



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 02:15 AM UTC

PDB ID : 9GUX / pdb_00009gux
EMDB ID : EMD-51623
Title : 30S-TEC (TEC in expressome position) Inactive state 1
Authors : Rahil, H.; Weixlbaumer, A.; Webster, M.W.
Deposited on : 2024-09-20
Resolution : 3.30 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:

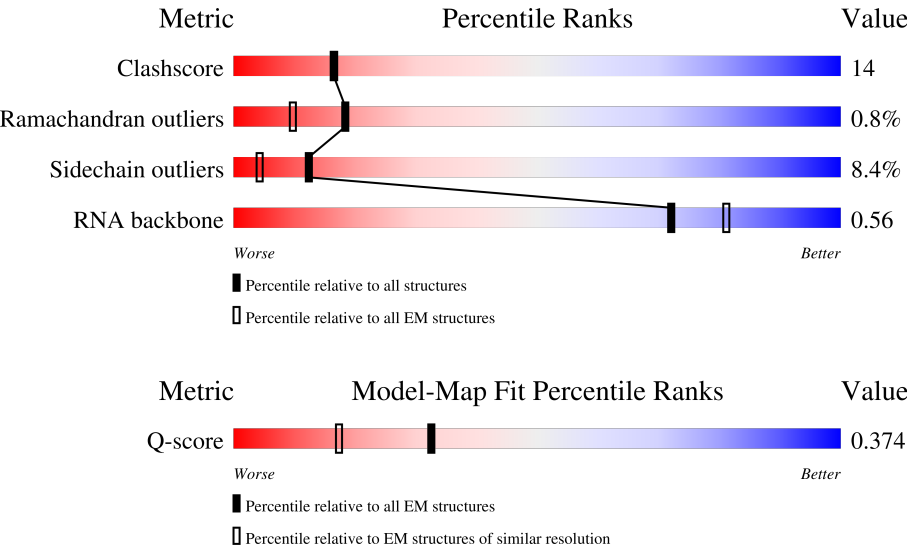
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 3.30 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.



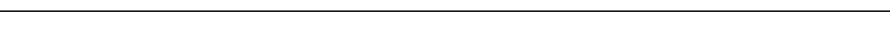
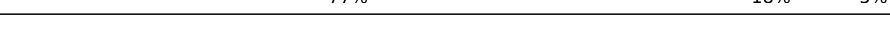
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	A	1542	
2	B	557	
3	C	241	

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Mol	Chain	Length	Quality of chain
4	D	233	
5	E	206	
6	F	157	
7	G	131	
8	H	156	
9	I	130	
10	J	130	
11	K	103	
12	L	129	
13	M	124	
14	N	118	
15	O	101	
16	P	89	
17	Q	82	
18	R	84	
19	S	75	
20	T	92	
21	U	87	
22	V	71	
23	X	53	
24	1	329	
24	2	329	
25	3	1342	
26	4	1406	
27	5	91	

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Mol	Chain	Length	Quality of chain
28	Z	180	50%32%15%
29	6	38	18%61%21%
30	7	39	28%49%23%

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 81286 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1512	Total	C	N	O	P	0	0
			32443	14476	5947	10508	1512		

- Molecule 2 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	260	Total	C	N	O	0	0
			1761	1092	318	351		

- Molecule 3 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	226	Total	C	N	O	S	0	0
			1765	1116	317	324	8		

- Molecule 4 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	211	Total	C	N	O	S	0	0
			1653	1046	310	293	4		

- Molecule 5 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 6 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 7 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 8 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 9 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 10 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	128	Total	C	N	O	S	0	0
			1031	639	207	182	3		

- Molecule 11 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	101	Total	C	N	O	S	0	0
			808	504	155	148	1		

- Molecule 12 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 13 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	122	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 14 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 15 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 16 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 17 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 18 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 19 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 20 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 21 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 22 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 23 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	21	Total	C	N	O	P	0	0
			458	204	93	140	21		

- Molecule 24 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	1	229	Total	C	N	O	S	0	0
			1775	1106	313	350	6		
24	2	219	Total	C	N	O	S	0	0
			1684	1051	295	332	6		

- Molecule 25 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	3	1320	Total	C	N	O	S	0	0
			10415	6535	1815	2021	44		

- Molecule 26 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	1333	Total	C	N	O	S	0	0
			10375	6518	1851	1956	50		

- Molecule 27 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	5	90	Total	C	N	O	S	0	0
			709	430	136	142	1		

- Molecule 28 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	153	Total	C	N	O	S	0	0
			1225	782	209	227	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Z	121	ALA	LYS	conflict	UNP P0AFG0

- Molecule 29 is a DNA chain called Non-Template DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	6	30	Total	C	N	O	P	0	0
			618	294	114	180	30		

- Molecule 30 is a DNA chain called Template DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	7	30	Total	C	N	O	P	0	0
			606	288	105	183	30		

- Molecule 31 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
31	A	131	Total	Mg	0
			131	131	
31	D	1	Total	Mg	0
			1	1	

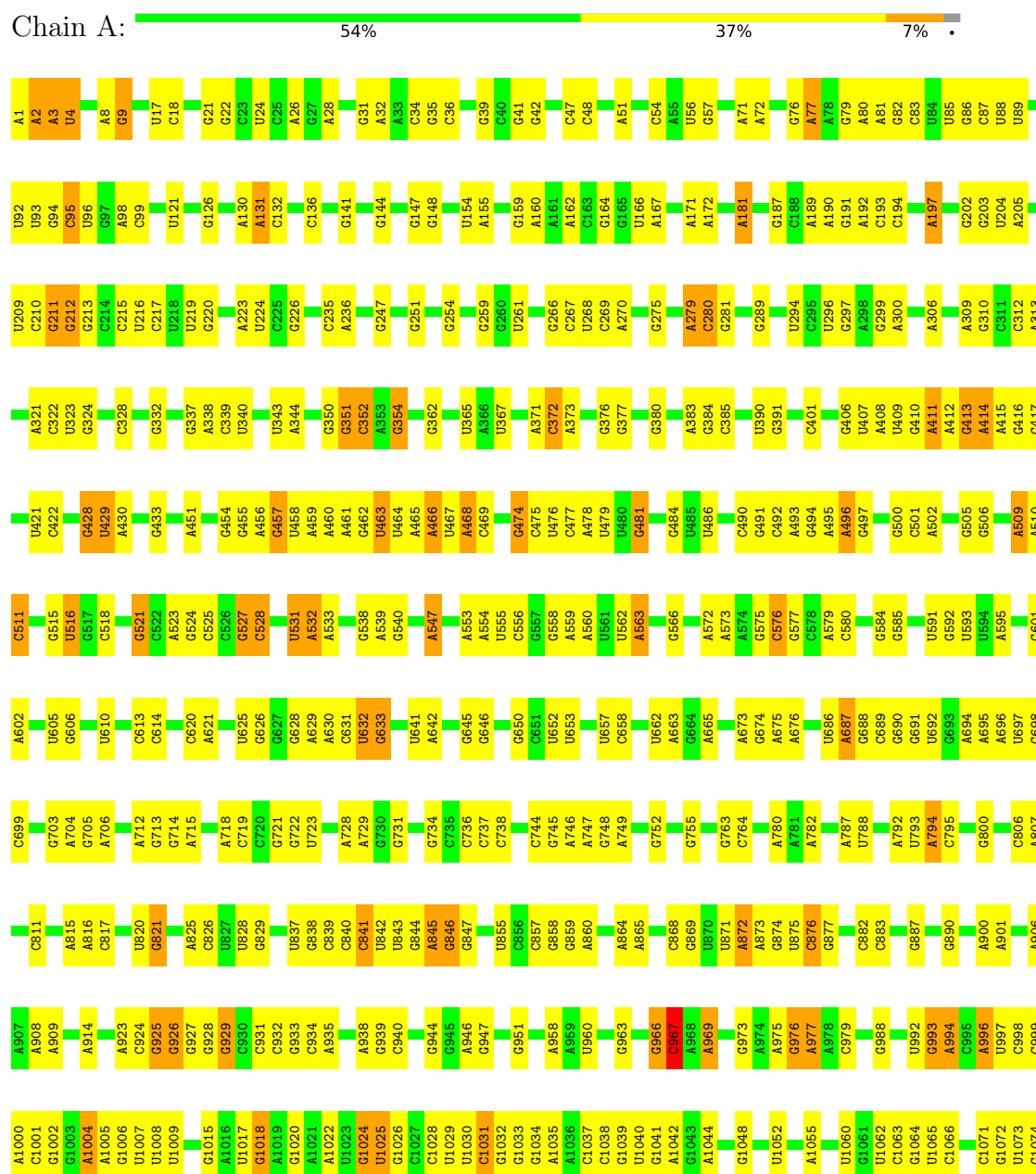
- Molecule 32 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
32	4	2	Total	Zn	0
			2	2	

3 Residue-property plots

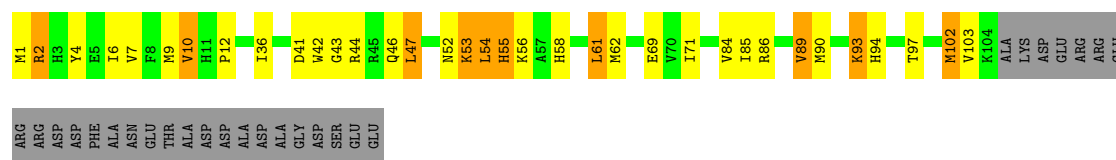
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S ribosomal RNA



