47:ARG:HH22	1.44	0.81
19:R:66:VAL:CG1	19:R:69:ILE:CB	2.58	0.80
1:2:1335:G:H1	1:2:1492:U:H3	1.25	0.80
1:2:1652:G:H1	1:2:1672:U:H3	1.26	0.80
1:2:146:G:H1	1:2:173:A:H61	1.29	0.80
19:R:32:LYS:CE	19:R:47:ARG:HH22	1.95	0.80
1:2:1260:A:H61	1:2:1617:G:N2	1.79	0.79
1:2:1605:G:H21	1:2:1634:A:H62	1.27	0.79
7:F:146:ARG:HH22	29:c:57:THR:H	1.30	0.78
1:2:1864:U:H2'	35:y:409:VAL:HG12	1.65	0.77
19:R:66:VAL:HG12	19:R:69:ILE:HG12	1.01	0.76
4:C:133:TYR:CE1	4:C:216:MET:HA	2.21	0.75
1:2:1143:A:H5'	4:C:190:SER:HB3	1.69	0.74
33:g:17:TRP:HB2	33:g:36:ARG:HD3	1.70	0.74
1:2:16:G:H21	1:2:1195:A:H62	1.34	0.73
7:F:78:MET:HB3	7:F:159:ARG:HH22	1.54	0.72
4:C:103:LYS:CD	4:C:133:TYR:CE2	2.50	0.72
19:R:67:ARG:HG3	19:R:67:ARG:NH1	2.03	0.72
4:C:104:ASP:OD1	4:C:104:ASP:N	2.20	0.72
4:C:103:LYS:HD2	4:C:133:TYR:CD2	2.24	0.71
4:C:133:TYR:HD1	4:C:215:MET:O	1.73	0.71
4:C:133:TYR:CD1	4:C:216:MET:HA	2.25	0.70
19:R:32:LYS:HG2	19:R:47:ARG:HH22	1.44	0.69
1:2:1271:C:N4	1:2:1511:U:H3	1.89	0.69
2:A:81:ASN:HA	2:A:84:GLN:HG2	1.75	0.68
8:G:209:TYR:O	8:G:213:LEU:HB3	1.92	0.68
19:R:32:LYS:HE3	19:R:47:ARG:HH12	1.58	0.68
1:2:1867:U:OP2	35:y:393:GLY:HA2	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1602:U:H4'	20:S:24:ARG:HH12	1.57	0.68
1:2:1868:U:OP1	34:x:87:PRO:HG3	1.92	0.68
19:R:32:LYS:HE3	19:R:47:ARG:NH2	2.07	0.68
33:g:260:ASP:HB3	33:g:265:ILE:HB	1.76	0.68
19:R:58:MET:HE3	19:R:61:ILE:HD12	1.76	0.68
1:2:1222:G:H5''	7:F:78:MET:HE3	1.76	0.68
2:A:38:ILE:HD11	2:A:47:TYR:HB3	1.76	0.68
1:2:1867:U:P	35:y:393:GLY:HA2	2.35	0.67
23:V:73:ALA:HB1	23:V:78:ILE:HB	1.77	0.67
1:2:155:G:H21	8:G:56:ASN:HD21	1.41	0.67
1:2:1758:G:C2	1:2:1775:U:O2	2.48	0.67
14:M:52:LEU:HD11	14:M:62:VAL:HG13	1.76	0.67
1:2:1867:U:OP1	35:y:393:GLY:CA	2.43	0.66
7:F:145:ARG:HB2	29:c:49:PRO:HD2	1.76	0.66
1:2:918:U:H5''	15:N:64:ARG:HH22	1.60	0.66
1:2:1567:G:OP1	1:2:1568:C:N4	2.29	0.66
3:B:82:ARG:NH1	3:B:188:LEU:O	2.28	0.66
2:A:130:ASP:OD1	2:A:130:ASP:N	2.29	0.66
1:2:991:G:N2	35:y:403:ALA:O	2.29	0.66
19:R:5:ARG:HB2	19:R:10:LYS:HE3	1.78	0.66
1:2:1865:C:OP1	34:x:187:GLY:HA2	1.96	0.66
23:V:40:ASP:HB2	23:V:44:GLY:H	1.59	0.65
5:D:26:THR:O	5:D:30:ALA:HB2	1.97	0.65
10:I:99:ASN:ND2	10:I:174:CYS:SG	2.70	0.65
2:A:80:ARG:NH2	2:A:165:ASN:O	2.30	0.65
16:O:85:CYS:HB3	16:O:90:ILE:HB	1.77	0.65
1:2:1285:G:H22	14:M:56:CYS:HA	1.62	0.65
5:D:98:ALA:HB2	5:D:188:ILE:HG12	1.79	0.65
4:C:133:TYR:CE1	4:C:215:MET:O	2.49	0.65
1:2:1373:C:O2'	19:R:10:LYS:NZ	2.30	0.65
1:2:1679:A:OP1	29:c:20:ARG:NH2	2.30	0.64
27:Z:69:THR:HB	27:Z:72:VAL:H	1.62	0.64
2:A:212:LYS:O	2:A:216:ALA:HB3	1.98	0.64
14:M:25:ALA:HA	14:M:30:GLY:H	1.62	0.64
1:2:1608:U:O4	1:2:1632:G:N2	2.31	0.64
3:B:90:ASP:HB2	3:B:97:LEU:HB2	1.79	0.63
1:2:126:G:OP1	8:G:198:ARG:NH1	2.31	0.63
1:2:1466:G:OP2	19:R:5:ARG:NH1	2.31	0.63
6:E:31:PRO:HG3	6:E:43:PRO:HG3	1.80	0.63
1:2:1454:A:H5'	19:R:3:ARG:HD3	1.78	0.63
1:2:1542:C:H5''	21:T:62:ARG:HH22	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:104:ASP:HB3	4:C:130:ILE:HB	1.80	0.63
6:E:100:ARG:NH2	6:E:121:TYR:O	2.32	0.63
1:2:1722:G:O6	1:2:1812:U:O2	2.17	0.63
1:2:1869:A:O2'	35:y:118:HIS:CE1	2.52	0.63
2:A:52:LYS:HD2	19:R:109:LEU:HD22	1.81	0.63
15:N:4:MET:SD	15:N:124:ARG:NH1	2.72	0.63
34:x:213:GLY:H	34:x:218:ILE:HD11	1.63	0.63
1:2:155:G:H4'	8:G:15:LEU:HD22	1.81	0.62
19:R:66:VAL:HG11	19:R:69:ILE:HD13	1.80	0.62
3:B:72:ALA:HB3	16:O:128:ARG:HH22	1.64	0.62
1:2:1453:C:OP1	19:R:48:ASN:ND2	2.32	0.62
13:L:13:GLN:NE2	13:L:36:TYR:O	2.32	0.62
14:M:76:LEU:O	14:M:131:LYS:NZ	2.32	0.62
20:S:12:ILE:HG23	20:S:19:ASN:HD21	1.64	0.62
25:X:98:ASP:OD1	25:X:140:ARG:NH2	2.32	0.62
14:M:69:CYS:HA	14:M:74:ILE:HB	1.79	0.62
7:F:125:SER:HB3	7:F:136:ARG:HG2	1.82	0.62
1:2:643:A:OP1	11:J:39:ASN:ND2	2.33	0.62
1:2:1704:C:O2'	1:2:1831:A:N1	2.32	0.62
18:Q:16:LYS:NZ	18:Q:123:ASP:OD2	2.33	0.62
1:2:885:U:O2	1:2:901:G:N2	2.30	0.61
12:K:14:LEU:O	12:K:18:GLU:HB2	2.00	0.61
35:y:324:TYR:HB3	35:y:401:PRO:HG2	1.76	0.61
1:2:1858:G:OP2	16:O:146:ARG:NH2	2.32	0.61
16:O:31:CYS:HB3	16:O:95:ILE:HG12	1.82	0.61
1:2:65:C:N4	8:G:134:GLY:O	2.32	0.61
1:2:1368:U:O3'	19:R:2:GLY:N	2.33	0.61
7:F:51:HIS:HB2	7:F:90:VAL:HG11	1.82	0.61
20:S:84:LEU:HD22	20:S:97:GLN:HB2	1.81	0.61
33:g:15:ASN:O	33:g:305:ASN:ND2	2.33	0.61
34:x:227:ASN:ND2	34:x:232:ASN:OD1	2.32	0.61
35:y:111:LYS:HG3	35:y:307:HIS:HB3	1.83	0.61
1:2:1606:G:N2	1:2:1633:A:C8	2.68	0.61
12:K:15:LEU:HD23	12:K:79:LEU:HD21	1.82	0.61
21:T:9:VAL:O	21:T:11:GLN:NE2	2.34	0.61
1:2:1709:G:C6	1:2:1824:A:N1	2.69	0.61
19:R:32:LYS:CG	19:R:47:ARG:NH2	2.47	0.61
20:S:39:ARG:HH22	21:T:37:VAL:HA	1.66	0.61
17:P:108:LYS:HB2	17:P:111:MET:HE3	1.81	0.61
35:y:213:ASN:HA	35:y:216:GLN:HB2	1.83	0.61
2:A:198:MET:HE3	2:A:200:ASP:HB3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:954:U:O2	16:O:55:ARG:NH2	2.33	0.61
18:Q:70:VAL:HG11	18:Q:84:ILE:HG23	1.82	0.61
1:2:751:G:O6	1:2:791:C:N4	2.34	0.61
1:2:663:C:OP2	25:X:3:LYS:NZ	2.32	0.60
5:D:57:ASN:O	5:D:65:ARG:NH1	2.34	0.60
21:T:34:VAL:O	21:T:52:TRP:NE1	2.29	0.60
1:2:496:C:OP1	6:E:49:ARG:NH2	2.33	0.60
1:2:1366:G:H4'	35:y:353:GLN:HG3	1.82	0.60
1:2:1398:G:H1'	33:g:63:SER:HB3	1.84	0.60
1:2:1605:G:N2	1:2:1634:A:H62	1.97	0.60
21:T:11:GLN:OE1	21:T:62:ARG:NH1	2.35	0.60
1:2:441:C:OP2	10:I:2:GLY:N	2.34	0.60
1:2:797:C:O2	1:2:798:G:N2	2.33	0.60
5:D:45:ARG:HG2	5:D:83:SER:HA	1.82	0.60
1:2:1868:U:C5	35:y:399:LEU:HD11	2.36	0.60
7:F:199:VAL:O	7:F:203:ASN:ND2	2.35	0.60
19:R:58:MET:CE	19:R:61:ILE:HD12	2.30	0.60
27:Z:85:ARG:NH2	27:Z:103:HIS:O	2.35	0.60
33:g:107:ASP:HB2	33:g:125:ARG:HD2	1.83	0.60
1:2:1139:C:H41	1:2:1149:A:H62	1.48	0.60
4:C:134:ASN:HA	4:C:218:GLY:HA3	1.83	0.60
1:2:1551:U:OP1	5:D:9:ARG:NH2	2.35	0.60
1:2:1138:C:OP1	2:A:155:ARG:NH1	2.35	0.60
18:Q:58:LEU:HB3	18:Q:62:ARG:HD2	1.84	0.60
1:2:830:A:OP2	1:2:846:G:N2	2.35	0.60
1:2:1240:A:N3	1:2:1267:C:O2'	2.35	0.60
29:c:43:ILE:H	35:y:364:PRO:HG2	1.67	0.60
1:2:942:G:N2	16:O:138:ASP:OD2	2.35	0.60
5:D:169:ASP:O	5:D:187:LYS:HA	2.02	0.60
18:Q:76:GLY:H	18:Q:79:ALA:HB3	1.67	0.60
21:T:29:LYS:HD2	21:T:106:ALA:HA	1.82	0.60
2:A:142:LEU:O	23:V:60:ARG:NH2	2.34	0.59
1:2:1607:A:N6	1:2:1632:G:O2'	2.35	0.59
7:F:175:ASP:O	7:F:179:ASN:ND2	2.35	0.59
18:Q:28:GLY:HA3	18:Q:67:ASP:HB2	1.84	0.59
5:D:54:ARG:HB3	5:D:57:ASN:HD22	1.68	0.59
1:2:1036:A:N3	1:2:1844:U:O2'	2.35	0.59
1:2:1261:C:O2	30:d:10:HIS:NE2	2.36	0.59
19:R:32:LYS:HE3	19:R:47:ARG:NH1	2.18	0.59
1:2:913:A:OP2	9:H:99:ARG:NH1	2.34	0.59
2:A:20:ALA:O	35:y:287:HIS:NE2	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:229:MET:O	3:B:233:GLY:N	2.33	0.59
1:2:146:G:H1	1:2:173:A:N6	1.99	0.59
1:2:878:G:O6	1:2:908:A:N1	2.36	0.59
29:c:66:ARG:HG3	34:x:155:LEU:HG	1.84	0.59
35:y:400:ASN:OD1	35:y:400:ASN:N	2.27	0.59
1:2:659:G:O2'	1:2:662:G:O2'	2.21	0.59
3:B:136:ARG:HB2	3:B:218:LEU:HD11	1.85	0.59
1:2:1864:U:C6	35:y:408:PHE:HB2	2.37	0.58
14:M:21:VAL:HG12	14:M:111:VAL:HG21	1.84	0.58
6:E:100:ARG:HB2	6:E:114:ILE:HD11	1.85	0.58
28:b:40:CYS:SG	28:b:41:TYR:N	2.76	0.58
1:2:302:A:N3	10:I:64:ASN:ND2	2.52	0.58
1:2:959:G:OP2	16:O:38:ASN:ND2	2.35	0.58
1:2:1677:U:OP1	7:F:71:ARG:NH2	2.37	0.58
7:F:110:GLN:HE21	7:F:114:ASN:HD21	1.49	0.58
1:2:1602:U:O2'	20:S:24:ARG:NH2	2.32	0.58
1:2:1606:G:H5'	21:T:86:GLY:HA2	1.86	0.58
1:2:1622:U:H3	17:P:122:THR:HG1	1.46	0.58
3:B:180:ASP:O	3:B:184:VAL:N	2.34	0.58
19:R:71:ILE:HG22	19:R:73:LEU:H	1.68	0.58
1:2:1690:U:O3'	35:y:381:ARG:NH1	2.37	0.58
8:G:37:ALA:HA	8:G:49:VAL:HG13	1.85	0.58
4:C:102:LEU:HG	4:C:130:ILE:HD11	1.83	0.58
1:2:1673:U:OP1	18:Q:79:ALA:N	2.37	0.58
3:B:157:GLN:O	3:B:161:VAL:N	2.37	0.58
5:D:167:TYR:OH	5:D:202:LYS:O	2.21	0.58
15:N:99:ARG:NH2	15:N:119:GLU:OE2	2.37	0.58
19:R:66:VAL:HG13	19:R:69:ILE:CG1	1.92	0.58
34:x:79:PRO:HA	34:x:115:ASN:HD22	1.69	0.58
1:2:297:A:H5'	6:E:132:GLY:HA2	1.86	0.58
1:2:925:G:OP1	15:N:121:ARG:NH1	2.36	0.58
1:2:1541:G:H5''	21:T:59:SER:HB2	1.85	0.58
1:2:1608:U:OP1	20:S:134:GLN:NE2	2.37	0.58
4:C:222:CYS:SG	4:C:223:TYR:N	2.74	0.58
1:2:1274:G:N7	30:d:7:TYR:OH	2.36	0.57
1:2:1286:G:N2	1:2:1287:A:N7	2.52	0.57
6:E:48:LEU:HD23	6:E:61:VAL:HG13	1.85	0.57
14:M:42:LEU:HA	14:M:47:ALA:HB3	1.86	0.57
1:2:1865:C:H42	34:x:204:LEU:HB3	1.69	0.57
6:E:60:GLU:OE1	26:Y:20:ARG:NH2	2.37	0.57
33:g:107:ASP:OD2	33:g:125:ARG:NH1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:71:LEU:HD11	3:B:189:ILE:HG23	1.86	0.57
18:Q:33:LYS:HA	18:Q:38:PRO:HA	1.87	0.57
22:U:20:ILE:HG12	22:U:116:ILE:HG12	1.86	0.57
7:F:34:SER:HA	29:c:55:VAL:HG13	1.86	0.57
17:P:18:ARG:NH1	20:S:89:ASP:O	2.38	0.57
1:2:1276:A:H62	1:2:1321:G:H21	1.53	0.57
33:g:116:ASP:O	33:g:118:ARG:NH1	2.38	0.57
1:2:637:U:O2	31:e:56:ASN:ND2	2.37	0.57
1:2:1270:G:O2'	1:2:1301:A:N1	2.36	0.57
1:2:1865:C:H5''	34:x:187:GLY:C	2.29	0.57
4:C:102:LEU:CG	4:C:130:ILE:CD1	2.82	0.57
8:G:5:ILE:HG12	8:G:111:LEU:HD12	1.87	0.57
12:K:71:LEU:HB3	12:K:75:GLY:HA3	1.86	0.57
2:A:147:LEU:O	2:A:165:ASN:ND2	2.38	0.57
3:B:146:ARG:HB2	3:B:149:GLN:HB2	1.86	0.57
6:E:70:ILE:HG12	6:E:92:ILE:HG12	1.86	0.57
12:K:21:MET:HB2	12:K:49:MET:HE3	1.85	0.57
16:O:151:LEU:HB3	34:x:168:VAL:HG12	1.86	0.57
5:D:52:ALA:HB3	5:D:55:THR:HG22	1.86	0.57
16:O:98:ARG:HH21	16:O:134:PRO:HG2	1.70	0.57
1:2:1865:C:H42	34:x:204:LEU:CB	2.17	0.57
1:2:1865:C:C4	34:x:204:LEU:HB2	2.40	0.57
9:H:166:VAL:HG12	9:H:169:LYS:HD2	1.86	0.57
35:y:209:ILE:O	35:y:213:ASN:ND2	2.37	0.57
9:H:11:PRO:HD2	9:H:14:GLU:HA	1.87	0.57
1:2:1709:G:N1	1:2:1824:A:H2	1.96	0.56
1:2:126:G:H21	1:2:180:G:H21	1.54	0.56
2:A:80:ARG:O	2:A:84:GLN:NE2	2.37	0.56
13:L:104:LYS:O	25:X:11:ARG:NH2	2.33	0.56
1:2:43:U:OP2	1:2:485:A:N6	2.37	0.56
1:2:1288:U:HO2'	1:2:1315:U:HO2'	1.48	0.56
4:C:171:GLY:O	24:W:98:GLN:NE2	2.37	0.56
7:F:19:LEU:HD23	7:F:109:LEU:HD11	1.86	0.56
9:H:170:VAL:HG13	9:H:187:PHE:HB2	1.87	0.56
9:H:181:THR:HG21	9:H:183:LYS:HE2	1.87	0.56
1:2:197:U:O4	1:2:202:G:O6	2.23	0.56
1:2:1013:U:OP1	1:2:1129:G:O2'	2.24	0.56
1:2:1680:G:OP1	7:F:60:ARG:NH1	2.39	0.56
13:L:131:CYS:SG	13:L:132:ARG:N	2.79	0.56
29:c:44:ARG:NH1	29:c:60:GLU:O	2.39	0.56
35:y:324:TYR:HB2	35:y:401:PRO:HG2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1829:G:C6	1:2:1830:U:N3	2.74	0.56
8:G:2:LYS:HD3	8:G:15:LEU:HD21	1.88	0.56
1:2:685:A:N6	1:2:917:U:O4	2.38	0.56
3:B:104:ASP:OD1	3:B:104:ASP:N	2.37	0.56
35:y:263:ALA:HB3	35:y:300:VAL:HB	1.86	0.55
1:2:1255:G:O6	1:2:1257:G:N2	2.38	0.55
1:2:1256:G:H21	1:2:1659:U:H5'	1.70	0.55
1:2:1615:U:OP2	17:P:43:ARG:NH1	2.38	0.55
4:C:221:ASP:OD1	4:C:221:ASP:N	2.37	0.55
30:d:30:LEU:HA	30:d:39:CYS:HA	1.88	0.55
1:2:431:G:OP1	6:E:6:LYS:NZ	2.39	0.55
1:2:490:C:O2'	1:2:574:A:N1	2.38	0.55
1:2:1061:U:O4	1:2:1850:A:N6	2.38	0.55
1:2:1309:C:H41	32:f:95:ARG:HH21	1.54	0.55
1:2:1513:C:OP1	30:d:12:ARG:NH2	2.40	0.55
4:C:102:LEU:HG	4:C:130:ILE:CD1	2.35	0.55
5:D:6:SER:O	5:D:10:LYS:N	2.39	0.55
5:D:16:ILE:HD11	30:d:36:LEU:HD12	1.89	0.55
1:2:1709:G:C2	1:2:1824:A:H2	2.25	0.55
17:P:81:ARG:NH2	17:P:120:SER:O	2.40	0.55
19:R:33:ARG:HH21	33:g:64:HIS:HE1	1.54	0.55
22:U:17:ILE:HD12	22:U:95:SER:H	1.70	0.55
1:2:379:C:O2	10:I:5:ARG:NH1	2.39	0.55
1:2:659:G:HO2'	1:2:662:G:HO2'	1.54	0.55
2:A:53:ARG:NH2	23:V:82:ASN:O	2.40	0.55
4:C:146:GLU:O	4:C:150:ALA:N	2.40	0.55
18:Q:86:GLN:NE2	18:Q:118:THR:O	2.39	0.55
1:2:878:G:C6	1:2:908:A:N1	2.74	0.55
1:2:1451:G:N7	19:R:44:LYS:NZ	2.47	0.55
1:2:1473:G:N1	1:2:1476:A:OP2	2.39	0.55
5:D:27:ARG:HB3	12:K:61:GLN:HE22	1.71	0.55
7:F:100:ILE:HG12	7:F:178:ILE:HD11	1.89	0.55
8:G:78:SER:OG	8:G:79:LYS:N	2.40	0.55
9:H:95:ILE:HD11	9:H:133:LEU:HD13	1.88	0.55
1:2:1790:A:O2'	8:G:64:LYS:NZ	2.40	0.55
6:E:125:LYS:HB2	6:E:226:PHE:HD1	1.70	0.55
7:F:100:ILE:O	7:F:104:THR:N	2.39	0.55
2:A:53:ARG:NH1	2:A:56:GLU:OE1	2.40	0.55
3:B:107:ARG:NH1	16:O:133:THR:O	2.38	0.55
5:D:41:VAL:HG22	5:D:46:THR:HG23	1.89	0.55
33:g:176:VAL:HB	33:g:186:THR:HB	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:165:G:OP2	1:2:165:G:N2	2.38	0.54
2:A:128:ARG:HH22	35:y:326:LEU:HD13	1.71	0.54
7:F:74:ASN:HA	7:F:77:MET:HE3	1.89	0.54
1:2:57:U:O2'	1:2:499:G:N3	2.40	0.54
24:W:112:ASP:HB2	24:W:115:GLU:H	1.71	0.54
33:g:110:SER:HB2	33:g:153:CYS:HA	1.88	0.54
1:2:482:G:N1	1:2:485:A:OP2	2.41	0.54
1:2:1245:G:O2'	1:2:1492:U:OP1	2.22	0.54
15:N:13:GLN:O	28:b:20:LYS:NZ	2.40	0.54
1:2:1669:G:OP1	22:U:79:ARG:NH1	2.41	0.54
13:L:73:LEU:HD12	13:L:140:PHE:HE2	1.72	0.54
33:g:152:SER:OG	33:g:168:CYS:SG	2.66	0.54
1:2:148:U:H2'	1:2:149:A:H8	1.71	0.54
1:2:1544:C:O2'	18:Q:80:GLN:NE2	2.41	0.54
1:2:1709:G:C6	1:2:1824:A:C2	2.95	0.54
1:2:1722:G:O6	1:2:1812:U:C2	2.61	0.54
1:2:1565:C:OP2	21:T:101:ARG:NH1	2.36	0.54
1:2:1737:G:OP1	8:G:94:ARG:NH2	2.40	0.54
4:C:172:ASN:ND2	11:J:95:ASP:OD2	2.37	0.54
35:y:10:ASP:HB2	35:y:236:THR:HG22	1.89	0.54
35:y:94:GLU:HG3	35:y:250:LEU:HD21	1.88	0.54
1:2:801:U:O4	9:H:106:ARG:NH2	2.41	0.54
1:2:988:C:O2'	3:B:118:GLN:O	2.24	0.54
1:2:1380:C:H1'	2:A:113:GLN:HE22	1.73	0.54
1:2:1589:A:N3	1:2:1653:U:O2'	2.37	0.54
1:2:30:C:O2'	1:2:596:U:OP1	2.26	0.54
1:2:828:G:OP1	6:E:22:LYS:NZ	2.40	0.54
1:2:1241:A:HO2'	1:2:1266:C:HO2'	1.52	0.54
2:A:42:LYS:HD3	2:A:48:ILE:HD11	1.88	0.54
4:C:133:TYR:HE1	4:C:215:MET:C	2.16	0.54
1:2:1005:G:OP2	3:B:162:ARG:NH2	2.41	0.54
1:2:1113:A:H5''	1:2:1114:U:H4'	1.89	0.54
21:T:51:ASN:HB3	21:T:54:TYR:HB2	1.90	0.54
1:2:1335:G:O6	1:2:1492:U:O4	2.26	0.53
3:B:182:LYS:O	3:B:186:ASN:ND2	2.42	0.53
29:c:65:ALA:HB2	35:y:364:PRO:HA	1.89	0.53
1:2:818:A:OP1	11:J:80:ARG:NH2	2.35	0.53
8:G:181:THR:O	8:G:185:LEU:N	2.40	0.53
1:2:1387:G:N2	5:D:206:ASP:OD1	2.34	0.53
4:C:70:VAL:HG21	4:C:93:ILE:HG23	1.90	0.53
7:F:30:ILE:HG13	7:F:36:GLN:HG3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:c:67:ARG:HD3	35:y:372:PRO:HA	1.90	0.53
1:2:617:G:H4'	25:X:88:ASP:HB3	1.89	0.53
3:B:149:GLN:NE2	3:B:153:THR:O	2.41	0.53
10:I:13:LYS:NZ	13:L:108:ASN:O	2.41	0.53
12:K:42:ASN:HA	12:K:45:VAL:HB	1.91	0.53
15:N:129:TYR:O	15:N:133:ARG:N	2.42	0.53
16:O:57:THR:HG23	16:O:60:MET:HE3	1.89	0.53
1:2:616:A:OP1	25:X:68:LYS:NZ	2.41	0.53
11:J:32:ILE:O	11:J:36:GLY:N	2.40	0.53
17:P:111:MET:HE2	20:S:117:ILE:HG12	1.91	0.53
1:2:67:C:H41	8:G:163:ASN:HA	1.73	0.53
1:2:1061:U:H5'	1:2:1062:A:H5''	1.89	0.53
1:2:1562:C:OP1	21:T:74:SER:N	2.42	0.53
1:2:1720:U:O4	1:2:1814:G:N2	2.42	0.53
27:Z:103:HIS:CD2	27:Z:104:ARG:H	2.27	0.53
33:g:114:SER:HB3	33:g:119:GLN:HB2	1.90	0.53
1:2:1068:G:N2	1:2:1069:U:O4	2.42	0.53
1:2:1374:C:O2'	1:2:1464:C:O2	2.26	0.53
1:2:1477:U:OP2	19:R:3:ARG:NH2	2.39	0.53
23:V:22:ARG:NH2	24:W:19:LYS:O	2.41	0.53
1:2:185:G:N2	1:2:214:U:O2	2.33	0.53
1:2:1082:A:O2'	1:2:1842:C:O2'	2.23	0.53
1:2:1536:G:H2'	1:2:1537:A:H8	1.73	0.53
3:B:49:VAL:HG21	3:B:62:LEU:HD22	1.90	0.53
7:F:74:ASN:OD1	7:F:86:LYS:NZ	2.35	0.53
7:F:115:ALA:O	7:F:119:SER:HB3	2.08	0.53
20:S:137:LYS:O	20:S:141:ARG:NH2	2.40	0.53
27:Z:91:LEU:O	27:Z:95:GLY:N	2.42	0.53
33:g:42:MET:O	33:g:56:GLN:N	2.35	0.53
35:y:239:PHE:HE1	35:y:263:ALA:HB1	1.73	0.53
2:A:137:ALA:HB1	2:A:142:LEU:HB2	1.91	0.53
17:P:59:ARG:HH22	17:P:77:LYS:HE2	1.74	0.53
1:2:5:U:H2'	1:2:6:G:H8	1.73	0.53
2:A:24:HIS:O	2:A:49:ILE:N	2.40	0.53
2:A:63:ARG:HB3	23:V:37:ALA:H	1.74	0.53
3:B:92:GLN:HB2	3:B:95:ASN:HB2	1.90	0.53
15:N:85:PRO:O	15:N:89:TYR:N	2.42	0.53
19:R:66:VAL:HG13	19:R:69:ILE:HG23	1.90	0.53
24:W:24:GLN:NE2	24:W:64:ASN:OD1	2.41	0.53
1:2:1060:A:O2'	1:2:1062:A:N7	2.34	0.52
1:2:1535:U:O4	7:F:159:ARG:NE	2.33	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:g:71:ILE:HA	33:g:78:ALA:HA	1.91	0.52
35:y:210:THR:O	35:y:212:SER:N	2.40	0.52
1:2:520:A:O2'	1:2:825:A:N3	2.42	0.52
1:2:918:U:O2'	1:2:919:A:O4'	2.27	0.52
12:K:15:LEU:HD21	12:K:71:LEU:HD21	1.90	0.52
34:x:171:LEU:HD22	34:x:175:HIS:HB3	1.91	0.52
6:E:91:SER:OG	6:E:93:ASP:OD1	2.27	0.52
7:F:40:ALA:HB3	7:F:68:ILE:HB	1.92	0.52
19:R:22:THR:HG23	33:g:212:LYS:HE2	1.92	0.52
1:2:1216:C:N4	1:2:1342:U:OP1	2.42	0.52
4:C:102:LEU:HG	4:C:130:ILE:HG13	1.91	0.52
10:I:70:GLU:OE2	13:L:21:LYS:NZ	2.42	0.52
12:K:24:LYS:H	12:K:42:ASN:HD21	1.57	0.52
17:P:51:ARG:NH2	30:d:5:GLN:OE1	2.42	0.52
33:g:255:SER:HB3	33:g:271:LYS:HD3	1.91	0.52
35:y:70:SER:O	35:y:74:GLY:N	2.42	0.52
1:2:380:G:OP1	10:I:31:ARG:NH1	2.35	0.52
1:2:1210:G:OP1	34:x:242:ARG:NH2	2.43	0.52
1:2:1594:A:OP1	27:Z:103:HIS:ND1	2.43	0.52
9:H:153:LEU:HD21	9:H:186:ASN:HD22	1.74	0.52
12:K:35:LEU:HB3	12:K:38:LYS:HB2	1.90	0.52
33:g:82:SER:HB3	33:g:86:THR:O	2.09	0.52
2:A:185:MET:HE1	23:V:39:VAL:HG12	1.91	0.52
33:g:109:LEU:HD11	33:g:125:ARG:HE	1.75	0.52
1:2:333:G:OP2	8:G:190:ARG:NH1	2.43	0.52
6:E:18:TRP:NE1	6:E:41:CYS:O	2.42	0.52
35:y:8:VAL:O	35:y:235:LEU:N	2.43	0.52
21:T:14:PHE:HZ	21:T:131:LEU:HD22	1.75	0.52
34:x:106:GLN:HG2	35:y:210:THR:H	1.74	0.52
5:D:44:THR:HG22	5:D:45:ARG:HG3	1.91	0.52
10:I:10:LYS:HB3	10:I:18:ARG:HH21	1.75	0.52
12:K:47:LYS:NZ	12:K:50:GLN:OE1	2.34	0.52
13:L:23:VAL:O	13:L:27:GLU:N	2.42	0.52
15:N:118:ILE:HG12	15:N:121:ARG:HH21	1.75	0.52
19:R:62:GLN:OE1	19:R:62:GLN:HA	2.09	0.52
1:2:65:C:OP2	8:G:136:LYS:NZ	2.39	0.52
1:2:420:G:O2'	1:2:660:C:N3	2.40	0.52
7:F:35:LEU:HD12	7:F:117:ILE:HG12	1.93	0.52
1:2:28:U:H2'	1:2:29:G:H8	1.75	0.51
24:W:102:ILE:HB	24:W:113:HIS:HB3	1.91	0.51
32:f:139:HIS:HB2	32:f:148:TYR:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:66:LEU:HD11	4:C:81:ILE:HG12	1.93	0.51
25:X:67:ARG:HG3	25:X:115:ILE:HG12	1.92	0.51
1:2:1413:G:H2'	1:2:1414:A:H8	1.76	0.51
1:2:1415:C:H5''	21:T:129:ARG:HG2	1.92	0.51
1:2:1709:G:C2	1:2:1824:A:C2	2.97	0.51
1:2:1868:U:H5	35:y:399:LEU:HD11	1.75	0.51
2:A:77:ILE:HD12	2:A:122:LEU:HD11	1.92	0.51
6:E:71:LYS:HA	6:E:76:VAL:HA	1.91	0.51
16:O:97:LEU:HD21	16:O:108:PRO:HB3	1.91	0.51
22:U:19:ARG:HG3	22:U:117:ALA:HA	1.92	0.51
24:W:31:SER:H	24:W:34:ILE:HB	1.75	0.51
27:Z:85:ARG:NH1	27:Z:104:ARG:O	2.43	0.51
35:y:321:GLY:CA	35:y:400:ASN:HB3	2.41	0.51
1:2:15:U:O2'	1:2:669:A:N6	2.42	0.51
1:2:1033:G:N1	1:2:1080:A:O2'	2.41	0.51
1:2:1130:G:OP2	1:2:1130:G:N2	2.32	0.51
1:2:1567:G:H2'	21:T:37:VAL:HG21	1.93	0.51
1:2:203:G:OP2	10:I:146:GLN:NE2	2.41	0.51
30:d:21:CYS:HB3	30:d:26:ASN:H	1.76	0.51
33:g:72:SER:HB2	33:g:77:PHE:HB2	1.91	0.51
1:2:1324:G:O6	1:2:1504:U:O2	2.29	0.51
1:2:1608:U:H5''	20:S:134:GLN:HE22	1.74	0.51
2:A:76:VAL:HG12	2:A:87:VAL:HG13	1.92	0.51
4:C:105:GLU:O	4:C:128:VAL:HG13	2.11	0.51
26:Y:44:LEU:HD23	26:Y:55:ILE:HD12	1.91	0.51
1:2:446:G:OP2	10:I:47:ARG:NH2	2.43	0.51
1:2:1144:A:N3	1:2:1199:A:O2'	2.39	0.51
1:2:1577:G:O2'	1:2:1579:A:N3	2.39	0.51
1:2:1622:U:O4	17:P:81:ARG:NH2	2.37	0.51
10:I:7:ASN:O	10:I:18:ARG:NH2	2.43	0.51
18:Q:37:ARG:HH21	21:T:7:LYS:HZ2	1.59	0.51
34:x:157:ASP:OD1	34:x:157:ASP:N	2.43	0.51
1:2:163:U:OP2	8:G:87:ARG:NH2	2.37	0.51
1:2:197:U:O2	1:2:202:G:N2	2.30	0.51
1:2:1184:G:OP1	36:z:557:ARG:NH2	2.41	0.51
3:B:33:VAL:HA	3:B:96:CYS:HB2	1.93	0.51
4:C:171:GLY:HA2	24:W:97:ARG:HD2	1.93	0.51
33:g:38:LYS:HE3	33:g:64:HIS:HA	1.93	0.51
13:L:80:MET:HE1	13:L:120:VAL:HG12	1.91	0.51
14:M:94:ILE:HA	14:M:100:PRO:HA	1.93	0.51
1:2:594:A:H61	1:2:643:A:H5''	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:100:PRO:HB2	14:M:103:VAL:HG22	1.93	0.50
17:P:37:TYR:HB3	17:P:41:GLN:HB2	1.92	0.50
1:2:1137:U:H5''	35:y:328:THR:HG23	1.94	0.50
1:2:1206:G:O6	1:2:1692:U:O4	2.29	0.50
1:2:1614:A:OP2	17:P:42:ARG:NH2	2.41	0.50
6:E:153:LEU:HD12	8:G:216:ARG:HH21	1.75	0.50
12:K:61:GLN:HB3	12:K:68:TYR:O	2.11	0.50
14:M:30:GLY:HA2	14:M:112:LYS:HB2	1.93	0.50
16:O:99:ALA:H	16:O:133:THR:HG22	1.75	0.50
5:D:138:VAL:HG22	5:D:184:ILE:HG22	1.93	0.50
11:J:84:ILE:O	11:J:108:ARG:NE	2.44	0.50
14:M:25:ALA:HB1	14:M:31:LEU:HG	1.94	0.50
22:U:17:ILE:HB	22:U:94:PRO:HA	1.93	0.50
25:X:67:ARG:HB3	25:X:84:PHE:HE1	1.77	0.50
30:d:19:ARG:HH11	30:d:32:ARG:HD2	1.76	0.50
1:2:588:G:OP2	1:2:588:G:N2	2.43	0.50
1:2:928:G:H2'	1:2:929:G:C8	2.47	0.50
1:2:1616:U:H5	17:P:43:ARG:HH21	1.60	0.50
8:G:44:GLU:HA	8:G:119:LYS:HD2	1.93	0.50
10:I:162:LEU:HD23	10:I:165:GLN:HG3	1.93	0.50
19:R:58:MET:HE2	19:R:58:MET:CA	2.26	0.50
1:2:663:C:O2'	4:C:227:ARG:NH2	2.42	0.50
5:D:106:ARG:O	5:D:110:LEU:HB2	2.12	0.50
1:2:1868:U:OP2	35:y:395:GLY:HA3	2.11	0.50
33:g:248:LEU:HB2	33:g:261:LEU:HD11	1.94	0.50
1:2:223:C:H2'	1:2:224:A:H8	1.77	0.50
6:E:124:CYS:HB3	6:E:141:THR:HB	1.93	0.50
9:H:144:ILE:HG12	9:H:154:ILE:HG23	1.92	0.50
1:2:561:A:HO2'	11:J:134:HIS:HE2	1.56	0.50
1:2:1360:U:O2'	1:2:1379:A:OP2	2.25	0.50
1:2:1587:G:H5''	21:T:77:LYS:HE2	1.92	0.50
16:O:44:VAL:O	16:O:53:ILE:HB	2.11	0.50
2:A:216:ALA:HA	35:y:63:VAL:HG11	1.93	0.50
14:M:85:LEU:HD13	14:M:107:SER:HA	1.93	0.50
1:2:1324:G:O2'	1:2:1510:G:O2'	2.27	0.49
9:H:144:ILE:HB	24:W:52:ILE:HB	1.94	0.49
13:L:101:ARG:HG3	25:X:7:LEU:HA	1.93	0.49
4:C:110:MET:HE3	4:C:127:PHE:HE2	1.77	0.49
4:C:137:VAL:HG11	4:C:217:ALA:HB2	1.94	0.49
19:R:60:ARG:CZ	19:R:60:ARG:CA	2.86	0.49
32:f:130:VAL:HG11	32:f:143:LYS:HE3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:71:G:H1'	1:2:79:A:H61	1.77	0.49
1:2:1192:U:OP2	25:X:119:ARG:NH2	2.37	0.49
1:2:1413:G:H2'	1:2:1414:A:C8	2.47	0.49
22:U:43:ALA:O	22:U:48:LEU:N	2.44	0.49
1:2:24:C:OP1	11:J:11:LYS:NZ	2.37	0.49
1:2:1221:G:O2'	1:2:1676:U:O2	2.28	0.49
2:A:42:LYS:NZ	19:R:99:ASP:OD2	2.34	0.49
4:C:102:LEU:HG	4:C:130:ILE:CG1	2.43	0.49
7:F:73:THR:HG21	7:F:90:VAL:HG12	1.94	0.49
1:2:1317:C:H2'	1:2:1318:G:C8	2.47	0.49
11:J:138:ARG:HG2	11:J:156:HIS:CD2	2.48	0.49
34:x:152:LEU:HD23	34:x:158:LEU:HB2	1.94	0.49
1:2:1307:U:OP2	32:f:96:LYS:NZ	2.45	0.49
1:2:1865:C:N4	34:x:204:LEU:CB	2.76	0.49
5:D:108:LYS:HB3	5:D:113:LEU:HD12	1.94	0.49
10:I:104:ILE:HD11	10:I:171:LEU:HD12	1.95	0.49
14:M:92:CYS:HB3	14:M:100:PRO:HB3	1.93	0.49
21:T:9:VAL:HG21	21:T:135:ALA:HB1	1.93	0.49
1:2:223:C:H2'	1:2:224:A:C8	2.48	0.49
2:A:85:ARG:NH2	19:R:82:ASP:O	2.45	0.49
9:H:65:PRO:HG2	9:H:68:GLN:HB2	1.94	0.49
13:L:102:PHE:N	25:X:7:LEU:O	2.45	0.49
17:P:56:LEU:HD23	17:P:83:MET:HG2	1.94	0.49
26:Y:14:THR:HG22	26:Y:21:LYS:HG2	1.94	0.49
2:A:176:TRP:CD2	2:A:199:PRO:HB3	2.48	0.49
4:C:133:TYR:CE1	4:C:215:MET:C	2.90	0.49
5:D:226:GLN:HG2	33:g:186:THR:HA	1.95	0.49
19:R:66:VAL:HG13	19:R:69:ILE:H	1.78	0.49
34:x:165:ILE:HG13	34:x:229:ILE:HD12	1.94	0.49
1:2:302:A:O5'	10:I:74:ARG:NH1	2.46	0.49
1:2:1550:G:H21	1:2:1559:C:H1'	1.78	0.49
7:F:142:SER:O	7:F:146:ARG:N	2.46	0.49
10:I:67:TRP:CD1	10:I:70:GLU:H	2.29	0.49
18:Q:53:GLU:OE1	18:Q:85:ARG:NH2	2.46	0.49
29:c:32:VAL:HG21	29:c:44:ARG:HB2	1.93	0.49
35:y:104:LYS:NZ	35:y:303:ASP:OD1	2.40	0.49
35:y:298:VAL:HG12	35:y:308:MET:HG2	1.94	0.49
1:2:144:U:H2'	1:2:145:G:H8	1.78	0.49
1:2:145:G:H2'	1:2:146:G:C8	2.48	0.49
1:2:1615:U:O4	17:P:40:ARG:NH1	2.44	0.49
17:P:83:MET:HB3	17:P:116:LEU:HD12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:453:C:O2'	8:G:92:ARG:O	2.26	0.48
1:2:1373:C:OP1	19:R:7:LYS:N	2.46	0.48
1:2:1609:C:N3	1:2:1630:A:N6	2.60	0.48
6:E:43:PRO:HD2	6:E:46:ILE:HD13	1.95	0.48
11:J:53:ILE:HD13	11:J:81:LEU:HD21	1.95	0.48
1:2:16:G:N2	1:2:1195:A:H62	2.07	0.48
1:2:375:U:H2'	1:2:376:A:C8	2.48	0.48
1:2:500:A:H3'	1:2:501:C:H6	1.78	0.48
7:F:50:PRO:HG3	7:F:69:VAL:HG12	1.95	0.48
33:g:44:LYS:O	33:g:54:ILE:N	2.44	0.48
26:Y:55:ILE:HG22	26:Y:75:ILE:HG23	1.94	0.48
33:g:11:LEU:HB2	33:g:307:VAL:HB	1.95	0.48
1:2:1293:A:H2'	1:2:1294:G:H8	1.78	0.48
1:2:1601:A:H4'	1:2:1602:U:H5'	1.95	0.48
1:2:1705:C:H42	1:2:1830:U:H3	1.62	0.48
1:2:1864:U:H5''	35:y:408:PHE:HB3	1.95	0.48
17:P:44:ARG:HH12	17:P:53:GLN:HE22	1.60	0.48
35:y:285:CYS:HB2	35:y:289:GLY:H	1.76	0.48
1:2:65:C:O2'	1:2:67:C:OP2	2.31	0.48
1:2:878:G:N1	1:2:908:A:C2	2.82	0.48
1:2:943:U:OP1	3:B:214:LYS:NZ	2.35	0.48
6:E:191:ARG:HH21	6:E:245:ARG:HD2	1.78	0.48
1:2:1260:A:N6	1:2:1617:G:N2	2.44	0.48
2:A:41:ARG:HD3	2:A:47:TYR:CZ	2.48	0.48
9:H:51:ILE:HD13	9:H:179:LYS:HD2	1.94	0.48
19:R:60:ARG:HH21	19:R:63:ARG:HB2	1.78	0.48
1:2:1048:G:N1	1:2:1069:U:OP2	2.36	0.48
1:2:1284:A:H8	14:M:104:VAL:HG12	1.79	0.48
1:2:1317:C:H2'	1:2:1318:G:H8	1.79	0.48
1:2:1560:U:H2'	1:2:1561:A:H8	1.78	0.48
1:2:1736:G:H2'	1:2:1737:G:C8	2.49	0.48
13:L:78:THR:OG1	13:L:79:LYS:N	2.47	0.48
24:W:17:ALA:O	24:W:22:LYS:N	2.45	0.48
1:2:495:U:O2'	6:E:27:PHE:O	2.28	0.48
1:2:1601:A:OP2	1:2:1636:G:N1	2.41	0.48
1:2:1661:A:OP2	30:d:32:ARG:NH1	2.46	0.48
1:2:1865:C:N4	34:x:204:LEU:HB3	2.29	0.48
3:B:32:ASP:O	3:B:96:CYS:N	2.46	0.48
5:D:98:ALA:HB3	5:D:169:ASP:HB2	1.96	0.48
19:R:32:LYS:HE3	19:R:47:ARG:CZ	2.44	0.48
26:Y:41:ARG:NH2	26:Y:52:PRO:O	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:g:73:SER:HB3	33:g:117:ASN:HD21	1.79	0.48
1:2:1868:U:H5'	34:x:83:ASN:O	2.13	0.48
4:C:169:TYR:OH	4:C:175:GLY:O	2.32	0.48
10:I:38:ILE:HD11	10:I:81:VAL:HG23	1.95	0.48
21:T:124:THR:O	21:T:128:GLN:N	2.47	0.48
1:2:122:G:H21	6:E:146:THR:HG21	1.78	0.48
9:H:99:ARG:HB2	9:H:120:ARG:HG2	1.96	0.48
15:N:99:ARG:NH1	15:N:141:TYR:OH	2.47	0.48
20:S:99:LEU:O	20:S:103:LEU:N	2.47	0.48
1:2:1113:A:N6	1:2:1121:G:O6	2.47	0.47
5:D:47:GLU:HG2	5:D:85:GLU:HB2	1.96	0.47
7:F:104:THR:HG22	7:F:106:GLU:H	1.78	0.47
8:G:50:VAL:HG11	8:G:111:LEU:HB3	1.96	0.47
29:c:12:ALA:HA	29:c:33:GLU:O	2.13	0.47
1:2:179:C:H2'	1:2:180:G:H8	1.79	0.47
1:2:980:A:H2'	1:2:981:A:C8	2.50	0.47
1:2:1232:U:O2	1:2:1526:G:N2	2.37	0.47
1:2:1605:G:H21	1:2:1634:A:N6	2.05	0.47
1:2:1615:U:H5''	17:P:43:ARG:HH12	1.79	0.47
1:2:1865:C:H5''	34:x:187:GLY:CA	2.44	0.47
2:A:16:LEU:HD21	19:R:114:LEU:HD22	1.96	0.47
11:J:114:VAL:HG13	11:J:119:LEU:HB2	1.95	0.47
34:x:75:THR:OG1	34:x:76:ARG:N	2.42	0.47
1:2:64:A:H2	1:2:83:A:H62	1.62	0.47
1:2:1259:A:H61	1:2:1519:U:H5'	1.79	0.47
1:2:1549:U:H5'	30:d:34:TYR:HE1	1.79	0.47
7:F:35:LEU:O	7:F:39:ILE:N	2.40	0.47
13:L:88:ILE:HG21	13:L:126:VAL:HG11	1.96	0.47
20:S:71:MET:HG2	20:S:99:LEU:HD21	1.96	0.47
33:g:164:ILE:HG23	33:g:176:VAL:HG13	1.95	0.47
1:2:1313:A:H5'	12:K:5:LYS:HD2	1.97	0.47
3:B:104:ASP:HA	3:B:214:LYS:HA	1.96	0.47
18:Q:85:ARG:NH2	18:Q:116:ASP:OD2	2.47	0.47
19:R:98:VAL:HG13	19:R:102:THR:HB	1.96	0.47
21:T:38:LYS:HA	21:T:47:PRO:HD3	1.96	0.47
35:y:63:VAL:HG13	35:y:85:GLN:HE22	1.79	0.47
1:2:1608:U:O2'	20:S:130:ARG:NH1	2.48	0.47
1:2:1260:A:C6	1:2:1617:G:N2	2.72	0.47
1:2:1736:G:H2'	1:2:1737:G:H8	1.79	0.47
1:2:1808:U:H2'	1:2:1809:A:C8	2.49	0.47
6:E:87:MET:HE1	6:E:236:ILE:HG21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:17:ALA:HB1	24:W:22:LYS:HB2	1.96	0.47
1:2:598:G:O2'	1:2:605:A:N1	2.41	0.47
1:2:823:U:H5	11:J:143:ASN:HB3	1.79	0.47
1:2:957:A:H3'	1:2:958:G:H21	1.78	0.47
1:2:1209:A:O3'	34:x:242:ARG:NH1	2.47	0.47
3:B:46:LYS:HG3	16:O:19:PRO:HB3	1.97	0.47
6:E:206:ASP:HB2	6:E:222:LEU:HB2	1.96	0.47
11:J:112:THR:HG22	11:J:123:ILE:HD11	1.97	0.47
17:P:63:ALA:HB1	17:P:74:GLU:HB3	1.97	0.47
20:S:70:ILE:HG23	20:S:77:TYR:HB2	1.97	0.47
33:g:172:LYS:HE2	33:g:193:GLY:H	1.78	0.47
35:y:269:ARG:HH11	35:y:274:PHE:HD1	1.60	0.47
1:2:851:C:O2'	1:2:852:G:N2	2.48	0.47
1:2:1101:U:H2'	1:2:1102:G:C8	2.50	0.47
1:2:1443:C:O2	18:Q:71:ARG:NH1	2.48	0.47
26:Y:54:VAL:HG22	26:Y:76:TYR:HB2	1.97	0.47
1:2:1205:C:H2'	1:2:1206:G:C8	2.49	0.47
1:2:1274:G:C6	12:K:43:LEU:HD21	2.50	0.47
1:2:1299:A:N6	1:2:1301:A:N7	2.63	0.47
4:C:182:CYS:HB2	24:W:95:PRO:HB2	1.97	0.47
5:D:226:GLN:NE2	33:g:223:GLU:O	2.40	0.47
13:L:39:ASN:ND2	13:L:40:ILE:O	2.48	0.47
1:2:818:A:H5''	11:J:76:ALA:HB1	1.97	0.47
1:2:1491:G:O2'	22:U:70:CYS:SG	2.60	0.47
2:A:128:ARG:HD3	2:A:153:PRO:HD2	1.97	0.47
6:E:139:LEU:HG	6:E:150:PRO:HG3	1.97	0.47
11:J:170:PRO:HB2	11:J:174:LYS:HB3	1.96	0.47
13:L:23:VAL:HG12	13:L:25:LEU:H	1.80	0.47
13:L:135:SER:OG	13:L:136:LYS:N	2.48	0.47
26:Y:29:HIS:NE2	26:Y:69:THR:OG1	2.39	0.47
29:c:32:VAL:HB	29:c:42:ILE:O	2.15	0.47
1:2:385:G:H3'	13:L:136:LYS:HB2	1.97	0.46
1:2:1101:U:H2'	1:2:1102:G:H8	1.80	0.46
1:2:1172:U:H2'	1:2:1173:A:H8	1.79	0.46
1:2:1488:C:O2'	1:2:1490:G:O5'	2.34	0.46
6:E:148:ARG:NH2	8:G:202:ASN:OD1	2.38	0.46
11:J:122:SER:H	11:J:125:HIS:HB3	1.80	0.46
17:P:96:VAL:HB	17:P:120:SER:HB2	1.96	0.46
17:P:122:THR:HB	17:P:123:TYR:HD1	1.79	0.46
32:f:106:TYR:HD1	32:f:114:ILE:HG21	1.80	0.46
1:2:61:A:H5'	1:2:316:G:H4'	1.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1298:G:H5'	17:P:78:THR:HA	1.96	0.46
1:2:1590:C:H5''	1:2:1591:C:H5	1.80	0.46
4:C:196:ILE:HB	4:C:223:TYR:HB2	1.97	0.46
16:O:90:ILE:HG22	16:O:124:MET:HE1	1.96	0.46
19:R:71:ILE:HB	19:R:74:GLN:HB2	1.98	0.46
35:y:324:TYR:CG	35:y:401:PRO:CG	2.84	0.46
1:2:871:U:H3'	1:2:872:A:H4'	1.97	0.46
1:2:1869:A:C5	35:y:120:GLU:HG3	2.50	0.46
7:F:50:PRO:HB3	7:F:70:GLU:HA	1.98	0.46
8:G:57:ASP:HA	8:G:106:LEU:HA	1.96	0.46
2:A:4:ALA:HB2	23:V:80:SER:HB2	1.98	0.46
7:F:78:MET:HE1	7:F:152:TRP:HE1	1.81	0.46
19:R:57:LEU:O	19:R:61:ILE:HG13	2.16	0.46
1:2:28:U:H2'	1:2:29:G:C8	2.50	0.46
1:2:878:G:O6	1:2:908:A:C6	2.69	0.46
1:2:1662:U:O4	1:2:1663:A:N6	2.49	0.46
2:A:109:THR:HG21	2:A:139:TYR:HD2	1.79	0.46
4:C:166:ARG:HB3	4:C:247:THR:HB	1.97	0.46
6:E:118:GLU:OE2	6:E:237:SER:N	2.49	0.46
1:2:1213:C:H2'	1:2:1214:A:C8	2.51	0.46
4:C:254:ASP:HB3	23:V:1:MET:HG2	1.97	0.46
7:F:201:LYS:O	7:F:204:ARG:NE	2.44	0.46
1:2:874:G:H2'	1:2:875:A:H8	1.81	0.46
1:2:1485:U:OP1	5:D:151:LYS:NZ	2.46	0.46
19:R:42:PRO:HG2	19:R:46:LEU:HD23	1.97	0.46
34:x:99:ILE:HG22	34:x:105:LEU:HB2	1.98	0.46
29:c:67:ARG:HB2	35:y:372:PRO:HA	1.98	0.46
33:g:166:VAL:HG11	33:g:198:VAL:HG11	1.97	0.46
34:x:98:PRO:HG2	34:x:150:LEU:HD21	1.98	0.46
1:2:1578:U:H4'	1:2:1579:A:C8	2.50	0.46
2:A:127:PRO:HD3	2:A:146:ALA:HB1	1.98	0.46
10:I:6:ASP:OD1	10:I:6:ASP:N	2.49	0.46
11:J:138:ARG:HH21	11:J:153:SER:HB2	1.81	0.46
12:K:16:PHE:HB2	12:K:79:LEU:HD13	1.98	0.46
1:2:1140:G:HO2'	1:2:1151:G:HO2'	1.59	0.46
1:2:1724:A:H2'	1:2:1725:U:H6	1.81	0.46
1:2:1868:U:C5'	34:x:83:ASN:O	2.64	0.46
19:R:41:ILE:H	19:R:41:ILE:HG13	1.56	0.46
34:x:92:TRP:O	34:x:96:PHE:CB	2.64	0.46
1:2:185:G:O6	1:2:214:U:O4	2.34	0.45
1:2:941:C:H2'	1:2:942:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1354:G:N1	1:2:1357:A:OP2	2.47	0.45
1:2:1606:G:H1	1:2:1632:G:H2'	1.82	0.45
5:D:47:GLU:HB3	5:D:87:TYR:HE2	1.81	0.45
17:P:22:LEU:HD23	17:P:25:LEU:HD12	1.98	0.45
35:y:39:ASP:OD2	35:y:42:THR:HG23	2.16	0.45
3:B:52:THR:HG22	3:B:54:GLY:H	1.82	0.45
4:C:134:ASN:O	4:C:167:ARG:NH1	2.49	0.45
1:2:560:A:OP2	11:J:177:ASN:ND2	2.50	0.45
1:2:925:G:N2	1:2:1017:U:O2	2.36	0.45
1:2:991:G:O6	35:y:405:ARG:NE	2.50	0.45
1:2:1650:A:H3'	1:2:1651:A:H8	1.81	0.45