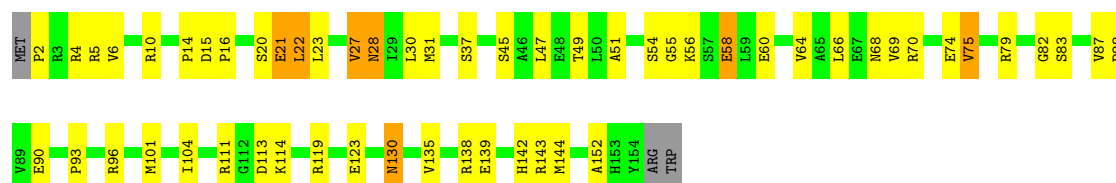


Chain G:  53% 19% 8% 21%



• Molecule 8: 30S ribosomal protein S7

Chain H:  62% 31% 7%



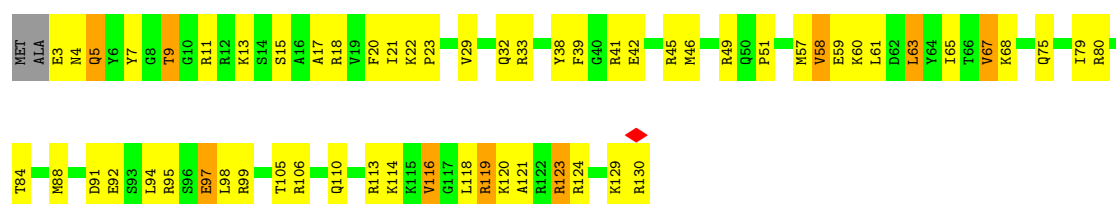
• Molecule 9: 30S ribosomal protein S8

Chain I:  73% 24% 3%



• Molecule 10: 30S ribosomal protein S9

Chain J:  52% 39% 7%



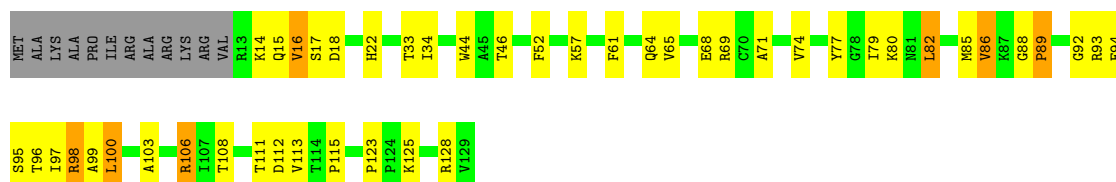
• Molecule 11: 30S ribosomal protein S10

Chain K:  61% 32% 7%

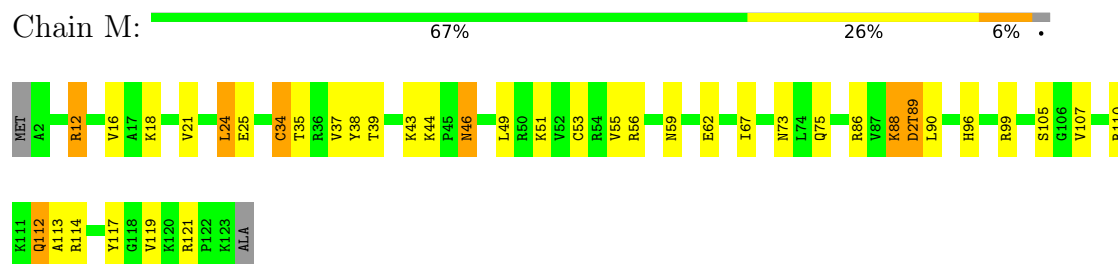


• Molecule 12: 30S ribosomal protein S11

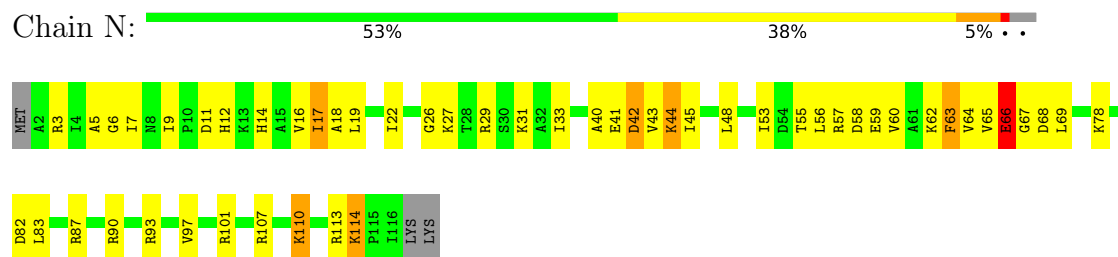
Chain L:  55% 30% 5% 9%



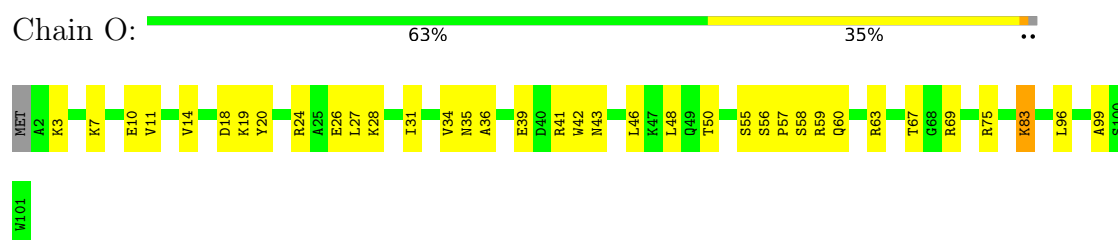
• Molecule 13: 30S ribosomal protein S12



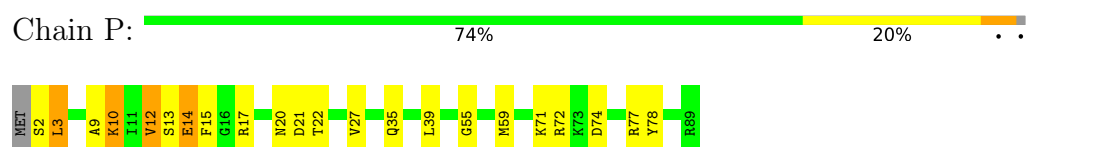
• Molecule 14: 30S ribosomal protein S13



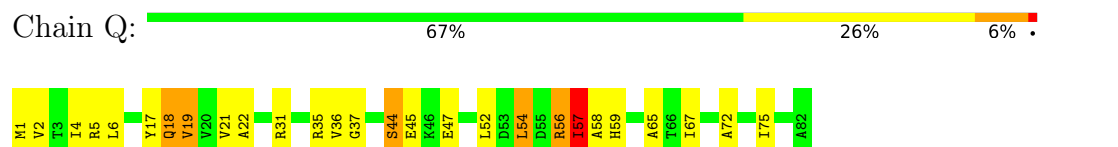
• Molecule 15: 30S ribosomal protein S14



• Molecule 16: Small ribosomal subunit protein uS15



• Molecule 17: 30S ribosomal protein S16



- Molecule 18: 30S ribosomal protein S17

Chain R:  77% 18% 5%



- Molecule 19: 30S ribosomal protein S18

Chain S:  73% 15% 12%



- Molecule 20: 30S ribosomal protein S19

Chain T:  64% 20% 10%



- Molecule 21: 30S ribosomal protein S20

Chain U:  75% 22% ..



- Molecule 22: 30S ribosomal protein S21

Chain V:  68% 30% ..



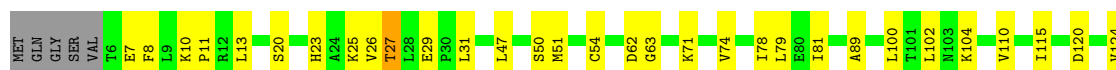
- Molecule 23: mRNA

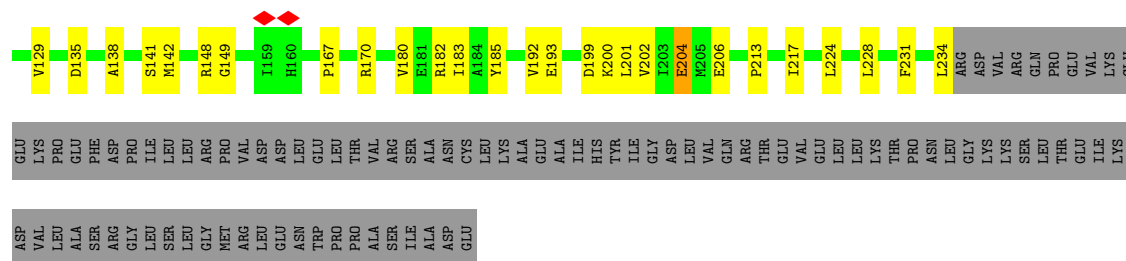
Chain X:  11% 25% 60%



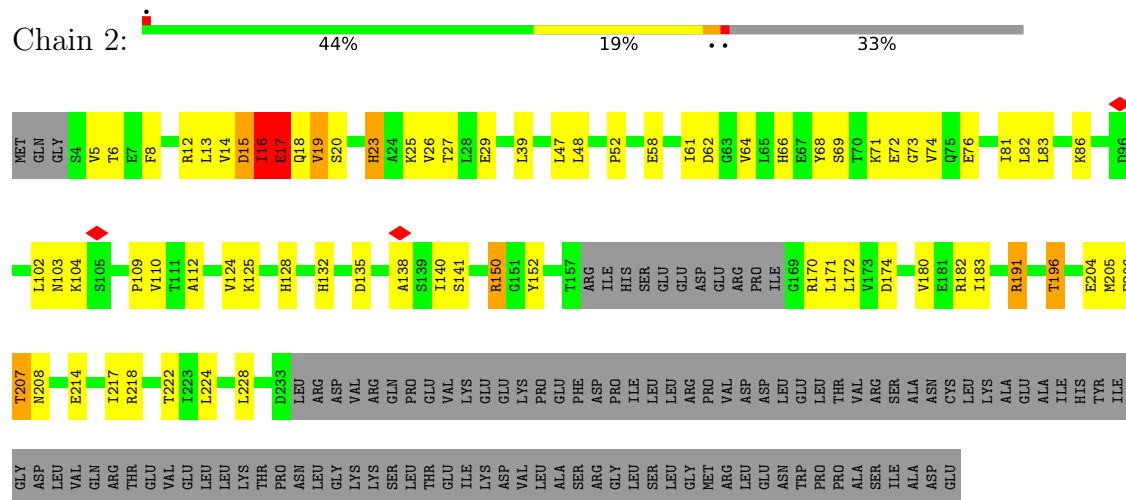
- Molecule 24: DNA-directed RNA polymerase subunit alpha