6:E:45:ILE:HA	6:E:61:VAL:HG11	1.97	0.45
6:E:123:LEU:HD22	6:E:159:THR:HG22	1.98	0.45
15:N:84:LEU:HA	15:N:85:PRO:HD3	1.82	0.45
17:P:68:PRO:HD2	17:P:71:GLU:HG3	1.98	0.45
1:2:5:U:H2'	1:2:6:G:C8	2.51	0.45
1:2:455:A:O2'	1:2:1735:A:N3	2.35	0.45
33:g:296:GLN:HB3	33:g:312:VAL:H	1.81	0.45
1:2:51:U:H2'	1:2:52:G:C8	2.52	0.45
9:H:66:VAL:HG22	9:H:96:ALA:HB1	1.98	0.45
16:O:62:VAL:HG11	16:O:67:ASP:HB2	1.98	0.45
1:2:456:C:HO2'	1:2:1801:A:HO2'	1.62	0.45
8:G:226:GLU:O	8:G:230:LYS:N	2.50	0.45
12:K:29:MET:HB3	12:K:42:ASN:HB3	1.98	0.45
29:c:14:VAL:HB	29:c:53:GLY:H	1.82	0.45
1:2:1337:C:OP1	30:d:44:ARG:NH2	2.35	0.45
4:C:127:PHE:HD1	4:C:141:VAL:HG22	1.81	0.45
13:L:124:ASP:N	13:L:124:ASP:OD1	2.48	0.45
13:L:135:SER:O	13:L:139:ARG:NH1	2.50	0.45
25:X:72:VAL:HG21	25:X:102:VAL:HG21	1.99	0.45
34:x:100:VAL:HA	34:x:105:LEU:H	1.81	0.45
1:2:1218:C:H2'	1:2:1219:C:H6	1.81	0.45
13:L:109:MET:HE2	13:L:109:MET:HB3	1.71	0.45
22:U:43:ALA:HB1	22:U:48:LEU:HB2	1.98	0.45
34:x:111:LEU:N	35:y:129:HIS:O	2.50	0.45
1:2:940:U:H3	1:2:1002:U:H3	1.64	0.45
1:2:1047:C:H5''	16:O:143:LYS:HA	1.98	0.45
1:2:1255:G:C6	1:2:1257:G:N1	2.85	0.45
1:2:1779:G:H2'	1:2:1780:G:C8	2.51	0.45
28:b:14:GLU:HG3	28:b:17:ARG:HH22	1.81	0.45
1:2:1465:A:O3'	19:R:10:LYS:NZ	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:57:ASP:OD1	8:G:61:PHE:N	2.49	0.45
8:G:84:TYR:OH	8:G:91:GLU:O	2.25	0.45
19:R:6:THR:H	19:R:9:VAL:HB	1.81	0.45
33:g:269:GLU:HG2	33:g:271:LYS:HE2	1.99	0.45
34:x:182:ARG:HH11	34:x:229:ILE:HA	1.82	0.45
1:2:500:A:H5'	1:2:501:C:H5	1.82	0.44
1:2:916:A:O2'	15:N:73:ARG:NH1	2.48	0.44
2:A:29:ASN:HB2	2:A:151:ASP:HB2	1.99	0.44
7:F:19:LEU:N	7:F:23:TRP:O	2.41	0.44
9:H:121:THR:O	9:H:125:VAL:N	2.45	0.44
12:K:35:LEU:HD22	12:K:38:LYS:HD2	1.99	0.44
21:T:56:ARG:HH21	21:T:79:TYR:HD2	1.64	0.44
1:2:384:U:O4	10:I:5:ARG:NH2	2.48	0.44
1:2:560:A:C8	11:J:173:VAL:HG11	2.51	0.44
3:B:137:LEU:HD11	3:B:176:VAL:HG21	1.99	0.44
6:E:154:ILE:HG21	6:E:160:ILE:HD11	1.98	0.44
11:J:63:LEU:HD11	11:J:69:ARG:HH11	1.82	0.44
23:V:10:ASP:OD1	23:V:11:LEU:N	2.49	0.44
26:Y:74:MET:HE2	26:Y:74:MET:HB3	1.92	0.44
33:g:63:SER:OG	33:g:84:ASP:OD2	2.30	0.44
33:g:260:ASP:N	33:g:265:ILE:O	2.50	0.44
1:2:925:G:O6	1:2:1017:U:O4	2.36	0.44
1:2:1010:G:H2'	1:2:1011:A:C8	2.53	0.44
4:C:102:LEU:HD12	4:C:102:LEU:HA	1.87	0.44
5:D:126:ILE:HD12	5:D:188:ILE:HD11	2.00	0.44
6:E:42:LEU:HD13	6:E:47:PHE:HB2	2.00	0.44
7:F:119:SER:HB2	7:F:180:ALA:HB1	1.99	0.44
28:b:49:HIS:CD2	28:b:70:LYS:HG2	2.53	0.44
33:g:18:VAL:HB	33:g:301:GLY:HA3	2.00	0.44
1:2:63:U:O2'	1:2:170:A:N3	2.46	0.44
1:2:1213:C:H2'	1:2:1214:A:H8	1.83	0.44
1:2:1455:A:OP1	19:R:5:ARG:NH2	2.50	0.44
4:C:127:PHE:CD1	4:C:141:VAL:HG22	2.53	0.44
12:K:47:LYS:HB3	12:K:47:LYS:HE3	1.75	0.44
19:R:59:LYS:HZ1	19:R:63:ARG:CG	2.17	0.44
1:2:103:A:H5'	10:I:12:ARG:CZ	2.48	0.44
1:2:671:A:H4'	1:2:672:A:H5''	1.99	0.44
1:2:678:U:OP2	1:2:1026:C:N4	2.37	0.44
5:D:11:PHE:HD1	5:D:11:PHE:HA	1.71	0.44
15:N:98:VAL:HB	15:N:115:LEU:HD13	1.99	0.44
1:2:31:U:O2'	1:2:643:A:N1	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:433:A:OP1	10:I:25:ARG:NH2	2.49	0.44
1:2:563:G:N7	11:J:172:ARG:NH2	2.66	0.44
4:C:133:TYR:CE1	4:C:216:MET:CA	2.99	0.44
27:Z:68:ILE:HG21	27:Z:97:ILE:HD13	1.99	0.44
27:Z:69:THR:HG22	27:Z:71:ALA:H	1.82	0.44
1:2:1376:A:O2'	35:y:348:GLN:N	2.42	0.44
1:2:1753:C:H2'	1:2:1754:G:C8	2.53	0.44
4:C:244:ILE:HA	4:C:247:THR:HG23	1.98	0.44
7:F:39:ILE:HD13	7:F:113:VAL:HG13	1.99	0.44
22:U:56:MET:HB2	22:U:86:LYS:HB3	1.99	0.44
34:x:202:ILE:HG22	34:x:211:ILE:HG22	2.00	0.44
1:2:944:A:H5''	16:O:134:PRO:HB3	2.00	0.44
1:2:1243:U:O4	1:2:1265:A:N6	2.51	0.44
1:2:1312:G:H1	14:M:34:GLY:HA3	1.83	0.44
1:2:1426:U:H1'	21:T:5:THR:HG21	2.00	0.44
25:X:140:ARG:HD2	25:X:141:PRO:HD2	2.00	0.44
1:2:33:G:O2'	1:2:564:A:O2'	2.36	0.44
1:2:156:G:OP1	8:G:2:LYS:NZ	2.51	0.44
2:A:81:ASN:OD1	2:A:81:ASN:N	2.49	0.44
3:B:197:ILE:HB	3:B:210:VAL:HG21	2.00	0.44
4:C:78:LEU:HD13	4:C:97:PHE:HD2	1.81	0.44
4:C:137:VAL:CG1	4:C:217:ALA:HA	2.48	0.44
6:E:71:LYS:HG2	6:E:76:VAL:HG22	2.00	0.44
19:R:60:ARG:HH21	19:R:63:ARG:CG	2.31	0.44
28:b:24:LEU:HD12	28:b:24:LEU:HA	1.85	0.44
33:g:68:ASP:OD2	33:g:111:VAL:N	2.38	0.44
1:2:1707:U:C4	1:2:1828:C:N3	2.86	0.43
4:C:95:ASP:O	4:C:99:GLY:HA2	2.18	0.43
4:C:174:ILE:O	4:C:200:ARG:NH2	2.51	0.43
4:C:193:VAL:HG11	4:C:240:THR:HB	1.99	0.43
32:f:104:LYS:HG2	32:f:118:ARG:HH22	1.83	0.43
33:g:130:LYS:NZ	33:g:141:THR:OG1	2.39	0.43
34:x:87:PRO:HA	34:x:90:GLU:HB2	2.00	0.43
1:2:1565:C:P	21:T:102:ARG:HH21	2.41	0.43
8:G:122:PRO:O	8:G:127:THR:OG1	2.33	0.43
13:L:68:ILE:HG21	13:L:143:LEU:HD11	1.99	0.43
18:Q:34:VAL:N	18:Q:37:ARG:O	2.51	0.43
25:X:93:PHE:O	25:X:140:ARG:NH1	2.51	0.43
34:x:80:VAL:HG11	34:x:109:PHE:HE1	1.83	0.43
1:2:72:C:H2'	1:2:73:C:C6	2.53	0.43
1:2:1297:U:H2'	1:2:1298:G:H3'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1309:C:H41	32:f:95:ARG:HE	1.65	0.43
1:2:1529:C:O2'	21:T:87:VAL:O	2.29	0.43
1:2:1652:G:N2	1:2:1672:U:O2	2.42	0.43
2:A:41:ARG:HE	2:A:45:GLY:HA2	1.84	0.43
11:J:127:ARG:HD3	31:e:31:ARG:HD3	2.01	0.43
21:T:6:VAL:HG21	21:T:131:LEU:HD13	1.99	0.43
35:y:90:THR:HG22	35:y:250:LEU:HD13	2.00	0.43
1:2:527:C:H4'	11:J:121:LYS:HD2	2.00	0.43
1:2:678:U:OP1	15:N:127:ARG:NH2	2.51	0.43
1:2:991:G:C6	1:2:1134:G:H4'	2.53	0.43
1:2:1304:U:OP1	32:f:93:HIS:N	2.52	0.43
12:K:15:LEU:HD22	12:K:49:MET:HE1	2.00	0.43
13:L:60:CYS:SG	13:L:114:SER:OG	2.67	0.43
35:y:258:MET:SD	35:y:258:MET:N	2.92	0.43
1:2:561:A:O2'	11:J:134:HIS:NE2	2.38	0.43
1:2:869:A:C8	9:H:114:GLN:HB2	2.53	0.43
3:B:106:THR:HG22	3:B:108:ASP:H	1.83	0.43
6:E:11:ARG:HA	6:E:28:ALA:HB2	2.00	0.43
7:F:35:LEU:HD21	7:F:146:ARG:HD2	2.00	0.43
9:H:145:ARG:HA	24:W:51:GLU:HA	2.00	0.43
10:I:172:LEU:HB3	10:I:190:LEU:HD12	2.00	0.43
12:K:52:LEU:O	12:K:56:GLY:N	2.49	0.43
17:P:38:SER:HB2	17:P:41:GLN:HG2	2.01	0.43
17:P:108:LYS:HD3	20:S:116:LYS:HE2	2.01	0.43
1:2:1018:U:O2'	15:N:86:GLU:OE2	2.36	0.43
1:2:1084:A:OP1	1:2:1858:G:O2'	2.28	0.43
1:2:1293:A:H2'	1:2:1294:G:C8	2.53	0.43
2:A:2:SER:O	23:V:80:SER:N	2.51	0.43
14:M:95:ASP:N	14:M:99:LYS:O	2.46	0.43
33:g:114:SER:OG	33:g:118:ARG:N	2.52	0.43
34:x:111:LEU:HB3	35:y:130:LEU:HA	2.00	0.43
1:2:973:C:N3	16:O:55:ARG:NH1	2.67	0.43
1:2:1256:G:N2	1:2:1658:G:O3'	2.51	0.43
3:B:81:PHE:HD2	3:B:109:LYS:HG2	1.83	0.43
4:C:168:GLY:N	4:C:179:THR:O	2.44	0.43
11:J:47:LYS:HG3	11:J:102:ILE:HD12	2.01	0.43
16:O:34:PHE:HA	16:O:98:ARG:HB3	2.01	0.43
22:U:43:ALA:O	22:U:47:ASN:N	2.52	0.43
26:Y:17:LEU:H	26:Y:17:LEU:HG	1.61	0.43
28:b:33:MET:HE3	28:b:48:SER:HA	2.00	0.43
35:y:377:ASP:OD2	35:y:382:SER:OG	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:975:G:N2	16:O:50:LYS:O	2.51	0.43
2:A:128:ARG:HA	2:A:128:ARG:HD2	1.80	0.43
9:H:146:VAL:HG22	9:H:152:ARG:HG2	2.01	0.43
16:O:35:ALA:HB2	16:O:112:ALA:HB2	2.00	0.43
19:R:60:ARG:HH21	19:R:63:ARG:HG3	1.84	0.43
20:S:55:ARG:NH2	27:Z:80:ARG:HE	2.17	0.43
22:U:60:THR:HG22	22:U:62:ARG:HG3	2.01	0.43
25:X:60:LYS:HD2	25:X:116:PRO:HB3	2.00	0.43
30:d:29:GLY:O	30:d:40:ARG:N	2.50	0.43
1:2:88:G:N2	1:2:499:G:O3'	2.52	0.43
1:2:981:A:H2'	1:2:982:G:C8	2.54	0.43
2:A:38:ILE:HD12	2:A:38:ILE:HA	1.89	0.43
7:F:35:LEU:HD21	7:F:146:ARG:HB3	2.01	0.43
34:x:92:TRP:O	34:x:96:PHE:HB2	2.19	0.43
2:A:63:ARG:O	2:A:67:ALA:N	2.50	0.43
6:E:137:PRO:HG2	6:E:150:PRO:HD2	2.01	0.43
9:H:147:LYS:HE2	9:H:153:LEU:HB3	2.01	0.43
17:P:95:GLY:HA2	17:P:103:ASN:O	2.18	0.43
20:S:38:ARG:HD2	21:T:45:LEU:HD21	2.01	0.43
23:V:64:GLU:O	23:V:68:SER:OG	2.33	0.43
1:2:388:U:H2'	1:2:389:A:C8	2.53	0.42
1:2:1622:U:H3'	1:2:1623:A:H4'	2.01	0.42
1:2:1721:U:H4'	1:2:1722:G:H4'	2.00	0.42
1:2:1786:U:H2'	1:2:1787:G:C8	2.54	0.42
19:R:60:ARG:NH2	19:R:63:ARG:HG3	2.34	0.42
22:U:54:VAL:HG22	22:U:88:LEU:HB2	2.00	0.42
2:A:68:ILE:HG23	2:A:120:ARG:HH11	1.84	0.42
9:H:109:ARG:HD3	9:H:111:LYS:HE3	2.01	0.42
19:R:60:ARG:HH11	19:R:60:ARG:HB2	1.84	0.42
1:2:1228:A:H2'	1:2:1229:G:H8	1.84	0.42
1:2:1351:G:H1	1:2:1360:U:H3	1.67	0.42
4:C:133:TYR:CZ	4:C:216:MET:HG2	2.55	0.42
27:Z:46:ASN:HB2	27:Z:80:ARG:HG3	2.01	0.42
27:Z:74:SER:OG	27:Z:74:SER:O	2.37	0.42
34:x:84:ARG:HA	34:x:84:ARG:HD3	1.86	0.42
1:2:1615:U:H3'	17:P:43:ARG:HH22	1.84	0.42
20:S:36:VAL:HG13	20:S:40:TYR:HB3	2.00	0.42
35:y:398:ARG:HH11	35:y:398:ARG:CG	2.32	0.42
1:2:56:G:OP1	26:Y:111:LYS:NZ	2.52	0.42
1:2:535:G:H2'	1:2:536:A:H8	1.85	0.42
1:2:1082:A:HO2'	1:2:1842:C:HO2'	1.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1232:U:H2'	1:2:1233:G:H8	1.84	0.42
1:2:1593:C:H5	27:Z:104:ARG:HH21	1.68	0.42
1:2:1618:C:H3'	1:2:1619:A:H8	1.85	0.42
4:C:129:ALA:CB	4:C:213:LEU:HD21	2.49	0.42
10:I:48:VAL:HG11	10:I:54:LYS:HE3	2.01	0.42
15:N:13:GLN:HE21	28:b:21:LYS:HE2	1.84	0.42
35:y:75:ASP:OD2	35:y:244:VAL:HG22	2.19	0.42
35:y:343:ASP:N	35:y:343:ASP:OD1	2.50	0.42
1:2:913:A:H2	9:H:98:ARG:HA	1.85	0.42
14:M:35:ILE:HG12	32:f:102:VAL:HG11	2.02	0.42
20:S:3:LEU:HD22	20:S:54:LYS:HE2	2.02	0.42
1:2:10:G:O4'	1:2:1697:A:O2'	2.38	0.42
1:2:924:G:H21	15:N:87:ASP:HB3	1.85	0.42
1:2:1206:G:H2'	1:2:1208:A:H8	1.84	0.42
1:2:1865:C:N4	34:x:204:LEU:HB2	2.35	0.42
11:J:113:GLN:OE1	11:J:154:GLN:NE2	2.52	0.42
1:2:540:U:O2'	1:2:543:C:N4	2.52	0.42
1:2:1312:G:N1	14:M:34:GLY:HA3	2.35	0.42
1:2:1575:G:H2'	1:2:1576:G:H8	1.85	0.42
6:E:6:LYS:O	6:E:30:ARG:NH2	2.52	0.42
1:2:798:G:H1'	9:H:107:LYS:HA	2.02	0.42
1:2:869:A:H1'	1:2:915:G:H21	1.84	0.42
1:2:893:U:H2'	1:2:894:G:C8	2.54	0.42
1:2:1442:U:H2'	1:2:1443:C:C6	2.55	0.42
4:C:96:PHE:HD2	4:C:97:PHE:CD1	2.37	0.42
4:C:133:TYR:CE1	4:C:216:MET:HG2	2.54	0.42
4:C:210:PRO:HB3	4:C:240:THR:HG21	2.01	0.42
4:C:259:THR:HG21	23:V:15:ARG:HA	2.02	0.42
6:E:192:ILE:N	6:E:243:GLY:O	2.45	0.42
10:I:25:ARG:HA	10:I:25:ARG:HD3	1.86	0.42
1:2:1462:U:O2	35:y:348:GLN:NE2	2.53	0.42
1:2:1651:A:H2'	1:2:1652:G:H8	1.84	0.42
1:2:1867:U:OP1	35:y:393:GLY:HA2	2.18	0.42
3:B:217:MET:HG2	3:B:220:LYS:HE3	2.02	0.42
4:C:137:VAL:CG1	4:C:217:ALA:HB2	2.50	0.42
19:R:60:ARG:HH21	19:R:63:ARG:CB	2.32	0.42
21:T:64:LEU:HB3	21:T:122:LYS:HA	2.02	0.42
22:U:34:LYS:NZ	22:U:107:GLU:OE1	2.35	0.42
6:E:114:ILE:HG21	6:E:114:ILE:HD13	1.85	0.41
35:y:269:ARG:HA	35:y:276:THR:HA	2.02	0.41
1:2:1648:G:H5''	18:Q:125:ARG:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:144:LEU:HB3	29:c:49:PRO:HG2	2.03	0.41
9:H:60:ILE:HD11	9:H:90:LYS:HE3	2.02	0.41
15:N:40:LEU:HD23	15:N:43:LYS:HD2	2.02	0.41
20:S:13:LEU:O	20:S:19:ASN:ND2	2.53	0.41
21:T:107:LEU:HB3	21:T:112:MET:HB2	2.02	0.41
33:g:70:VAL:O	33:g:79:LEU:N	2.52	0.41
34:x:201:ARG:HD3	34:x:201:ARG:HA	1.87	0.41
1:2:641:A:O2'	1:2:645:C:OP1	2.38	0.41
1:2:1269:G:H21	1:2:1298:G:H1	1.68	0.41
1:2:1512:C:H2'	1:2:1513:C:C6	2.55	0.41
1:2:1631:U:H4'	20:S:103:LEU:HD21	2.02	0.41
6:E:164:LEU:HD23	6:E:164:LEU:HA	1.91	0.41
19:R:60:ARG:HB2	19:R:60:ARG:NH1	2.35	0.41
20:S:84:LEU:HD12	20:S:95:TYR:HB3	2.02	0.41
1:2:917:U:H2'	1:2:918:U:C6	2.56	0.41
1:2:1707:U:O4	1:2:1828:C:N3	2.53	0.41
10:I:119:LEU:HA	10:I:120:PRO:HD3	1.93	0.41
15:N:37:ILE:HG23	15:N:50:ILE:HG21	2.03	0.41
15:N:87:ASP:OD1	15:N:129:TYR:OH	2.38	0.41
16:O:62:VAL:HG12	16:O:64:ALA:H	1.85	0.41
33:g:140:TYR:HD2	33:g:142:VAL:HG22	1.84	0.41
1:2:1245:G:H2'	1:2:1246:A:H8	1.85	0.41
1:2:1668:U:OP2	18:Q:141:TYR:OH	2.30	0.41
5:D:167:TYR:HB3	5:D:189:MET:HG3	2.03	0.41
11:J:37:LEU:HD11	11:J:106:LEU:HD21	2.02	0.41
26:Y:55:ILE:HD13	26:Y:55:ILE:HG21	1.90	0.41
33:g:258:ILE:HD12	33:g:267:VAL:HB	2.01	0.41
1:2:317:C:OP2	8:G:183:ARG:NH1	2.36	0.41
1:2:381:C:H41	10:I:27:TYR:HB2	1.84	0.41
1:2:987:A:H61	3:B:120:MET:HE1	1.85	0.41
5:D:199:GLY:HA2	5:D:200:PRO:HD3	1.90	0.41
13:L:75:GLY:HA3	13:L:88:ILE:HD12	2.02	0.41
16:O:98:ARG:HE	16:O:134:PRO:HD3	1.84	0.41
19:R:17:ILE:HG22	19:R:71:ILE:HD11	2.01	0.41
29:c:43:ILE:HD12	35:y:363:ALA:HA	2.01	0.41
33:g:23:THR:HA	33:g:31:ILE:HG23	2.03	0.41
1:2:60:A:O2'	1:2:61:A:O5'	2.35	0.41
1:2:846:G:OP2	6:E:106:LYS:NZ	2.47	0.41
1:2:1678:A:OP2	7:F:63:LYS:NZ	2.43	0.41
6:E:62:LYS:HE3	6:E:62:LYS:HB2	1.87	0.41
12:K:24:LYS:HA	12:K:66:HIS:CE1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:78:VAL:HA	18:Q:81:ILE:HD12	2.02	0.41
19:R:66:VAL:HG13	19:R:69:ILE:CB	2.43	0.41
1:2:126:G:N2	1:2:180:G:H21	2.17	0.41
1:2:751:G:H2'	1:2:752:G:C8	2.55	0.41
1:2:1865:C:H5''	34:x:187:GLY:HA2	2.03	0.41
5:D:16:ILE:HD13	5:D:16:ILE:HG21	1.88	0.41
7:F:39:ILE:HG21	7:F:113:VAL:HG13	2.03	0.41
11:J:111:GLN:NE2	11:J:127:ARG:HB2	2.35	0.41
18:Q:101:ASP:N	18:Q:101:ASP:OD1	2.46	0.41
33:g:133:ASN:HD22	33:g:137:VAL:HB	1.85	0.41
1:2:319:C:H2'	1:2:320:G:C8	2.56	0.41
1:2:352:U:H2'	1:2:353:C:C6	2.56	0.41
1:2:388:U:H2'	1:2:389:A:H8	1.85	0.41
1:2:561:A:H2'	1:2:562:U:O4'	2.21	0.41
1:2:808:A:O2'	1:2:809:A:O5'	2.39	0.41
1:2:935:G:H2'	1:2:936:G:H8	1.85	0.41
1:2:1217:A:O2'	1:2:1684:C:O2	2.37	0.41
1:2:1869:A:C8	35:y:120:GLU:HG3	2.56	0.41
6:E:71:LYS:HE2	6:E:74:GLY:HA2	2.03	0.41
7:F:79:HIS:HB3	7:F:82:ASN:HD22	1.86	0.41
14:M:47:ALA:HB1	14:M:110:VAL:HG11	2.02	0.41
16:O:119:LEU:H	16:O:119:LEU:HG	1.66	0.41
19:R:59:LYS:HA	19:R:59:LYS:HD2	1.80	0.41
1:2:575:A:P	26:Y:93:ARG:HH21	2.44	0.41
1:2:1033:G:H1	1:2:1080:A:HO2'	1.65	0.41
1:2:1329:U:H3	1:2:1500:G:H1	1.68	0.41
1:2:1453:C:O2'	19:R:48:ASN:O	2.38	0.41
1:2:1753:C:H2'	1:2:1754:G:H8	1.85	0.41
3:B:49:VAL:HG22	3:B:65:ARG:HH22	1.86	0.41
4:C:129:ALA:HB2	4:C:139:LEU:HD13	2.03	0.41
9:H:158:LEU:HD23	9:H:158:LEU:HA	1.93	0.41
13:L:38:LYS:NZ	13:L:64:GLY:O	2.54	0.41
26:Y:105:LYS:HD2	26:Y:105:LYS:HA	1.90	0.41
34:x:78:ILE:HA	34:x:79:PRO:HD3	1.91	0.41
1:2:941:C:H2'	1:2:942:G:H8	1.87	0.40
1:2:1261:C:H41	1:2:1661:A:H62	1.67	0.40
1:2:1486:A:OP2	5:D:151:LYS:NZ	2.51	0.40
1:2:1724:A:H2'	1:2:1725:U:C6	2.55	0.40
2:A:60:LEU:HD22	2:A:159:ILE:HG12	2.03	0.40
7:F:19:LEU:HB3	7:F:23:TRP:HB2	2.04	0.40
23:V:1:MET:HG3	23:V:2:GLN:HG3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:X:68:LYS:HB3	25:X:91:LEU:HD22	2.04	0.40
26:Y:28:LEU:HD21	26:Y:68:LYS:HE2	2.03	0.40
33:g:124:SER:OG	33:g:125:ARG:N	2.54	0.40
1:2:748:C:H42	1:2:794:A:H61	1.69	0.40
2:A:159:ILE:HA	2:A:159:ILE:HD12	1.81	0.40
3:B:140:VAL:HG23	3:B:213:ARG:HG2	2.03	0.40
7:F:71:ARG:NH2	7:F:148:ASN:OD1	2.40	0.40
18:Q:37:ARG:HA	18:Q:38:PRO:HD3	1.96	0.40
33:g:40:ILE:HB	33:g:59:LEU:HB2	2.04	0.40
33:g:196:ASN:ND2	33:g:237:ASN:O	2.53	0.40
35:y:234:CYS:HB3	35:y:236:THR:HG23	2.02	0.40
1:2:1582:C:H2'	1:2:1583:C:C6	2.56	0.40
24:W:69:LEU:HD21	24:W:72:CYS:HB2	2.03	0.40
1:2:551:U:H4'	31:e:39:ASN:HB3	2.03	0.40
1:2:1206:G:H2'	1:2:1208:A:C8	2.56	0.40
1:2:1564:C:H3'	21:T:101:ARG:HH12	1.85	0.40
7:F:176:GLU:OE1	7:F:188:TYR:N	2.55	0.40
15:N:107:LYS:HB2	15:N:107:LYS:HE3	1.85	0.40
21:T:36:THR:HG22	21:T:37:VAL:HB	2.04	0.40
33:g:45:LEU:HD23	33:g:53:GLY:HA3	2.03	0.40
34:x:75:THR:OG1	34:x:118:ILE:O	2.36	0.40
35:y:270:CYS:HB2	35:y:275:LYS:H	1.87	0.40
1:2:841:G:H2'	1:2:842:C:C6	2.57	0.40
3:B:90:ASP:HB3	3:B:92:GLN:HE21	1.86	0.40
13:L:40:ILE:HD12	13:L:40:ILE:HA	1.88	0.40
17:P:42:ARG:HH11	17:P:42:ARG:HD2	1.73	0.40
25:X:28:LYS:HG2	25:X:32:LEU:HD22	2.04	0.40
34:x:103:LEU:HD22	34:x:129:ALA:HB1	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