Chain 1:  52% 17% 30%

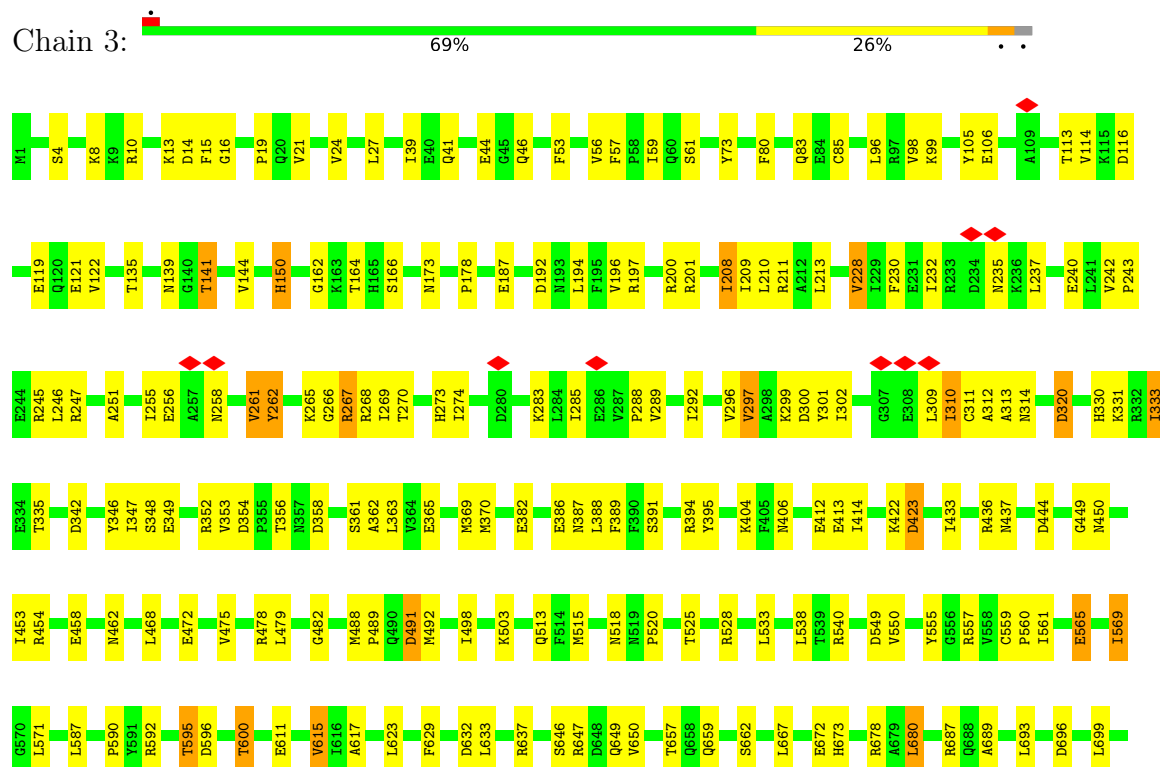


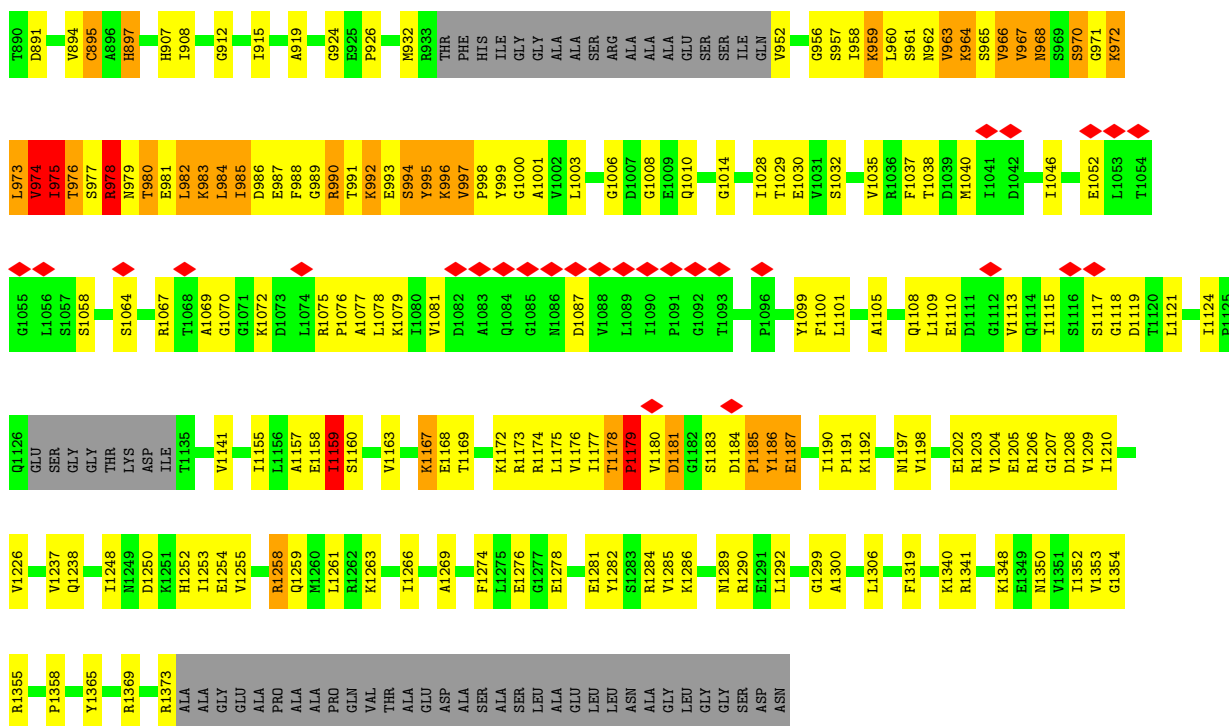


• Molecule 24: DNA-directed RNA polymerase subunit alpha



• Molecule 25: DNA-directed RNA polymerase subunit beta

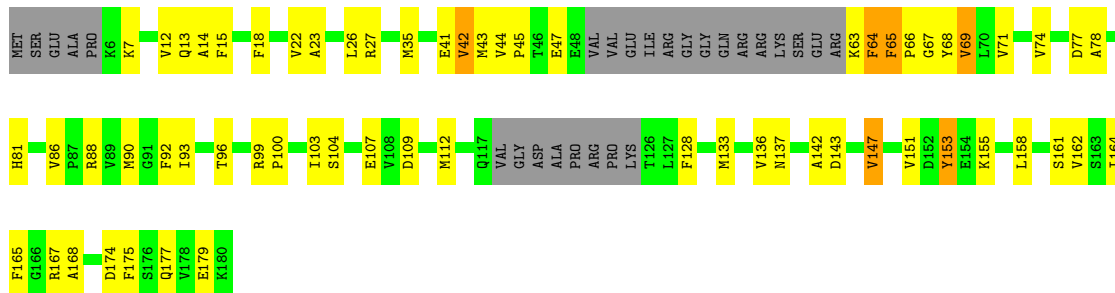




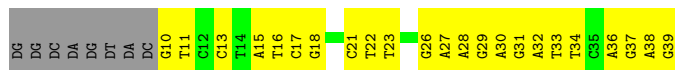
• Molecule 27: DNA-directed RNA polymerase subunit omega



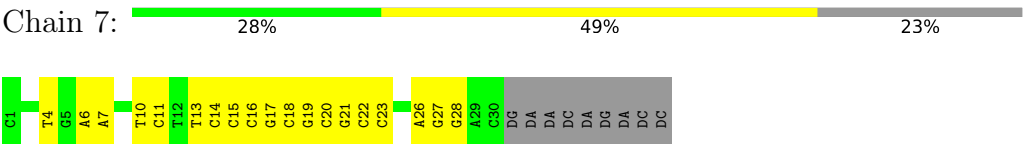
• Molecule 28: Transcription termination/antitermination protein NusG



• Molecule 29: Non-Template DNA strand



• Molecule 30: Template DNA strand



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11965	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49.95	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	4.625	Depositor
Minimum map value	-1.259	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.148	Depositor
Recommended contour level	0.303	Depositor
Map size (Å)	503.99997, 503.99997, 503.99997	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84, 0.84, 0.84	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: G7M, 2MG, MG, ZN, PSU, MA6, D2T, 5MC

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	A	0.38	1/36116 (0.0%)	0.42	9/56333 (0.0%)
2	B	0.45	0/1776	0.73	2/2413 (0.1%)
3	C	0.29	0/1796	0.60	0/2420
4	D	0.36	0/1680	0.63	0/2263
5	E	0.35	0/1665	0.68	5/2227 (0.2%)
6	F	0.32	0/1165	0.60	0/1568
7	G	0.30	0/867	0.60	0/1171
8	H	0.29	0/1219	0.58	0/1635
9	I	0.32	0/989	0.52	0/1326
10	J	0.35	0/1043	0.72	0/1387
11	K	0.41	0/818	0.81	0/1105
12	L	0.35	0/893	0.64	0/1205
13	M	0.36	0/954	0.58	0/1279
14	N	0.35	0/900	0.68	0/1204
15	O	0.37	0/817	0.61	0/1088
16	P	0.28	0/722	0.49	0/964
17	Q	0.46	0/659	0.79	1/884 (0.1%)
18	R	0.30	0/657	0.60	0/881
19	S	0.31	0/553	0.45	0/742
20	T	0.46	0/680	0.75	1/915 (0.1%)
21	U	0.31	0/676	0.57	0/895
22	V	0.37	0/597	0.70	1/792 (0.1%)
23	X	0.26	0/513	0.35	0/797
24	1	0.34	0/1797	0.49	0/2436
24	2	0.32	0/1703	0.53	0/2308
25	3	0.31	0/10581	0.47	2/14275 (0.0%)
26	4	0.35	1/10532 (0.0%)	0.56	9/14219 (0.1%)
27	5	0.27	0/711	0.45	0/956
28	Z	0.37	0/1251	0.63	1/1686 (0.1%)
29	6	0.26	0/693	0.43	0/1068
30	7	0.32	0/676	0.49	0/1039
All	All	0.36	2/85699 (0.0%)	0.51	31/123481 (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
20	T	0	1
25	3	0	1
26	4	0	1
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	G7M	O3'-P	5.44	1.61	1.56
26	4	1179	PRO	N-CA	5.13	1.53	1.47