There are no protein backbone outliers to report in this entry.

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	180/243 (74%)	178 (99%)	2 (1%)	65	74
3	B	194/231 (84%)	193 (100%)	1 (0%)	81	80
4	C	184/225 (82%)	180 (98%)	4 (2%)	45	65
5	D	189/202 (94%)	188 (100%)	1 (0%)	81	80
6	E	224/225 (100%)	221 (99%)	3 (1%)	61	72
7	F	159/170 (94%)	159 (100%)	0	100	100
8	G	200/218 (92%)	200 (100%)	0	100	100
9	H	167/174 (96%)	166 (99%)	1 (1%)	78	79
10	I	178/180 (99%)	178 (100%)	0	100	100
11	J	160/168 (95%)	159 (99%)	1 (1%)	78	79
12	K	86/136 (63%)	86 (100%)	0	100	100
13	L	135/142 (95%)	134 (99%)	1 (1%)	76	78
14	M	104/108 (96%)	104 (100%)	0	100	100
15	N	130/131 (99%)	129 (99%)	1 (1%)	73	77
16	O	105/119 (88%)	104 (99%)	1 (1%)	68	75
17	P	107/130 (82%)	107 (100%)	0	100	100
18	Q	115/121 (95%)	115 (100%)	0	100	100
19	R	110/122 (90%)	106 (96%)	4 (4%)	31	57
20	S	124/132 (94%)	124 (100%)	0	100	100
21	T	114/115 (99%)	113 (99%)	1 (1%)	70	76
22	U	93/107 (87%)	92 (99%)	1 (1%)	65	74
23	V	66/67 (98%)	66 (100%)	0	100	100
24	W	112/113 (99%)	112 (100%)	0	100	100
25	X	113/115 (98%)	113 (100%)	0	100	100
26	Y	108/115 (94%)	106 (98%)	2 (2%)	50	68
27	Z	64/103 (62%)	64 (100%)	0	100	100
28	b	74/76 (97%)	74 (100%)	0	100	100
29	c	54/62 (87%)	53 (98%)	1 (2%)	50	68
30	d	48/49 (98%)	47 (98%)	1 (2%)	47	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	e	45/48 (94%)	45 (100%)	0	100	100
32	f	56/140 (40%)	56 (100%)	0	100	100
33	g	272/275 (99%)	272 (100%)	0	100	100
34	x	146/208 (70%)	143 (98%)	3 (2%)	47	66
35	y	275/367 (75%)	273 (99%)	2 (1%)	76	78
36	z	28/512 (6%)	28 (100%)	0	100	100
All	All	4519/5649 (80%)	4488 (99%)	31 (1%)	73	78