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	3	1099	ASN	CA-C-N	9.04	131.14	119.84
25	3	1099	ASN	C-N-CA	9.04	131.14	119.84
1	A	1486	G	C4'-C3'-O3'	7.29	123.93	113.00
1	A	1531	A	C4'-C3'-O3'	7.26	120.29	109.40
1	A	1086	U	C3'-C2'-O2'	7.08	121.31	110.70
26	4	1178	THR	CA-C-N	7.05	128.65	119.84
26	4	1178	THR	C-N-CA	7.05	128.65	119.84
26	4	976	THR	CB-CA-C	6.62	121.91	110.72
26	4	850	LYS	CA-C-N	6.50	127.97	119.84
26	4	850	LYS	C-N-CA	6.50	127.97	119.84
28	Z	68	TYR	N-CA-CB	-6.32	101.40	110.44
20	T	29	LYS	CB-CA-C	6.25	119.22	109.42
5	E	107	PHE	CA-C-N	6.24	133.63	121.41
5	E	107	PHE	C-N-CA	6.24	133.63	121.41
5	E	182	PHE	CB-CA-C	6.04	121.76	111.68
17	Q	57	ILE	N-CA-C	-5.89	104.61	110.62
26	4	970	SER	N-CA-C	-5.68	106.69	113.97
2	B	163	ARG	N-CA-C	-5.62	106.19	113.16
26	4	427	PRO	N-CA-CB	-5.60	97.37	103.25
26	4	978	ARG	N-CA-C	-5.54	105.66	113.20
1	A	1086	U	C2'-C3'-O3'	5.50	121.94	113.70
2	B	162	LYS	N-CA-C	-5.39	105.32	111.14
5	E	177	LYS	CA-C-N	-5.29	114.84	122.36
5	E	177	LYS	C-N-CA	-5.29	114.84	122.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1305	G	C4'-C3'-O3'	-5.21	105.18	113.00
1	A	1411	C	C4'-C3'-O3'	-5.16	101.66	109.40
22	V	10	GLU	N-CA-C	-5.10	103.60	109.93
1	A	1401	G	O3'-P-O5'	-5.09	96.37	104.00
1	A	1403	C	O3'-P-O5'	-5.08	96.38	104.00
1	A	528	C	C4'-C3'-C2'	-5.08	97.52	102.60
26	4	212	THR	N-CA-C	-5.08	107.09	113.28

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
25	3	1112	ILE	Peptide
26	4	426	ALA	Peptide
20	T	32	ARG	Sidechain

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	A	32443	0	16346	544	0
2	B	1761	0	1537	145	0
3	C	1765	0	1792	52	0
4	D	1653	0	1727	42	0
5	E	1643	0	1707	62	0
6	F	1152	0	1196	40	0
7	G	848	0	846	21	0
8	H	1203	0	1254	36	0
9	I	979	0	1031	21	0
10	J	1031	0	1076	41	0
11	K	808	0	845	43	0
12	L	877	0	887	42	0
13	M	951	0	1012	29	0
14	N	891	0	952	41	0
15	O	805	0	844	26	0
16	P	714	0	734	13	0
17	Q	649	0	666	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	R	648	0	691	11	0
19	S	544	0	565	10	0
20	T	663	0	688	16	0
21	U	670	0	719	16	0
22	V	589	0	629	22	0
23	X	458	0	233	17	0
24	1	1775	0	1800	36	0
24	2	1684	0	1713	48	0
25	3	10415	0	10432	295	0
26	4	10375	0	10599	398	0
27	5	709	0	719	18	0
28	Z	1225	0	1203	52	0
29	6	618	0	339	22	0
30	7	606	0	338	26	0
31	A	131	0	0	0	0
31	D	1	0	0	0	0
32	4	2	0	0	0	0
All	All	81286	0	65120	2032	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 14.