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	130	ASP
2	A	140	VAL
3	B	210	VAL
4	C	104	ASP
4	C	117	ARG
4	C	130	ILE
4	C	134	ASN
5	D	208	VAL
6	E	38	LEU
6	E	46	ILE
6	E	162	ILE
9	H	122	LEU
11	J	29	LEU
13	L	22	ARG
15	N	84	LEU
16	O	119	LEU
19	R	41	ILE
19	R	58	MET
19	R	59	LYS
19	R	60	ARG
21	T	134	ILE
22	U	47	ASN
26	Y	17	LEU
26	Y	107	ARG
29	c	55	VAL
30	d	26	ASN
34	x	118	ILE
34	x	225	ILE
34	x	227	ASN

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Mol	Chain	Res	Type
35	y	398	ARG
35	y	400	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (61) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	50	ASN
2	A	131	HIS
2	A	141	ASN
3	B	92	GLN
3	B	159	GLN
3	B	186	ASN
4	C	272	HIS
5	D	57	ASN
5	D	174	HIS
6	E	36	HIS
6	E	209	HIS
7	F	114	ASN
7	F	203	ASN
8	G	56	ASN
8	G	81	HIS
9	H	33	ASN
9	H	73	GLN
9	H	157	HIS
9	H	186	ASN
10	I	87	ASN
10	I	99	ASN
10	I	116	HIS
11	J	156	HIS
12	K	61	GLN
12	K	77	GLN
13	L	39	ASN
13	L	65	ASN
14	M	28	HIS
15	N	13	GLN
15	N	62	GLN
15	N	105	ASN
15	N	123	HIS
17	P	53	GLN
17	P	79	HIS
17	P	103	ASN
18	Q	29	ASN

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Mol	Chain	Res	Type
18	Q	80	GLN
20	S	19	ASN
20	S	120	HIS
20	S	134	GLN
21	T	91	HIS
22	U	47	ASN
23	V	21	ASN
24	W	15	ASN
25	X	61	GLN
26	Y	63	HIS
28	b	9	HIS
29	c	24	GLN
31	e	56	ASN
32	f	139	HIS
33	g	64	HIS
33	g	133	ASN
33	g	237	ASN
33	g	311	GLN
34	x	106	GLN
34	x	227	ASN
34	x	232	ASN
35	y	17	HIS
35	y	216	GLN
35	y	307	HIS
35	y	339	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1644/1882 (87%)	534 (32%)	0

All (534) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	3	C
1	2	4	C
1	2	5	U
1	2	14	C
1	2	17	C
1	2	23	G
1	2	25	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	2	27	A
1	2	33	G
1	2	41	G
1	2	42	A
1	2	44	U
1	2	46	A
1	2	49	C
1	2	50	A
1	2	56	G
1	2	58	C
1	2	60	A
1	2	61	A
1	2	62	G
1	2	65	C
1	2	66	G
1	2	67	C
1	2	68	A
1	2	69	C
1	2	72	C
1	2	73	C
1	2	74	G
1	2	75	G
1	2	76	U
1	2	77	A
1	2	79	A
1	2	80	G
1	2	100	U
1	2	103	A
1	2	104	A
1	2	110	U
1	2	111	A
1	2	113	G
1	2	114	G
1	2	115	U
1	2	126	G
1	2	127	C
1	2	128	U
1	2	129	C
1	2	130	G
1	2	143	U
1	2	144	U
1	2	160	U

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Mol	Chain	Res	Type
1	2	161	U
1	2	163	U
1	2	167	G
1	2	168	C
1	2	171	A
1	2	179	C
1	2	181	A
1	2	182	C
1	2	183	G
1	2	184	G
1	2	188	C
1	2	189	U
1	2	191	A
1	2	192	C
1	2	202	G
1	2	208	G
1	2	209	A
1	2	214	U
1	2	215	G
1	2	217	A
1	2	290	U
1	2	291	G
1	2	292	A
1	2	295	C
1	2	306	C
1	2	307	G
1	2	309	G
1	2	310	C
1	2	312	G
1	2	315	C
1	2	318	A
1	2	321	C
1	2	332	G
1	2	333	G
1	2	335	G
1	2	338	G
1	2	340	C
1	2	341	C
1	2	343	A
1	2	347	G
1	2	360	A
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	377	G
1	2	381	C
1	2	384	U
1	2	385	G
1	2	386	C
1	2	398	A
1	2	400	C
1	2	407	G
1	2	408	A
1	2	409	C
1	2	413	G
1	2	417	C
1	2	418	A
1	2	421	G
1	2	426	A
1	2	438	G
1	2	441	C
1	2	442	C
1	2	447	A
1	2	448	A
1	2	450	C
1	2	451	G
1	2	459	C
1	2	464	A
1	2	465	A
1	2	466	G
1	2	467	G
1	2	471	G
1	2	472	C
1	2	473	A
1	2	474	G
1	2	482	G
1	2	483	C
1	2	487	U
1	2	489	A
1	2	492	C
1	2	500	A
1	2	502	C

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Mol	Chain	Res	Type
1	2	516	A
1	2	525	A
1	2	532	C
1	2	534	G
1	2	535	G
1	2	536	A
1	2	537	C
1	2	538	U
1	2	543	C
1	2	544	G
1	2	546	G
1	2	548	C
1	2	550	C
1	2	552	G
1	2	554	A
1	2	555	A
1	2	556	U
1	2	558	G
1	2	559	G
1	2	560	A
1	2	568	C
1	2	576	A
1	2	582	U
1	2	583	A
1	2	587	A
1	2	588	G
1	2	589	G
1	2	590	A
1	2	591	U
1	2	593	C
1	2	594	A
1	2	595	U
1	2	596	U
1	2	603	C
1	2	604	A
1	2	605	A
1	2	606	G
1	2	607	U
1	2	608	C
1	2	610	G
1	2	614	C
1	2	617	G

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Mol	Chain	Res	Type
1	2	621	C
1	2	627	U
1	2	637	U
1	2	638	C
1	2	639	C
1	2	640	A
1	2	643	A
1	2	644	G
1	2	655	A
1	2	658	U
1	2	660	C
1	2	662	G
1	2	664	A
1	2	668	A
1	2	669	A
1	2	671	A
1	2	672	A
1	2	673	G
1	2	683	G
1	2	685	A
1	2	687	C
1	2	688	U
1	2	749	U
1	2	750	C
1	2	751	G
1	2	792	C
1	2	794	A
1	2	797	C
1	2	799	U
1	2	800	U
1	2	809	A
1	2	812	A
1	2	821	G
1	2	827	A
1	2	830	A
1	2	833	C
1	2	842	C
1	2	845	G
1	2	847	A
1	2	856	C
1	2	859	G
1	2	861	A

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Mol	Chain	Res	Type
1	2	869	A
1	2	870	A
1	2	871	U
1	2	872	A
1	2	873	G
1	2	874	G
1	2	876	C
1	2	877	C
1	2	878	G
1	2	879	C
1	2	881	G
1	2	887	U
1	2	890	U
1	2	891	G
1	2	892	U
1	2	893	U
1	2	894	G
1	2	898	U
1	2	902	G
1	2	903	A
1	2	908	A
1	2	913	A
1	2	914	U
1	2	917	U
1	2	918	U
1	2	919	A
1	2	920	A
1	2	924	G
1	2	926	A
1	2	933	G
1	2	938	A
1	2	943	U
1	2	954	U
1	2	955	A
1	2	959	G
1	2	962	A
1	2	963	A
1	2	969	U
1	2	970	G
1	2	971	G
1	2	981	A
1	2	983	A

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Mol	Chain	Res	Type
1	2	985	G
1	2	989	C
1	2	990	A
1	2	991	G
1	2	999	G
1	2	1001	A
1	2	1002	U
1	2	1008	A
1	2	1017	U
1	2	1023	A
1	2	1027	A
1	2	1041	G
1	2	1042	A
1	2	1044	G
1	2	1045	U
1	2	1049	A
1	2	1057	C
1	2	1059	G
1	2	1060	A
1	2	1061	U
1	2	1062	A
1	2	1067	C
1	2	1072	U
1	2	1073	U
1	2	1078	C
1	2	1082	A
1	2	1083	A
1	2	1085	C
1	2	1086	G
1	2	1087	A
1	2	1088	U
1	2	1096	G
1	2	1097	G
1	2	1110	G
1	2	1113	A
1	2	1114	U
1	2	1115	U
1	2	1116	C
1	2	1117	C
1	2	1118	C
1	2	1119	A
1	2	1120	U

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Mol	Chain	Res	Type
1	2	1121	G
1	2	1133	A
1	2	1137	U
1	2	1138	C
1	2	1139	C
1	2	1141	G
1	2	1148	A
1	2	1149	A
1	2	1153	C
1	2	1154	U
1	2	1155	U
1	2	1157	G
1	2	1166	G
1	2	1171	G
1	2	1181	A
1	2	1195	A
1	2	1206	G
1	2	1207	G
1	2	1208	A
1	2	1210	G
1	2	1211	G
1	2	1215	C
1	2	1216	C
1	2	1217	A
1	2	1221	G
1	2	1224	G
1	2	1227	G
1	2	1232	U
1	2	1233	G
1	2	1241	A
1	2	1242	U
1	2	1243	U
1	2	1250	A
1	2	1251	A
1	2	1254	C
1	2	1257	G
1	2	1258	A
1	2	1259	A
1	2	1260	A
1	2	1261	C
1	2	1264	C
1	2	1270	G

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Mol	Chain	Res	Type
1	2	1271	C
1	2	1274	G
1	2	1275	G
1	2	1280	G
1	2	1281	G
1	2	1283	C
1	2	1284	A
1	2	1285	G
1	2	1286	G
1	2	1298	G
1	2	1301	A
1	2	1302	G
1	2	1303	C
1	2	1304	U
1	2	1313	A
1	2	1315	U
1	2	1317	C
1	2	1318	G
1	2	1325	G
1	2	1331	C
1	2	1333	U
1	2	1343	U
1	2	1354	G
1	2	1358	U
1	2	1366	G
1	2	1371	U
1	2	1372	U
1	2	1373	C
1	2	1378	A
1	2	1380	C
1	2	1382	A
1	2	1395	C
1	2	1398	G
1	2	1404	U
1	2	1405	A
1	2	1406	G
1	2	1416	C
1	2	1426	U
1	2	1429	G
1	2	1430	C
1	2	1431	G
1	2	1432	U

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Mol	Chain	Res	Type
1	2	1439	A
1	2	1441	U
1	2	1442	U
1	2	1444	U
1	2	1447	G
1	2	1450	G
1	2	1452	A
1	2	1453	C
1	2	1454	A
1	2	1460	C
1	2	1462	U
1	2	1463	U
1	2	1464	C
1	2	1465	A
1	2	1466	G
1	2	1477	U
1	2	1478	U
1	2	1487	A
1	2	1488	C
1	2	1489	A
1	2	1490	G
1	2	1493	C
1	2	1494	U
1	2	1495	G
1	2	1497	G
1	2	1498	A
1	2	1500	G
1	2	1505	U
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	1514	G
1	2	1515	G
1	2	1519	U
1	2	1520	G
1	2	1521	C
1	2	1522	A
1	2	1523	C
1	2	1526	G