All (2032) 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)
25:3:845:LEU:HB2	25:3:890:LYS:HD2	1.18	1.15
26:4:271:ARG:HB3	26:4:275:ARG:HH12	1.00	1.11
25:3:845:LEU:CB	25:3:890:LYS:HD2	1.83	1.08
26:4:271:ARG:HB3	26:4:275:ARG:NH1	1.69	1.05
2:B:158:LYS:HB3	2:B:167:VAL:HB	1.07	1.02
21:U:25:ARG:HG2	21:U:66:LEU:HD21	1.41	0.99
2:B:145:LEU:HA	2:B:148:GLU:HG2	1.48	0.96
26:4:965:SER:HA	26:4:976:THR:H	1.32	0.95
25:3:845:LEU:HB2	25:3:890:LYS:CD	1.95	0.94
26:4:425:ARG:HB2	26:4:466:MET:HE2	1.49	0.94
2:B:124:LEU:HD11	2:B:168:VAL:HG11	1.50	0.94
2:B:158:LYS:CB	2:B:167:VAL:HB	1.96	0.94
1:A:1376:U:O4	8:H:10:ARG:NH1	2.03	0.92
4:D:17:PRO:HG2	4:D:54:ARG:HH22	1.33	0.91
25:3:1044:PRO:O	25:3:1046:VAL:HG23	1.70	0.90
26:4:850:LYS:HD2	26:4:855:ASP:HB2	1.52	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:92:LEU:HB2	28:Z:165:PHE:HB3	1.54	0.89
25:3:841:ARG:HG2	25:3:1046:VAL:HG22	1.52	0.89
25:3:1105:SER:HB3	26:4:731:ARG:HB3	1.54	0.88
5:E:58:LYS:NZ	5:E:69:GLU:OE2	2.07	0.88
26:4:849:LEU:HA	26:4:856:ILE:HA	1.54	0.87
26:4:964:LYS:HG2	26:4:964:LYS:O	1.74	0.87
11:K:25:ILE:HD11	28:Z:165:PHE:CE1	2.09	0.87
2:B:170:ARG:HH11	2:B:170:ARG:HA	1.39	0.86
2:B:160:ASP:HB2	2:B:165:ASN:HB2	1.58	0.85
26:4:996:LYS:HB2	26:4:996:LYS:NZ	1.89	0.85
30:7:17:DG:OP1	30:7:17:DG:H4'	1.76	0.85
2:B:132:PRO:HG2	2:B:135:LEU:HD12	1.58	0.85
26:4:958:ILE:HD12	26:4:982:LEU:HD12	1.57	0.85
17:Q:1:MET:HG3	17:Q:2:VAL:H	1.42	0.85
2:B:112:ILE:HG13	2:B:148:GLU:HA	1.59	0.84
26:4:271:ARG:HH11	26:4:275:ARG:HH22	1.24	0.84
26:4:965:SER:HB2	26:4:975:ILE:HA	1.60	0.84
17:Q:52:LEU:HD21	17:Q:57:ILE:HG12	1.60	0.83
26:4:271:ARG:CB	26:4:275:ARG:HH12	1.88	0.83
24:2:17:GLU:HG3	24:2:25:LYS:HB3	1.62	0.82
26:4:981:GLU:HG2	26:4:996:LYS:HA	1.62	0.81
26:4:957:SER:HB3	26:4:985:ILE:HG23	1.61	0.81
2:B:115:LYS:HG2	2:B:144:THR:H	1.46	0.81
1:A:1531:A:OP1	1:A:1531:A:H3'	1.80	0.81
26:4:997:VAL:HG11	26:4:1003:LEU:HD21	1.63	0.81
2:B:98:LEU:HD22	2:B:166:VAL:HG21	1.62	0.80
30:7:17:DG:H5''	30:7:17:DG:C8	2.16	0.79
2:B:130:PHE:HB3	2:B:167:VAL:HG22	1.63	0.79
26:4:282:LEU:HD11	28:Z:65:PHE:HB3	1.65	0.79
2:B:147:LEU:HA	2:B:150:LYS:HD3	1.63	0.78
25:3:806:PRO:HD3	25:3:1100:PRO:HG3	1.65	0.78
30:7:17:DG:H5''	30:7:17:DG:H8	1.46	0.78
26:4:254:PRO:HA	26:4:260:PHE:HA	1.64	0.78
26:4:1350:ASN:HD22	26:4:1358:PRO:CD	1.97	0.78
1:A:1305:G:H21	1:A:1332:A:H2	1.30	0.77
2:B:131:LEU:HD13	2:B:169:SER:CB	2.15	0.76
26:4:849:LEU:HG	26:4:856:ILE:HG22	1.66	0.76
11:K:25:ILE:CD1	28:Z:165:PHE:CE1	2.69	0.76
12:L:93:ARG:NH2	12:L:112:ASP:OD2	2.19	0.76
26:4:848:VAL:HB	26:4:858:VAL:HB	1.69	0.75
26:4:974:VAL:O	26:4:974:VAL:HG12	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:4:985:ILE:HG12	26:4:989:GLY:HA2	1.69	0.75
1:A:1485:U:O2	1:A:1485:U:H2'	1.84	0.74
25:3:197:ARG:HD3	25:3:200:ARG:HA	1.69	0.74
2:B:131:LEU:HD11	2:B:136:VAL:HA	1.69	0.74
22:V:9:ASN:O	22:V:9:ASN:ND2	2.20	0.74
26:4:968:ASN:HB3	26:4:974:VAL:HG23	1.68	0.74
1:A:1218:C:H2'	1:A:1219:A:C8	2.22	0.74
2:B:163:ARG:HD2	2:B:163:ARG:H	1.53	0.74
25:3:1109:ILE:HG13	25:3:1112:ILE:HD11	1.68	0.73
26:4:965:SER:CA	26:4:976:THR:H	2.00	0.73
1:A:1356:G:H2'	1:A:1357:A:C8	2.24	0.73
26:4:1289:ASN:ND2	26:4:1300:ALA:O	2.22	0.73
1:A:261:U:OP2	21:U:74:ARG:NH2	2.22	0.73
3:C:151:ILE:HB	3:C:154:MET:HE3	1.70	0.72
21:U:25:ARG:CG	21:U:66:LEU:HD21	2.19	0.72
25:3:1138:VAL:HG21	25:3:1166:ASP:OD2	1.89	0.72
4:D:31:ASP:OD1	4:D:31:ASP:N	2.23	0.72
1:A:875:U:O2'	9:I:15:ARG:NH1	2.23	0.72
1:A:1398:A:H61	1:A:1498:U:H3	1.37	0.72
26:4:1177:ILE:HB	26:4:1186:TYR:HD2	1.54	0.72
2:B:166:VAL:HG12	2:B:168:VAL:HG23	1.69	0.72
2:B:154:PHE:HB3	2:B:168:VAL:HG13	1.72	0.72
25:3:358:ASP:N	25:3:361:SER:OG	2.22	0.72
26:4:72:CYS:HB2	26:4:87:LYS:HD3	1.72	0.72
15:O:20:TYR:HB2	15:O:55:SER:OG	1.90	0.72
26:4:960:LEU:HA	26:4:982:LEU:HA	1.71	0.72
26:4:975:ILE:CD1	26:4:997:VAL:HB	2.20	0.72
26:4:997:VAL:HG11	26:4:1003:LEU:CD2	2.20	0.72
2:B:157:ILE:HG22	2:B:167:VAL:HG12	1.72	0.71
26:4:965:SER:HA	26:4:976:THR:N	2.04	0.71
1:A:673:A:H2'	1:A:674:G:C8	2.25	0.71
1:A:1071:C:H2'	1:A:1072:G:H8	1.53	0.71
26:4:850:LYS:O	26:4:850:LYS:HD3	1.91	0.71
12:L:68:GLU:HG3	12:L:99:ALA:HB1	1.72	0.71
26:4:155:GLU:HB2	26:4:158:GLN:HB2	1.71	0.71
5:E:100:ASN:OD1	5:E:111:ARG:NH1	2.23	0.71
25:3:1002:LEU:HD21	25:3:1007:LYS:HB2	1.73	0.71
26:4:1177:ILE:HD12	26:4:1186:TYR:CE2	2.26	0.71
2:B:121:THR:HG23	2:B:121:THR:O	1.91	0.70
2:B:170:ARG:HH11	2:B:170:ARG:CA	2.03	0.70
1:A:562:U:H1'	13:M:12:ARG:HG2	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1305:G:H5''	1:A:1305:G:H8	1.56	0.70
25:3:732:ILE:HD11	25:3:769:PRO:HB3	1.71	0.70
1:A:749:A:O2'	16:P:20:ASN:OD1	2.09	0.70
1:A:1026:G:H1	1:A:1035:A:N6	1.88	0.70
2:B:131:LEU:HD11	2:B:136:VAL:CA	2.22	0.70
23:X:44:A:N7	25:3:1264:GLN:NE2	2.39	0.70
26:4:137:ARG:HG3	26:4:142:GLU:HB2	1.71	0.70
1:A:1397:C:H2'	1:A:1398:A:C8	2.26	0.70
21:U:67:ILE:HG12	21:U:71:LYS:HD3	1.72	0.70
1:A:926:G:H1	1:A:1391:U:H3	1.37	0.70
12:L:88:GLY:O	12:L:93:ARG:NH1	2.24	0.70
25:3:1314:GLN:HB2	27:5:28:ARG:HH12	1.56	0.70
1:A:938:A:N3	1:A:1376:U:O2'	2.24	0.70
1:A:1403:C:H42	1:A:1493:A:H61	1.39	0.70
1:A:1409:C:H5'	2:B:117:LYS:HE3	1.74	0.70
1:A:1363:A:O2'	1:A:1365:G:N7	2.20	0.70
15:O:41:ARG:NH2	20:T:6:LYS:O	2.25	0.70
22:V:31:GLU:OE1	22:V:34:ARG:NH2	2.24	0.70
1:A:297:G:N2	1:A:300:A:OP2	2.22	0.70
24:2:182:ARG:NH1	24:2:204:GLU:OE2	2.24	0.70
1:A:979:C:O2	15:O:59:ARG:NH1	2.24	0.70
2:B:131:LEU:HB2	2:B:169:SER:HB3	1.74	0.70
8:H:15:ASP:OD1	8:H:20:SER:N	2.25	0.70
11:K:88:MET:HG2	28:Z:164:ILE:HD13	1.73	0.70
25:3:758:ARG:NH2	25:3:762:ASN:OD1	2.22	0.70
26:4:982:LEU:HD23	26:4:982:LEU:O	1.92	0.70
2:B:158:LYS:HB3	2:B:167:VAL:CB	2.03	0.69
1:A:929:G:H4'	1:A:929:G:OP1	1.91	0.69
8:H:47:LEU:HB3	8:H:58:GLU:HB3	1.74	0.69
25:3:444:ASP:O	25:3:450:ASN:ND2	2.25	0.69
10:J:42:GLU:OE1	10:J:45:ARG:NE	2.25	0.69
26:4:957:SER:O	26:4:984:LEU:HA	1.92	0.69
1:A:1071:C:H2'	1:A:1072:G:C8	2.27	0.69
25:3:4:SER:O	25:3:8:LYS:N	2.25	0.69
5:E:105:MET:HG2	5:E:173:VAL:HG22	1.74	0.69
1:A:269:C:H2'	1:A:270:A:C8	2.27	0.69
4:D:191:THR:HG23	4:D:193:TYR:H	1.57	0.69
10:J:7:TYR:OH	10:J:9:THR:OG1	2.10	0.69
26:4:894:VAL:HG11	26:4:915:ILE:HD11	1.75	0.69
26:4:990:ARG:HB2	26:4:990:ARG:CZ	2.20	0.69
6:F:76:LEU:HD11	6:F:120:VAL:HG22	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1408:A:O2'	1:A:1491:G:N1	2.26	0.69
26:4:797:THR:HG22	26:4:924:GLY:HA3	1.75	0.69
2:B:135:LEU:HD22	2:B:171:ARG:HD3	1.75	0.68
26:4:975:ILE:HD12	26:4:1001:ALA:HB3	1.75	0.68
1:A:1147:C:O2	10:J:18:ARG:NH1	2.27	0.68
17:Q:5:ARG:HH12	17:Q:22:ALA:HB3	1.58	0.68
1:A:1507:A:H5''	1:A:1507:A:H8	1.57	0.68
14:N:17:ILE:H	14:N:17:ILE:HD12	1.57	0.68
26:4:981:GLU:CG	26:4:996:LYS:HA	2.22	0.68
21:U:17:ALA:O	21:U:21:ASN:ND2	2.26	0.68
26:4:996:LYS:HB2	26:4:996:LYS:HZ2	1.58	0.68
17:Q:2:VAL:HG13	17:Q:65:ALA:HA	1.74	0.68
22:V:69:ARG:HG2	22:V:71:TYR:H	1.57	0.68
26:4:1350:ASN:ND2	26:4:1358:PRO:HD3	2.08	0.68
1:A:87:C:H2'	1:A:88:U:C6	2.29	0.68
25:3:1246:ARG:NH1	25:3:1265:PHE:O	2.26	0.68
25:3:935:THR:HG23	25:3:1048:LYS:HB2	1.75	0.67
7:G:10:VAL:HG13	7:G:58:HIS:HB3	1.75	0.67
26:4:1350:ASN:HD22	26:4:1358:PRO:HD3	1.57	0.67
1:A:963:G:H21	11:K:57:VAL:HG11	1.60	0.67
10:J:97:GLU:OE1	10:J:97:GLU:N	2.24	0.67
10:J:51:PRO:HD3	10:J:80:ARG:HG3	1.76	0.67
2:B:5:PHE:CD2	3:C:44:GLU:HG2	2.29	0.67
26:4:804:ALA:HA	26:4:1259:GLN:HE21	1.57	0.67
1:A:1052:U:O2'	1:A:1055:A:OP2	2.10	0.67
1:A:1413:A:H2	1:A:1487:G:H1	1.41	0.67
14:N:66:GLU:O	14:N:69:LEU:N	2.28	0.67
25:3:230:PHE:HB2	25:3:333:ILE:HG22	1.77	0.67
1:A:1486:G:H8	1:A:1486:G:O5'	1.77	0.67
1:A:1497:G:H2'	1:A:1498:U:H6	1.60	0.67
11:K:92:LEU:HB3	28:Z:167:ARG:HH12	1.60	0.67
26:4:974:VAL:O	26:4:974:VAL:CG1	2.43	0.67
29:6:33:DT:H2''	29:6:34:DT:H5''	1.75	0.67
24:2:104:LYS:NZ	24:2:109:PRO:O	2.28	0.67
25:3:300:ASP:OD1	25:3:313:ALA:N	2.28	0.67
25:3:565:GLU:HG2	25:3:680:LEU:HD21	1.76	0.67
26:4:1064:SER:OG	26:4:1075:ARG:NH1	2.27	0.67
26:4:1077:ALA:HA	26:4:1100:PHE:HA	1.77	0.66
1:A:1484:C:H6	1:A:1484:C:O5'	1.78	0.66
26:4:1037:PHE:HB3	26:4:1040:MET:HB2	1.77	0.66
29:6:18:DG:H8	29:6:18:DG:H5''	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:93:ALA:O	28:Z:167:ARG:NH2	2.27	0.66
2:B:115:LYS:CG	2:B:144:THR:H	2.07	0.66
25:3:251:ALA:O	25:3:266:GLY:N	2.25	0.66
2:B:43:LYS:HB2	2:B:82:THR:HG23	1.76	0.66
24:2:14:VAL:HG13	24:2:15:ASP:HB2	1.77	0.66
25:3:557:ARG:NH2	25:3:611:GLU:OE1	2.28	0.66
25:3:1146:GLN:OE1	25:3:1161:LEU:N	2.25	0.66
1:A:492:C:H2'	1:A:493:A:C8	2.30	0.66
1:A:744:C:H2'	1:A:745:G:H8	1.61	0.66
1:A:890:G:O2'	1:A:906:A:N6	2.29	0.66
1:A:1092:A:OP2	8:H:4:ARG:NH2	2.28	0.66
1:A:1497:G:H2'	1:A:1498:U:C6	2.30	0.66
6:F:114:VAL:HG11	6:F:140:THR:HG21	1.76	0.66
26:4:1078:LEU:N	26:4:1099:TYR:O	2.26	0.66
26:4:1157:ALA:O	26:4:1207:GLY:N	2.26	0.66
1:A:999:C:H2'	1:A:1000:A:H8	1.61	0.66
26:4:1157:ALA:HB3	26:4:1208:ASP:HB3	1.76	0.66
2:B:129:ALA:HB1	2:B:168:VAL:HB	1.78	0.66
1:A:748:G:H2'	1:A:749:A:H8	1.60	0.66
22:V:12:PHE:CE2	22:V:16:LEU:HD22	2.31	0.66
25:3:423:ASP:OD1	25:3:423:ASP:N	2.25	0.66
25:3:525:THR:HG21	25:3:687:ARG:HD3	1.77	0.66
28:Z:42:VAL:HB	28:Z:71:VAL:HG22	1.78	0.66
2:B:132:PRO:CG	2:B:135:LEU:HD12	2.26	0.66
24:1:13:LEU:H	24:1:13:LEU:HD23	1.60	0.66
26:4:402:GLU:OE1	26:4:403:ARG:NH1	2.29	0.66
1:A:811:C:O2'	1:A:901:A:N1	2.29	0.65
12:L:106:ARG:HH21	22:V:6:VAL:HG11	1.61	0.65
2:B:43:LYS:O	3:C:206:ALA:HB2	1.97	0.65
26:4:534:GLU:OE2	26:4:538:ARG:NH2	2.28	0.65
1:A:159:G:N2	1:A:162:A:OP2	2.30	0.65
1:A:501:C:OP1	13:M:114:ARG:NH2	2.30	0.65
1:A:1531:A:H3'	1:A:1531:A:P	2.35	0.65
25:3:678:ARG:HE	25:3:1106:ARG:HB3	1.60	0.65
10:J:21:ILE:HD12	10:J:63:LEU:HD22	1.78	0.65
26:4:1263:LYS:HD3	26:4:1281:GLU:HA	1.78	0.65
28:Z:44:VAL:HG22	28:Z:69:VAL:HG12	1.79	0.65
1:A:87:C:H2'	1:A:88:U:H6	1.61	0.65
2:B:157:ILE:HG22	2:B:157:ILE:O	1.96	0.65
2:B:170:ARG:HG3	2:B:170:ARG:O	1.96	0.65
6:F:105:ILE:HD11	6:F:112:ARG:HA	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:8:LEU:HD13	18:R:25:ILE:HG21	1.78	0.65
25:3:1321:GLU:OE2	26:4:99:ARG:NH1	2.30	0.65
26:4:114:ILE:HG13	26:4:304:ASP:HA	1.79	0.65
2:B:124:LEU:CD1	2:B:168:VAL:HG21	2.27	0.65
25:3:1080:ASN:HD22	25:3:1085:MET:HE3	1.62	0.65
25:3:1314:GLN:OE1	27:5:28:ARG:NH1	2.29	0.65
26:4:789:LYS:HB2	26:4:932:MET:HB2	1.78	0.65
1:A:929:G:H8	1:A:929:G:H5''	1.62	0.65
1:A:1416:G:N2	1:A:1485:U:H1'	2.11	0.65
1:A:929:G:H5''	1:A:929:G:C8	2.32	0.65
1:A:1005:A:OP2	1:A:1024:G:N2	2.24	0.65
9:I:78:VAL:HG21	9:I:125:ILE:HG22	1.79	0.65
12:L:22:HIS:HB2	12:L:33:THR:HG23	1.78	0.64
26:4:830:ASP:O	26:4:832:LYS:NZ	2.30	0.64
26:4:984:LEU:HD13	26:4:993:GLU:HB3	1.79	0.64
26:4:891:ASP:OD2	26:4:1290:ARG:NH2	2.23	0.64
12:L:79:ILE:HG21	12:L:82:LEU:HD13	1.80	0.64
26:4:1176:VAL:CG1	26:4:1185:PRO:HA	2.27	0.64
24:1:20:SER:HG	24:1:23:HIS:H	1.43	0.64
26:4:894:VAL:HG11	26:4:915:ILE:CD1	2.27	0.64
25:3:678:ARG:HH21	25:3:1106:ARG:HG2	1.63	0.64
26:4:419:HIS:NE2	26:4:471:PRO:O	2.24	0.64
26:4:964:LYS:H	26:4:977:SER:HB2	1.62	0.64
7:G:69:GLU:OE1	7:G:69:GLU:N	2.31	0.64
25:3:862:LEU:HD23	25:3:865:LEU:HD12	1.79	0.64
26:4:194:LEU:HD21	26:4:227:PHE:HB3	1.78	0.64
26:4:985:ILE:O	26:4:985:ILE:HD13	1.96	0.64
5:E:14:ARG:HG3	5:E:56:ARG:NH2	2.12	0.64
6:F:24:THR:HA	6:F:29:ARG:HA	1.79	0.64
26:4:865:HIS:HD2	26:4:867:GLN:H	1.45	0.64
26:4:981:GLU:HG2	26:4:996:LYS:CA	2.28	0.64
12:L:16:VAL:HG22	12:L:18:ASP:H	1.62	0.64
26:4:850:LYS:HD3	26:4:850:LYS:C	2.23	0.64
25:3:1143:GLU:OE2	25:3:1147:ARG:NH1	2.22	0.64
26:4:1159:ILE:O	26:4:1206:ARG:N	2.31	0.64
26:4:1269:ALA:HB2	26:4:1276:GLU:HA	1.78	0.64
30:7:15:DC:O5'	30:7:15:DC:H6	1.80	0.64
16:P:35:GLN:HE21	16:P:39:LEU:HG	1.63	0.63
25:3:13:LYS:NZ	25:3:1149:TYR:O	2.27	0.63
25:3:73:TYR:HD2	25:3:96:LEU:HD11	1.64	0.63
26:4:71:LEU:H	26:4:90:VAL:HG11	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1239:A:H62	1:A:1299:A:H62	1.45	0.63
23:X:7:G:H2'	23:X:8:A:H8	1.62	0.63
26:4:664:ILE:HG22	26:4:678:ARG:HG2	1.80	0.63
26:4:850:LYS:CD	26:4:855:ASP:HB2	2.28	0.63
2:B:170:ARG:HD3	2:B:173:VAL:CB	2.28	0.63
25:3:342:ASP:O	25:3:437:ASN:ND2	2.30	0.63
26:4:807:LEU:HD12	26:4:1255:VAL:HG13	1.79	0.63
26:4:970:SER:HB2	26:4:972:LYS:HE3	1.79	0.63
26:4:1169:THR:HG21	26:4:1192:LYS:HB3	1.80	0.63
20:T:50:ALA:HB1	20:T:57:HIS:HB3	1.80	0.63
27:5:25:ARG:HD3	27:5:64:LEU:HD13	1.81	0.63
1:A:429:U:H5'	5:E:9:LEU:HD12	1.81	0.63
1:A:963:G:N2	11:K:57:VAL:HG11	2.12	0.63
25:3:1268:GLN:OE1	26:4:352:ARG:NH1	2.31	0.63
26:4:146:VAL:HG11	26:4:154:LEU:HB3	1.81	0.63