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Mol	Chain	Res	Type
1	2	1527	C
1	2	1531	A
1	2	1533	A
1	2	1534	C
1	2	1535	U
1	2	1536	G
1	2	1544	C
1	2	1548	G
1	2	1559	C
1	2	1560	U
1	2	1562	C
1	2	1563	G
1	2	1566	G
1	2	1567	G
1	2	1574	C
1	2	1575	G
1	2	1578	U
1	2	1579	A
1	2	1581	C
1	2	1582	C
1	2	1584	G
1	2	1585	U
1	2	1586	U
1	2	1587	G
1	2	1588	A
1	2	1589	A
1	2	1590	C
1	2	1591	C
1	2	1597	C
1	2	1599	U
1	2	1600	G
1	2	1601	A
1	2	1602	U
1	2	1603	G
1	2	1606	G
1	2	1609	C
1	2	1612	G
1	2	1617	G
1	2	1618	C
1	2	1619	A
1	2	1620	A
1	2	1621	U

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Mol	Chain	Res	Type
1	2	1623	A
1	2	1628	C
1	2	1630	A
1	2	1639	G
1	2	1641	A
1	2	1647	A
1	2	1648	G
1	2	1649	U
1	2	1650	A
1	2	1654	G
1	2	1663	A
1	2	1664	A
1	2	1665	G
1	2	1671	G
1	2	1675	A
1	2	1683	C
1	2	1687	C
1	2	1696	C
1	2	1697	A
1	2	1698	C
1	2	1705	C
1	2	1706	G
1	2	1711	U
1	2	1714	U
1	2	1719	A
1	2	1720	U
1	2	1721	U
1	2	1722	G
1	2	1723	G
1	2	1728	U
1	2	1729	U
1	2	1746	U
1	2	1751	C
1	2	1753	C
1	2	1773	C
1	2	1776	G
1	2	1778	C
1	2	1783	C
1	2	1786	U
1	2	1799	G
1	2	1801	A
1	2	1806	A

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Mol	Chain	Res	Type
1	2	1812	U
1	2	1814	G
1	2	1815	A
1	2	1816	G
1	2	1819	A
1	2	1822	A
1	2	1825	A
1	2	1826	G
1	2	1830	U
1	2	1831	A
1	2	1844	U
1	2	1849	G
1	2	1850	A
1	2	1855	G
1	2	1859	A
1	2	1860	A
1	2	1861	G
1	2	1863	A
1	2	1864	U
1	2	1865	C
1	2	1866	A
1	2	1868	U
1	2	1869	A

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

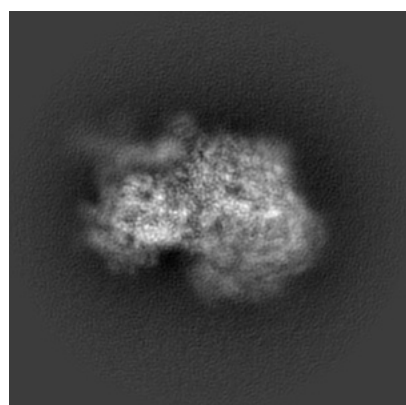
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4353. These allow visual inspection of the internal detail of the map and identification of artifacts.

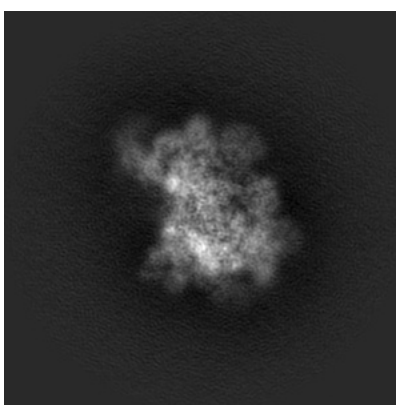
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

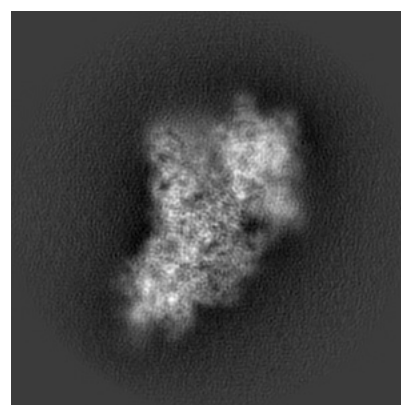
6.1.1 Primary map



X



Y

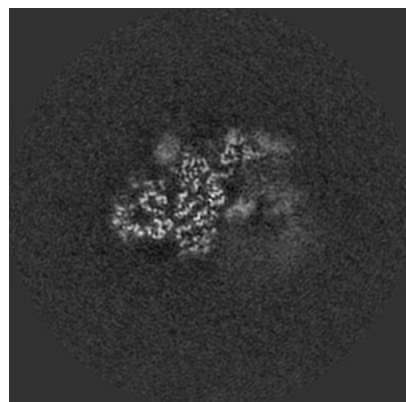


Z

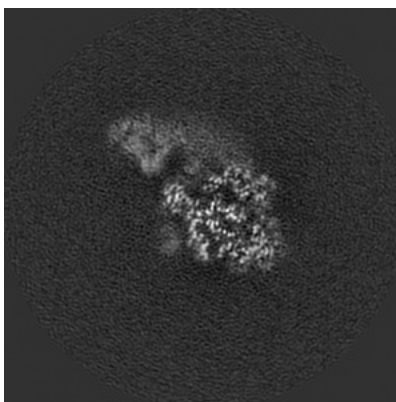
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

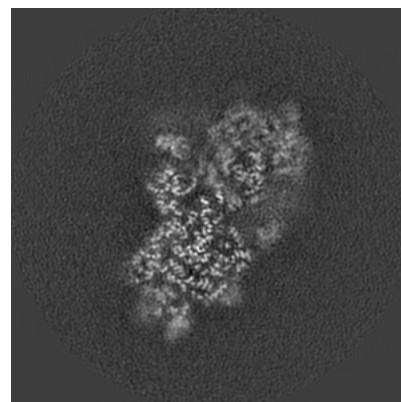
6.2.1 Primary map



X Index: 180



Y Index: 180

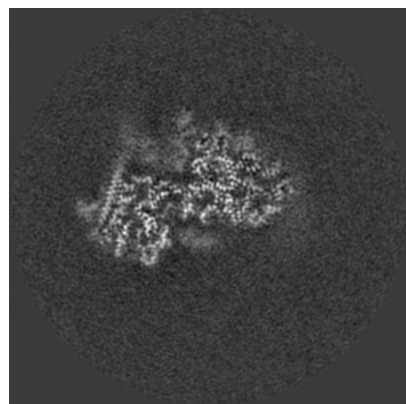


Z Index: 180

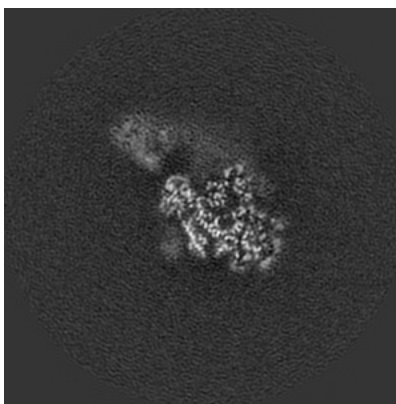
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

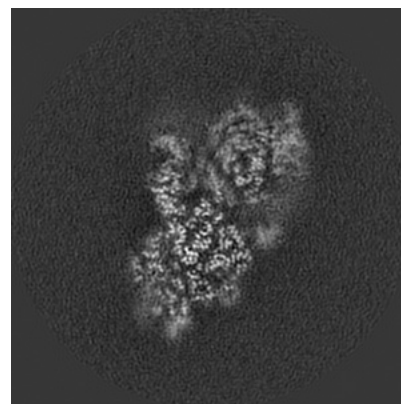
6.3.1 Primary map



X Index: 145



Y Index: 175

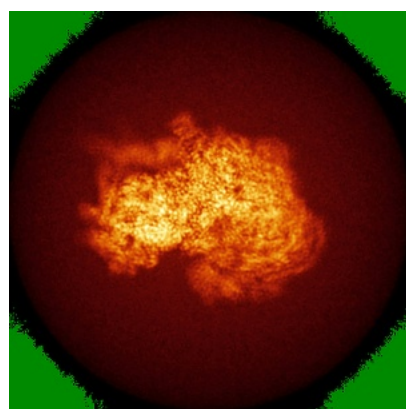


Z Index: 178

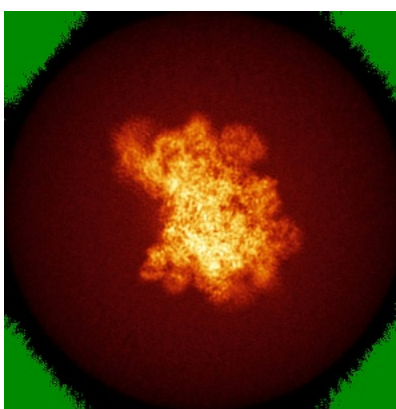
The images above show the largest variance slices of the map in three orthogonal directions.

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

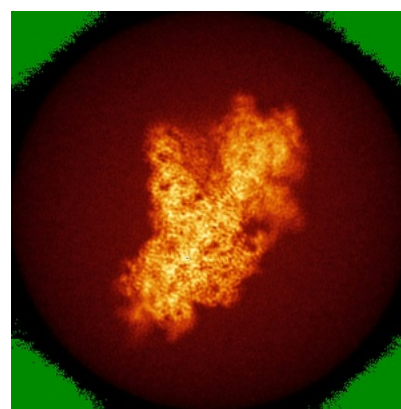
6.4.1 Primary map



X



Y



Z

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

This section was not generated.

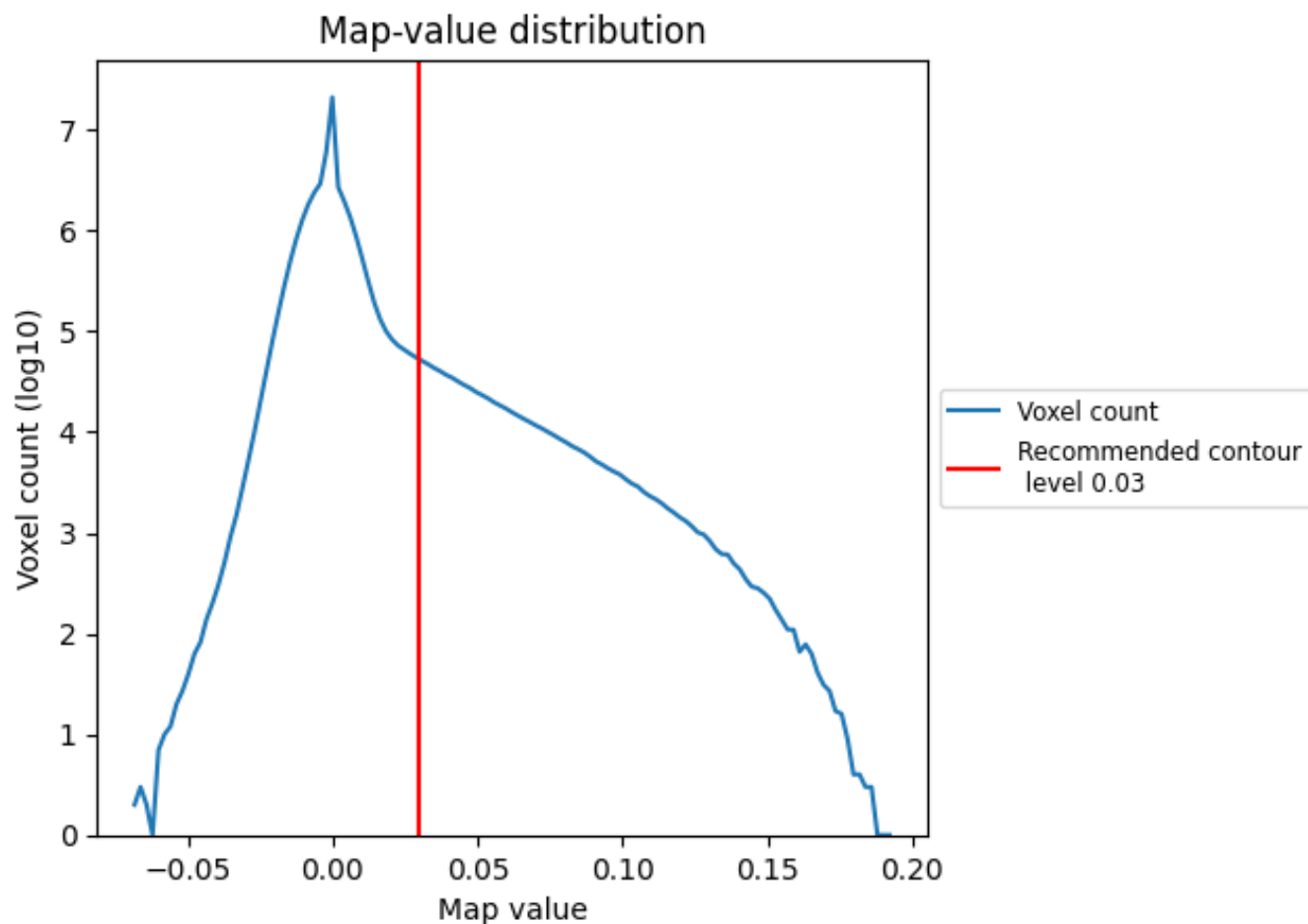
6.6 Mask visualisation

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

7 Map analysis [i](#)

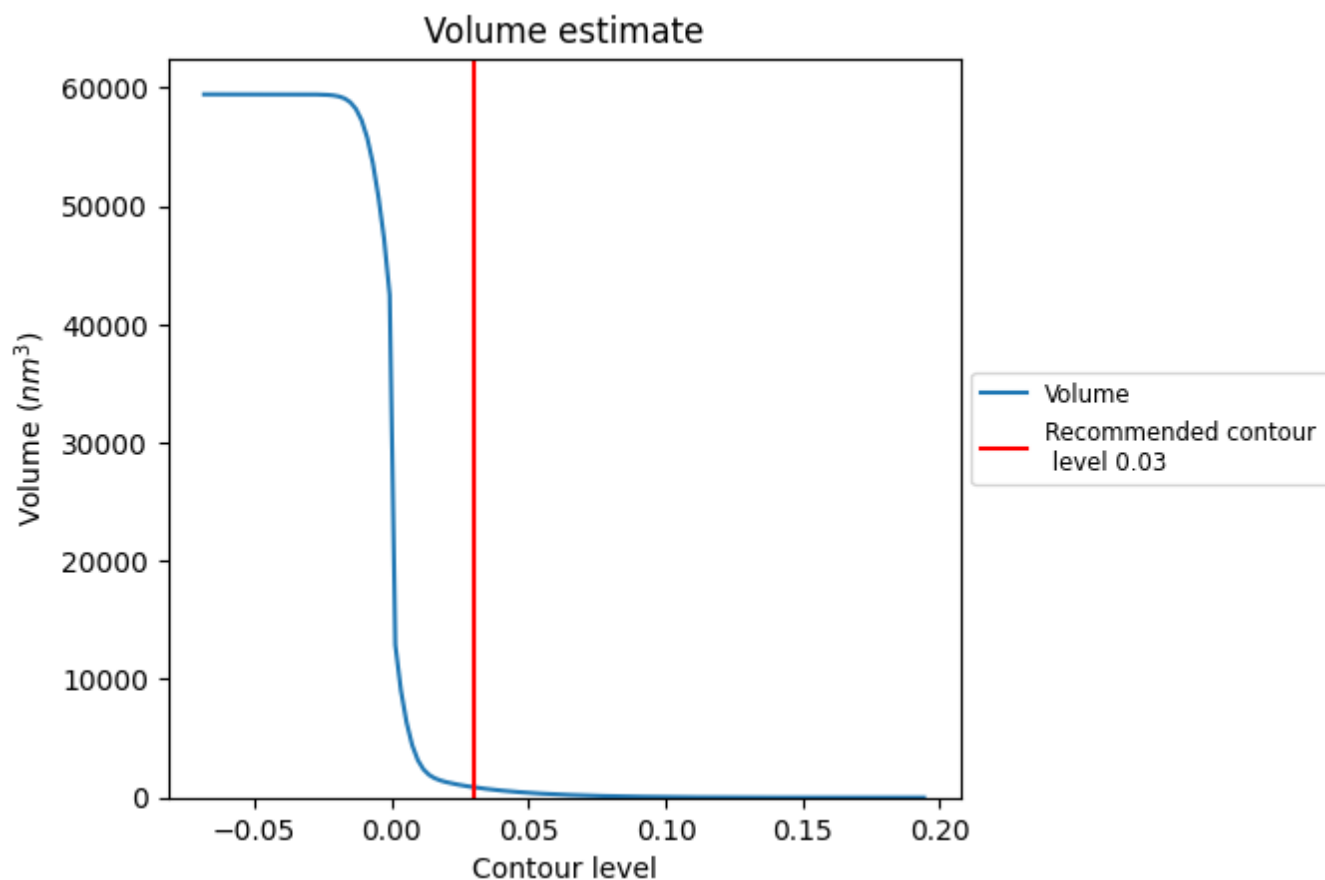
This section contains the results of statistical analysis of the map.