1:A:973:G:O4'	11:K:57:VAL:HG12	1.99	0.63
11:K:92:LEU:HB2	28:Z:165:PHE:CB	2.28	0.63
1:A:1537:U:H2'	1:A:1538:C:C6	2.32	0.63
3:C:169:GLU:N	3:C:169:GLU:OE1	2.31	0.63
1:A:714:G:H2'	1:A:715:A:C8	2.34	0.63
20:T:63:THR:HG22	20:T:66:MET:HG3	1.80	0.63
25:3:848:GLU:HG2	25:3:888:THR:HA	1.81	0.63
26:4:1350:ASN:ND2	26:4:1358:PRO:CD	2.60	0.63
28:Z:14:ALA:HB1	28:Z:22:VAL:HG21	1.79	0.63
2:B:122:VAL:HG11	2:B:154:PHE:CD2	2.34	0.62
11:K:25:ILE:CD1	28:Z:165:PHE:CZ	2.82	0.62
13:M:114:ARG:NH1	13:M:119:VAL:O	2.31	0.62
25:3:21:VAL:HG21	25:3:592:ARG:NH1	2.14	0.62
25:3:289:VAL:HA	25:3:292:ILE:HD12	1.79	0.62
25:3:1184:THR:HG23	25:3:1190:ALA:H	1.64	0.62
26:4:1157:ALA:HB2	26:4:1210:ILE:HD11	1.81	0.62
1:A:147:G:H2'	1:A:148:G:C8	2.35	0.62
1:A:1381:U:O2'	8:H:79:ARG:O	2.14	0.62
3:C:107:VAL:O	3:C:111:ILE:HG12	1.98	0.62
8:H:22:LEU:HD13	8:H:101:MET:HE2	1.80	0.62
25:3:842:ASP:O	25:3:842:ASP:OD1	2.18	0.62
29:6:38:DA:H2''	29:6:39:DG:C8	2.34	0.62
1:A:269:C:H2'	1:A:270:A:H8	1.64	0.62
1:A:676:A:H5''	12:L:115:PRO:HB3	1.82	0.62
1:A:999:C:H2'	1:A:1000:A:C8	2.34	0.62
10:J:17:ALA:HB2	10:J:67:VAL:HG13	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:88:MET:HG2	28:Z:164:ILE:CD1	2.30	0.62
12:L:34:ILE:HD12	12:L:74:VAL:HG11	1.82	0.62
5:E:194:ASP:OD1	5:E:194:ASP:N	2.31	0.62
12:L:98:ARG:HH11	12:L:98:ARG:CG	2.12	0.62
25:3:617:ALA:HB2	25:3:650:VAL:HG21	1.82	0.62
1:A:81:A:H2'	1:A:82:G:C8	2.35	0.62
2:B:108:VAL:O	2:B:154:PHE:N	2.33	0.62
2:B:115:LYS:CD	2:B:144:THR:H	2.13	0.62
2:B:159:LEU:HA	2:B:166:VAL:HG22	1.80	0.62
2:B:120:PHE:N	2:B:131:LEU:O	2.33	0.62
26:4:982:LEU:H	26:4:982:LEU:CD2	2.13	0.62
2:B:147:LEU:HD23	2:B:152:LEU:HD21	1.82	0.61
2:B:158:LYS:HG3	2:B:159:LEU:N	2.15	0.61
4:D:77:ILE:HA	4:D:84:VAL:HG23	1.82	0.61
14:N:5:ALA:HB1	14:N:66:GLU:HG2	1.80	0.61
25:3:201:ARG:NH1	25:3:370:MET:O	2.32	0.61
2:B:23:ILE:HD11	2:B:92:HIS:CD2	2.35	0.61
7:G:12:PRO:HD2	7:G:54:LEU:HD11	1.82	0.61
12:L:98:ARG:NH1	12:L:98:ARG:HG2	2.15	0.61
1:A:1413:A:H2	1:A:1487:G:H22	1.46	0.61
1:A:1487:G:C8	1:A:1487:G:O5'	2.54	0.61
5:E:85:ASN:HB2	5:E:88:GLU:HG2	1.83	0.61
6:F:99:ALA:HB2	6:F:124:LEU:HG	1.83	0.61
25:3:211:ARG:HB2	25:3:362:ALA:HB2	1.82	0.61
25:3:1058:ARG:NH2	25:3:1240:ASP:OD1	2.33	0.61
26:4:290:ILE:HG23	28:Z:93:ILE:CG2	2.30	0.61
26:4:814:CYS:SG	26:4:883:ARG:NH2	2.73	0.61
26:4:1155:ILE:HG13	26:4:1210:ILE:HB	1.82	0.61
16:P:74:ASP:OD1	16:P:77:ARG:HB2	1.99	0.61
26:4:271:ARG:NH1	26:4:275:ARG:HH22	1.98	0.61
26:4:985:ILE:CG1	26:4:989:GLY:HA2	2.30	0.61
1:A:1026:G:H1	1:A:1035:A:H61	1.46	0.61
2:B:42:LEU:O	3:C:208:ARG:NH2	2.34	0.61
12:L:71:ALA:HB1	12:L:103:ALA:CB	2.31	0.61
26:4:644:MET:HE1	26:4:740:LEU:HD13	1.82	0.61
1:A:21:G:H2'	1:A:22:G:C8	2.35	0.61
5:E:203:LEU:HD12	5:E:206:LYS:HE3	1.83	0.61
25:3:10:ARG:HH11	25:3:791:LEU:HD12	1.64	0.61
1:A:1287:A:H2'	1:A:1288:A:C8	2.35	0.61
12:L:64:GLN:HB2	12:L:95:SER:HB3	1.80	0.61
1:A:652:U:O4	1:A:752:G:O2'	2.18	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:946:A:H2'	1:A:947:G:C8	2.36	0.61
10:J:38:TYR:OH	10:J:75:GLN:NE2	2.33	0.61
12:L:17:SER:HB2	12:L:80:LYS:HG2	1.83	0.61
25:3:866:ASP:OD1	25:3:869:GLY:N	2.25	0.61
26:4:975:ILE:HG21	26:4:998:PRO:O	2.01	0.61
26:4:1177:ILE:HB	26:4:1186:TYR:CD2	2.36	0.61
1:A:924:C:O5'	1:A:924:C:H6	1.83	0.60
2:B:161:GLN:HA	2:B:164:ASN:HA	1.83	0.60
6:F:156:LYS:NZ	9:I:73:GLU:OE2	2.34	0.60
25:3:1222:GLU:HG3	26:4:634:ARG:HH21	1.65	0.60
1:A:1483:A:OP2	1:A:1483:A:H8	1.84	0.60
4:D:40:ARG:NH1	4:D:55:ILE:O	2.34	0.60
20:T:20:GLU:O	20:T:24:GLU:HG3	2.01	0.60
25:3:139:ASN:ND2	30:7:23:DC:OP1	2.29	0.60
26:4:1160:SER:HB2	26:4:1203:ARG:HH12	1.66	0.60
2:B:166:VAL:HG12	2:B:166:VAL:O	2.00	0.60
13:M:21:VAL:HG11	13:M:24:LEU:HD22	1.83	0.60
13:M:110:ARG:HH21	13:M:113:ALA:HB3	1.66	0.60
2:B:162:LYS:N	2:B:162:LYS:CD	2.64	0.60
5:E:163:GLU:O	5:E:167:LYS:NZ	2.35	0.60
26:4:527:LEU:HB2	26:4:550:VAL:HG12	1.84	0.60
26:4:1069:ALA:HA	26:4:1072:LYS:HB2	1.84	0.60
1:A:1483:A:H8	1:A:1483:A:P	2.24	0.60
1:A:859:G:H2'	1:A:860:A:H8	1.67	0.60
17:Q:18:GLN:HE21	17:Q:35:ARG:NE	1.99	0.60
24:2:86:LYS:NZ	26:4:532:GLU:OE2	2.34	0.60
29:6:17:DC:H4'	29:6:18:DG:H5'	1.82	0.60
2:B:162:LYS:N	2:B:162:LYS:HD2	2.16	0.60
26:4:1157:ALA:N	26:4:1208:ASP:O	2.20	0.60
2:B:155:LYS:O	2:B:157:ILE:HG13	2.02	0.60
1:A:976:G:OP2	1:A:1358:U:O2'	2.20	0.60
8:H:54:SER:OG	8:H:56:LYS:NZ	2.33	0.60
1:A:166:U:H2'	1:A:167:A:H8	1.67	0.60
1:A:1082:A:OP2	6:F:23:LYS:NZ	2.33	0.60
8:H:16:PRO:HA	10:J:46:MET:HE2	1.83	0.60
26:4:43:THR:HG22	26:4:56:LEU:HB2	1.83	0.60
1:A:259:G:P	21:U:78:ASN:HD21	2.25	0.59
26:4:368:LEU:HD22	26:4:439:PRO:HB2	1.84	0.59
1:A:1506:U:C6	1:A:1506:U:H5''	2.37	0.59
25:3:404:LYS:NZ	25:3:449:GLY:O	2.34	0.59
4:D:155:GLY:HA2	4:D:163:ALA:HB1	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:4:968:ASN:CB	26:4:1118:GLY:HA3	2.32	0.59
26:4:975:ILE:HD11	26:4:997:VAL:HB	1.82	0.59
26:4:995:TYR:N	26:4:995:TYR:CD1	2.70	0.59
25:3:994:ARG:HA	25:3:997:TRP:CE2	2.37	0.59
2:B:109:THR:HG22	2:B:153:GLU:HG2	1.84	0.59
1:A:1040:U:H2'	1:A:1041:G:C8	2.38	0.59
1:A:1484:C:H2'	1:A:1485:U:H6	1.68	0.59
1:A:713:G:H2'	1:A:714:G:C8	2.38	0.59
1:A:1268:G:H1'	1:A:1326:U:O2'	2.03	0.59
1:A:1392:G:N1	1:A:1504:G:H1'	2.17	0.59
1:A:1504:G:C8	1:A:1504:G:H5''	2.38	0.59
2:B:131:LEU:HD21	2:B:136:VAL:HG22	1.85	0.59
12:L:15:GLN:NE2	12:L:77:TYR:O	2.35	0.59
1:A:1077:G:N2	1:A:1080:A:OP2	2.31	0.59
2:B:170:ARG:NH1	2:B:170:ARG:HB2	2.17	0.59
25:3:533:LEU:HD21	25:3:571:LEU:HD13	1.84	0.59
25:3:1166:ASP:O	25:3:1166:ASP:OD1	2.21	0.59
25:3:1276:TRP:CZ2	26:4:801:VAL:HG21	2.38	0.59
1:A:539:A:OP2	13:M:112:GLN:NE2	2.35	0.59
11:K:94:ALA:HA	28:Z:167:ARG:NH2	2.17	0.59
17:Q:54:LEU:H	17:Q:54:LEU:HD12	1.67	0.59
25:3:302:ILE:HG22	25:3:309:LEU:HA	1.84	0.59
1:A:1218:C:H2'	1:A:1219:A:H8	1.64	0.58
3:C:50:PHE:O	3:C:54:LEU:HD22	2.03	0.58
4:D:22:TRP:CD1	4:D:59:ARG:HG3	2.37	0.58
5:E:70:ARG:O	5:E:74:ASN:ND2	2.34	0.58
25:3:320:ASP:OD1	25:3:320:ASP:N	2.32	0.58
25:3:520:PRO:HG3	25:3:714:VAL:HG11	1.85	0.58
1:A:1395:C:H3'	1:A:1396:A:H8	1.68	0.58
4:D:64:ILE:HG12	4:D:65:ARG:H	1.66	0.58
8:H:130:ASN:N	8:H:130:ASN:OD1	2.35	0.58
25:3:1166:ASP:HA	25:3:1169:VAL:HB	1.85	0.58
26:4:808:VAL:O	26:4:894:VAL:HG12	2.02	0.58
28:Z:43:MET:HE1	28:Z:112:MET:HG2	1.84	0.58