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.

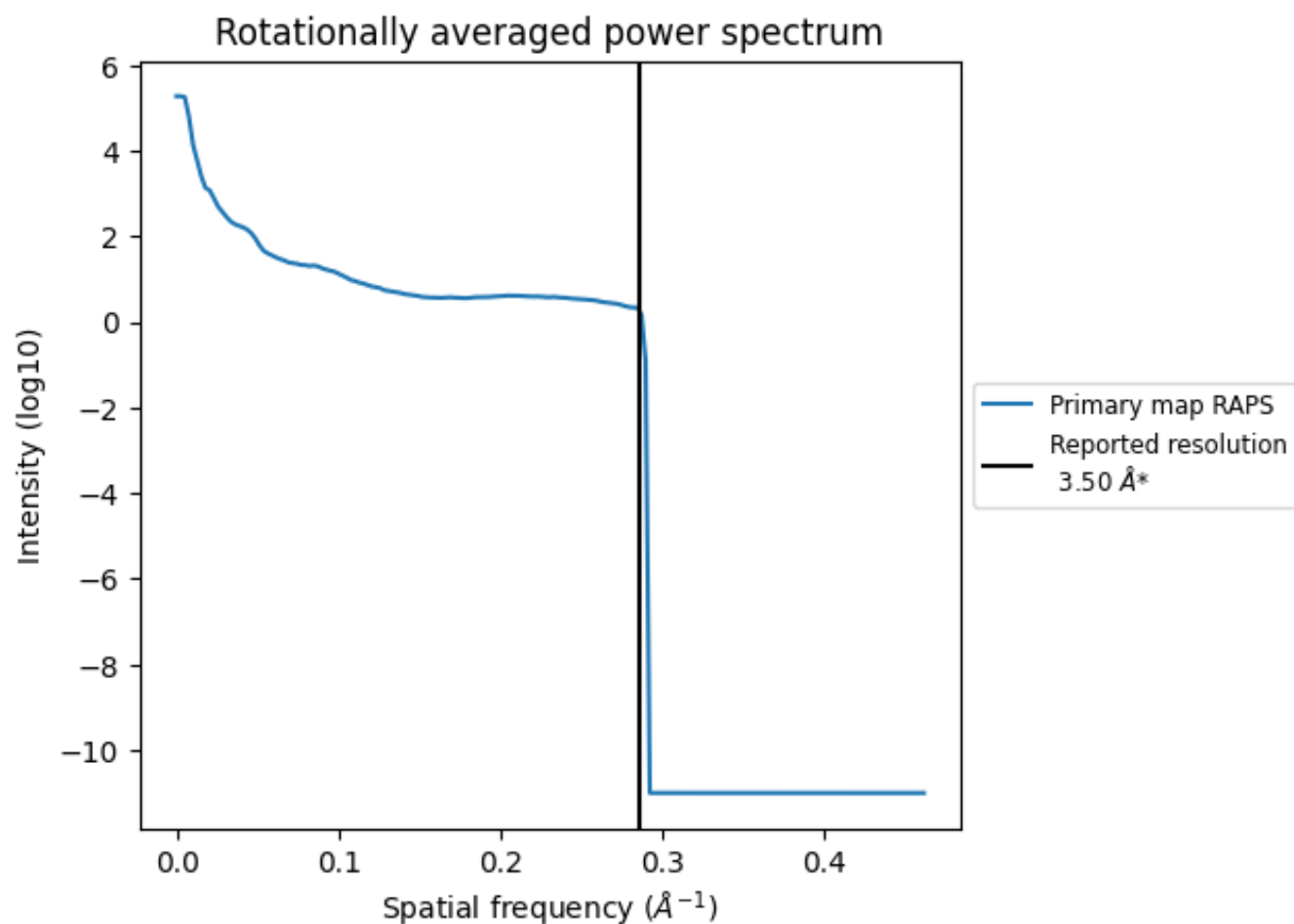
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 873 nm^3 ; this corresponds to an approximate mass of 789 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 ⓘ

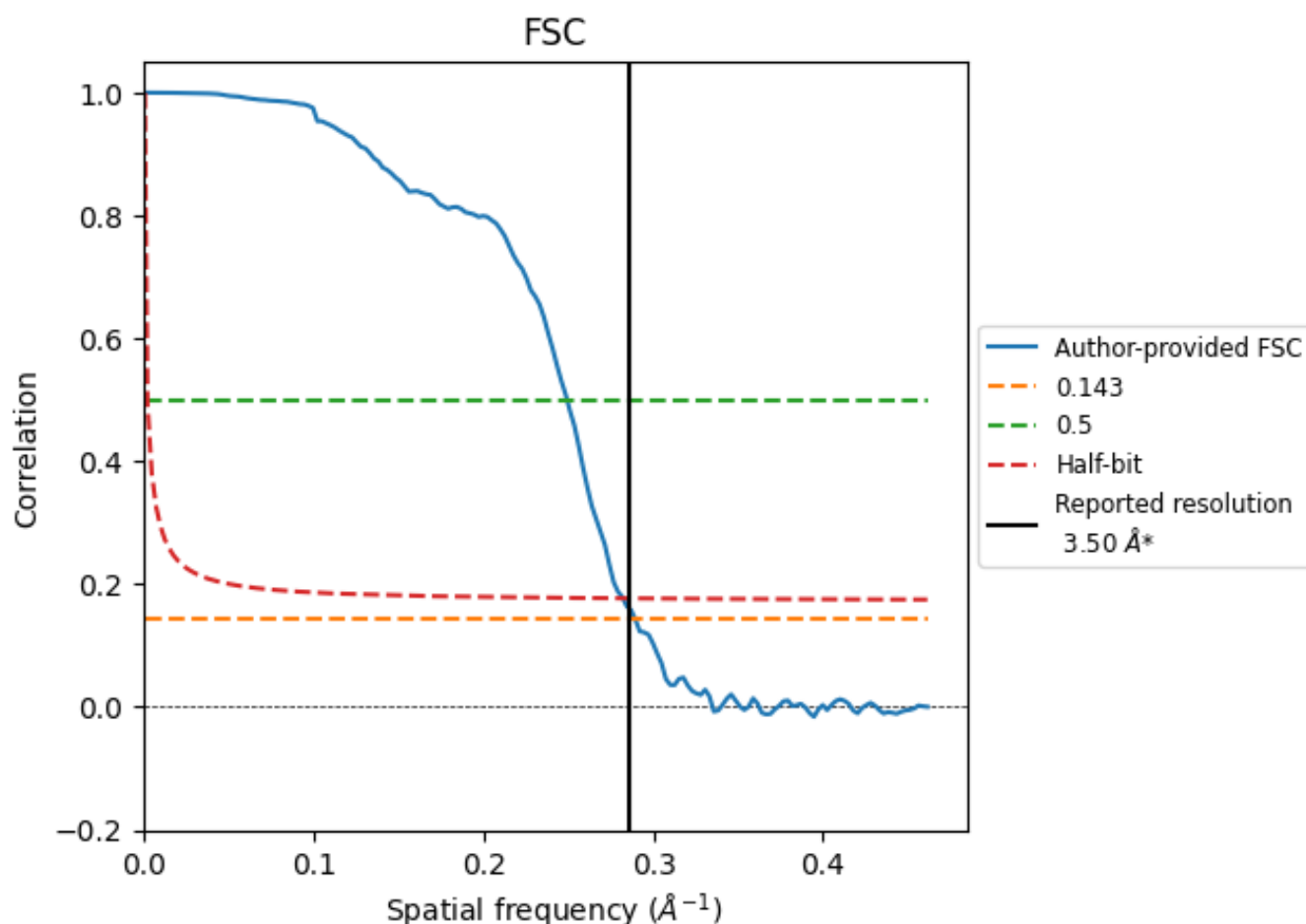


*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.46	4.01	3.54
Unmasked-calculated*	-	-	-

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

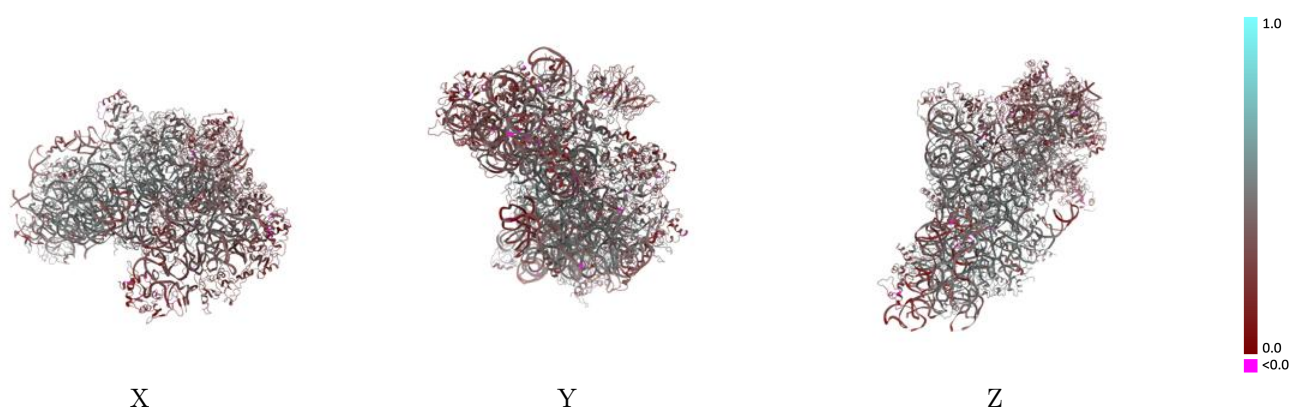
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4353 and PDB model 6G5I. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

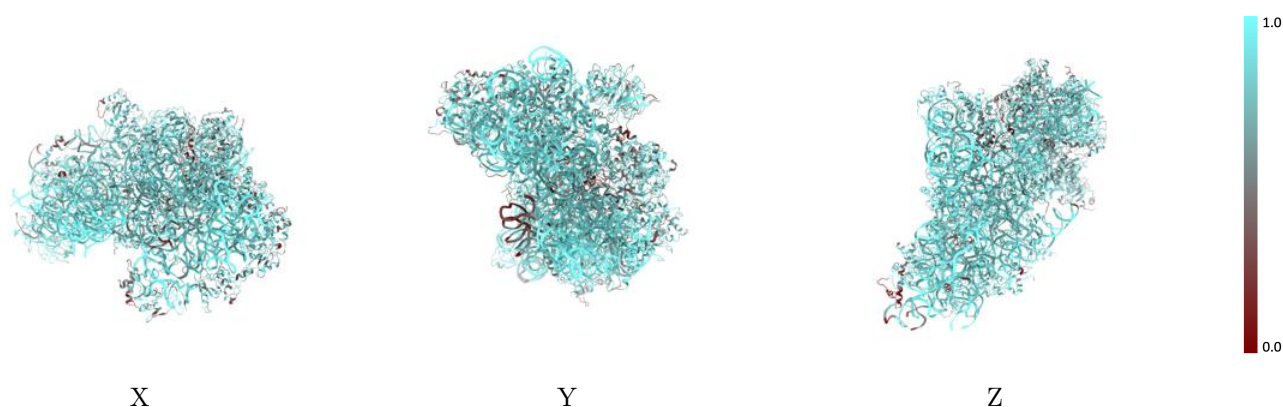
This section was not generated.

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



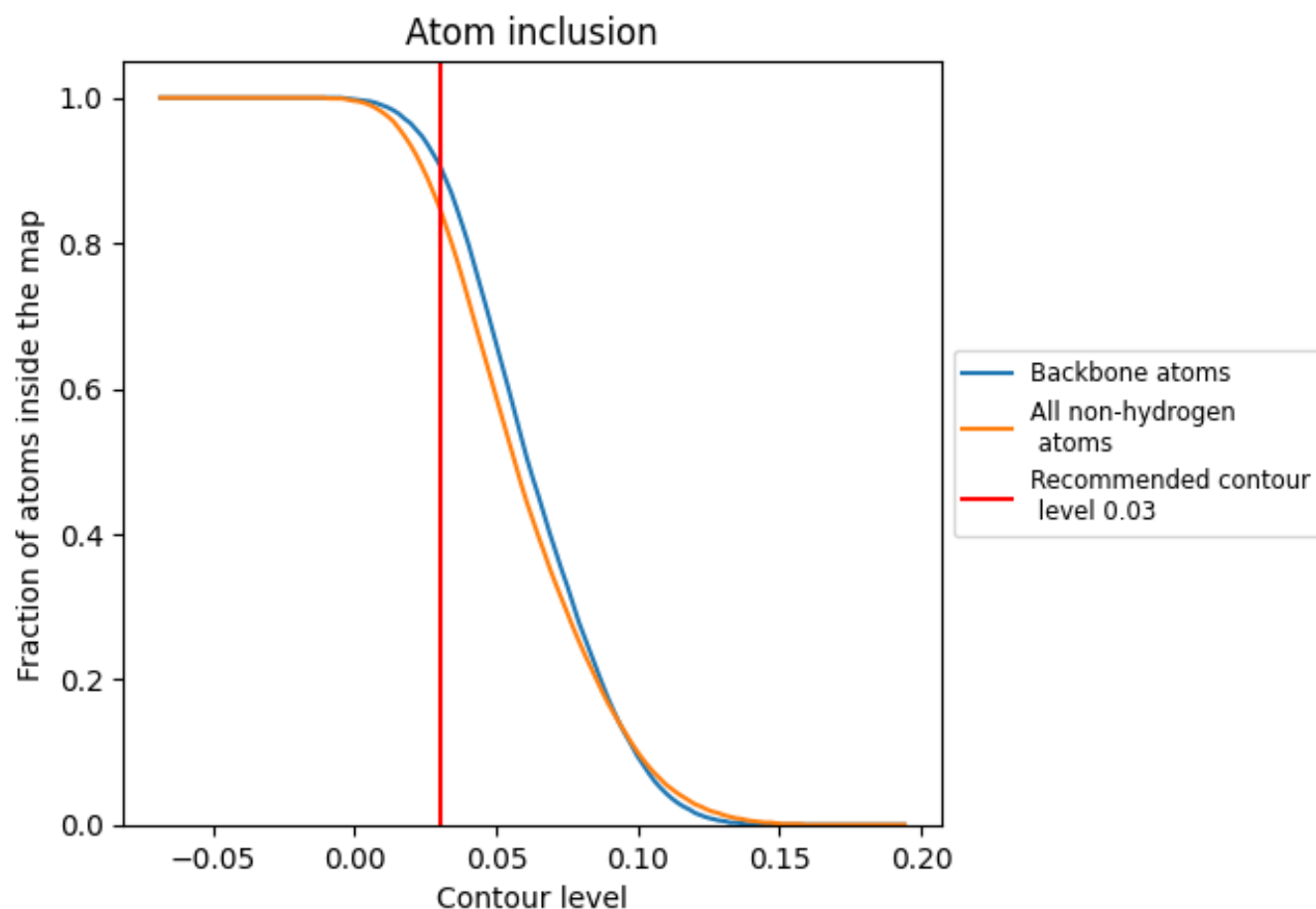
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 85% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8500	 0.3950
2	 0.9340	 0.4140
A	 0.8590	 0.4370
B	 0.8390	 0.4150
C	 0.8310	 0.4650
D	 0.7070	 0.3450
E	 0.8600	 0.4720
F	 0.7180	 0.2950
G	 0.8520	 0.4030
H	 0.7490	 0.3450
I	 0.7140	 0.3860
J	 0.8750	 0.4650
K	 0.8260	 0.3120
L	 0.8550	 0.4700
M	 0.6440	 0.2260
N	 0.8550	 0.4440
O	 0.8220	 0.4020
P	 0.7280	 0.3040
Q	 0.8130	 0.3760
R	 0.7280	 0.3800
S	 0.7230	 0.2690
T	 0.7780	 0.3090
U	 0.7770	 0.3640
V	 0.8300	 0.4530
W	 0.8490	 0.4890
X	 0.8420	 0.4800
Y	 0.9030	 0.4560
Z	 0.7090	 0.2580
b	 0.8090	 0.4300
c	 0.5710	 0.2700
d	 0.7300	 0.3990
e	 0.6580	 0.3720
f	 0.6400	 0.2300
g	 0.7890	 0.3220
x	 0.7490	 0.4010



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Chain	Atom inclusion	Q-score
y	 0.5770	 0.2950
z	 0.6100	 0.3640