1:A:1356:G:H2'	1:A:1357:A:H8	1.69	0.58
10:J:88:MET:SD	10:J:95:ARG:NE	2.76	0.58
25:3:714:VAL:O	25:3:767:GLN:NE2	2.36	0.58
25:3:1070:HIS:NE2	25:3:1114:GLU:OE1	2.34	0.58
25:3:1129:ASN:OD1	25:3:1177:ARG:NE	2.29	0.58
1:A:780:A:H5''	12:L:125:LYS:HD3	1.85	0.58
2:B:115:LYS:CD	2:B:143:ASP:HA	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:162:LYS:CD	2:B:162:LYS:H	2.16	0.58
7:G:4:TYR:CD2	7:G:71:ILE:HG13	2.39	0.58
10:J:5:GLN:HG3	10:J:20:PHE:HB3	1.84	0.58
26:4:474:LEU:HD21	27:5:27:ALA:HB3	1.86	0.58
26:4:848:VAL:HB	26:4:858:VAL:CB	2.34	0.58
26:4:45:ASN:ND2	26:4:48:THR:H	2.00	0.58
1:A:407:U:O2'	5:E:113:GLU:OE1	2.14	0.58
1:A:782:A:H62	1:A:800:G:H21	1.52	0.58
1:A:977:A:O2'	1:A:979:C:OP2	2.19	0.58
1:A:1425:U:H3	1:A:1475:G:H1	1.52	0.58
26:4:513:MET:HG3	26:4:544:LEU:HD21	1.84	0.58
1:A:1040:U:H2'	1:A:1041:G:H8	1.68	0.58
1:A:1487:G:O5'	1:A:1487:G:H8	1.85	0.58
8:H:2:PRO:HG2	8:H:5:ARG:H	1.67	0.58
26:4:720:ASN:HD22	26:4:723:TYR:H	1.49	0.58
30:7:19:DG:C8	30:7:19:DG:OP2	2.56	0.58
3:C:68:LEU:HB3	3:C:161:LEU:HD22	1.86	0.58
17:Q:1:MET:HG3	17:Q:2:VAL:N	2.15	0.58
1:A:8:A:N6	5:E:202:GLU:O	2.36	0.58
4:D:82:GLU:HG3	4:D:83:ASP:H	1.68	0.58
11:K:88:MET:HE2	28:Z:164:ILE:CD1	2.34	0.58
24:2:112:ALA:HB2	24:2:128:HIS:HB3	1.86	0.58
26:4:557:LYS:HB3	26:4:563:LEU:HD23	1.85	0.58
1:A:475:C:H2'	1:A:476:U:C6	2.39	0.57
1:A:528:C:N4	13:M:46:ASN:OD1	2.37	0.57
1:A:674:G:H2'	1:A:675:A:H8	1.69	0.57
1:A:923:A:H2'	1:A:924:C:C6	2.38	0.57
25:3:590:PRO:O	25:3:659:GLN:NE2	2.31	0.57
26:4:827:GLU:O	26:4:832:LYS:NZ	2.34	0.57
29:6:30:DA:H2''	29:6:31:DG:C8	2.39	0.57
29:6:36:DA:H2''	29:6:37:DG:C8	2.39	0.57
1:A:1169:A:H2'	1:A:1170:A:C8	2.39	0.57
1:A:1536:C:H2'	1:A:1537:U:H6	1.69	0.57
3:C:20:THR:HA	3:C:39:HIS:CD2	2.39	0.57
3:C:58:ASN:HB2	3:C:220:THR:HG22	1.86	0.57
10:J:39:PHE:O	10:J:45:ARG:NH1	2.38	0.57
11:K:66:GLU:OE2	11:K:68:ARG:NH2	2.29	0.57
11:K:88:MET:HE2	28:Z:164:ILE:HD11	1.86	0.57
26:4:802:ASP:OD1	26:4:1348:LYS:NZ	2.27	0.57
26:4:965:SER:CB	26:4:975:ILE:HA	2.32	0.57
5:E:102:VAL:HG13	5:E:114:ALA:HB1	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1151:A:HO2'	1:A:1152:A:H8	1.51	0.57
1:A:1485:U:O2	1:A:1485:U:C2'	2.53	0.57
1:A:1541:U:H2'	1:A:1542:A:C8	2.38	0.57
12:L:14:LYS:HD3	12:L:14:LYS:H	1.69	0.57
23:X:49:G:O2'	25:3:513:GLN:OE1	2.22	0.57
26:4:1176:VAL:HG13	26:4:1185:PRO:HA	1.86	0.57
4:D:17:PRO:HG2	4:D:54:ARG:NH2	2.11	0.57
20:T:25:SER:O	20:T:26:GLY:C	2.46	0.57
25:3:845:LEU:HB2	25:3:890:LYS:CE	2.35	0.57
1:A:464:U:O2'	1:A:466:A:N7	2.32	0.57
5:E:57:GLU:OE2	5:E:196:ASN:HB3	2.05	0.57
6:F:80:THR:HG23	6:F:122:ASN:O	2.04	0.57
25:3:228:VAL:HB	25:3:245:ARG:HH12	1.69	0.57
25:3:406:ASN:ND2	25:3:413:GLU:O	2.37	0.57
25:3:538:LEU:HD11	25:3:571:LEU:HD22	1.87	0.57
26:4:1177:ILE:HD12	26:4:1186:TYR:CD2	2.39	0.57
28:Z:147:VAL:HG13	28:Z:161:SER:HB3	1.86	0.57
1:A:691:G:H2'	1:A:692:U:H6	1.69	0.57
1:A:1485:U:C5	1:A:1485:U:OP2	2.58	0.57
12:L:68:GLU:CG	12:L:99:ALA:HB1	2.35	0.57
14:N:44:LYS:O	14:N:45:ILE:HD13	2.05	0.57
17:Q:6:LEU:HB3	17:Q:17:TYR:HB3	1.87	0.57
25:3:387:ASN:HA	25:3:391:SER:HB3	1.87	0.57
1:A:1239:A:H62	1:A:1299:A:N6	2.03	0.57
11:K:25:ILE:HD11	28:Z:165:PHE:CZ	2.40	0.57
1:A:203:G:H1'	1:A:465:A:H61	1.70	0.57
1:A:1390:U:H2'	1:A:1391:U:C6	2.40	0.57
9:I:90:ASP:N	9:I:90:ASP:OD1	2.36	0.57
13:M:53:CYS:HB3	13:M:67:ILE:HD11	1.86	0.57
26:4:1038:THR:HG21	26:4:1079:LYS:HE2	1.87	0.57
1:A:748:G:H2'	1:A:749:A:C8	2.39	0.56
7:G:93:LYS:O	7:G:94:HIS:ND1	2.38	0.56
26:4:963:VAL:HA	26:4:980:THR:HB	1.87	0.56
26:4:1319:PHE:HB3	26:4:1340:LYS:HD2	1.87	0.56
2:B:156:VAL:HA	2:B:168:VAL:HG22	1.86	0.56
2:B:170:ARG:HH11	2:B:170:ARG:CB	2.18	0.56
3:C:9:MET:HE1	3:C:47:VAL:HG22	1.87	0.56
11:K:56:HIS:ND1	11:K:57:VAL:HG13	2.20	0.56
30:7:17:DG:OP1	30:7:17:DG:C4'	2.51	0.56
1:A:1419:G:N2	1:A:1482:G:H1'	2.20	0.56
2:B:143:ASP:N	2:B:143:ASP:OD1	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:34:CYS:SG	13:M:37:VAL:HG23	2.45	0.56
25:3:300:ASP:HA	25:3:312:ALA:HA	1.87	0.56
25:3:347:ILE:HD11	25:3:433:ILE:HD11	1.87	0.56
26:4:576:ARG:HD3	26:4:593:ASN:HA	1.87	0.56
26:4:958:ILE:HG21	26:4:1006:GLY:HA2	1.87	0.56
30:7:19:DG:OP2	30:7:19:DG:H8	1.88	0.56
1:A:79:G:H2'	1:A:80:A:H8	1.71	0.56
1:A:337:G:H2'	1:A:338:A:C8	2.41	0.56
1:A:687:A:N3	1:A:688:G:H1'	2.20	0.56
1:A:696:A:H2'	1:A:697:U:C6	2.40	0.56
1:A:859:G:H2'	1:A:860:A:C8	2.40	0.56
3:C:168:HIS:HB3	3:C:169:GLU:OE1	2.06	0.56
4:D:126:ARG:O	4:D:127:ARG:HB2	2.05	0.56
5:E:15:GLU:HG2	5:E:60:LYS:HG3	1.86	0.56
12:L:97:ILE:HG22	22:V:12:PHE:CE1	2.41	0.56
26:4:656:GLU:OE1	26:4:692:ARG:NH2	2.29	0.56
26:4:907:HIS:ND1	26:4:908:ILE:O	2.34	0.56
1:A:235:C:H2'	1:A:236:A:H8	1.71	0.56
1:A:451:A:N6	1:A:481:G:OP2	2.34	0.56
20:T:69:HIS:ND1	20:T:73:GLU:OE1	2.39	0.56
26:4:405:GLU:HB2	26:4:408:VAL:HG23	1.88	0.56
27:5:38:LEU:N	27:5:53:GLU:OE2	2.27	0.56
1:A:92:U:H2'	1:A:93:U:C6	2.39	0.56
1:A:844:G:H2'	1:A:844:G:N3	2.20	0.56
1:A:1410:A:H5''	1:A:1410:A:H8	1.71	0.56
3:C:43:LEU:O	3:C:47:VAL:HG23	2.06	0.56
10:J:119:ARG:HB2	10:J:123:ARG:HD2	1.88	0.56
24:1:71:LYS:O	24:1:74:VAL:HG22	2.06	0.56
25:3:478:ARG:NH1	25:3:491:ASP:O	2.38	0.56
26:4:158:GLN:O	26:4:158:GLN:NE2	2.38	0.56
26:4:975:ILE:HB	26:4:1001:ALA:O	2.05	0.56
1:A:411:A:H4'	1:A:412:A:H5'	1.87	0.56
1:A:746:A:H2'	1:A:747:A:C8	2.41	0.56
1:A:844:G:N3	1:A:844:G:C2'	2.69	0.56
26:4:122:SER:HB2	26:4:132:LEU:HD12	1.88	0.56
26:4:965:SER:HB2	26:4:975:ILE:CA	2.34	0.56
1:A:337:G:H2'	1:A:338:A:H8	1.71	0.56
1:A:993:G:O2'	1:A:994:A:N7	2.39	0.56
1:A:1419:G:C2	1:A:1482:G:H1'	2.41	0.56
3:C:159:ASP:N	3:C:159:ASP:OD1	2.38	0.56
8:H:68:ASN:O	8:H:138:ARG:NH2	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:301:TYR:HB3	25:3:330:HIS:CD2	2.41	0.56
1:A:24:U:HO2'	1:A:524:G:HO2'	1.54	0.56
1:A:531:U:H4'	1:A:532:A:H5'	1.87	0.56
2:B:19:ARG:O	2:B:21:GLY:N	2.39	0.56
6:F:43:ASN:O	6:F:43:ASN:ND2	2.39	0.56
25:3:1291:LEU:HD11	26:4:1354:GLY:HA2	1.88	0.56
1:A:181:A:O2'	1:A:194:C:N4	2.39	0.55
5:E:107:PHE:HB3	5:E:155:VAL:HG22	1.87	0.55
28:Z:174:ASP:OD1	28:Z:175:PHE:N	2.39	0.55
30:7:15:DC:C2'	30:7:16:DC:H5'	2.36	0.55
1:A:28:A:O2'	1:A:296:U:OP1	2.24	0.55
1:A:1309:G:OP1	14:N:87:ARG:NH2	2.34	0.55
10:J:84:THR:HG23	10:J:98:LEU:HD13	1.88	0.55
1:A:745:G:H2'	1:A:746:A:H8	1.72	0.55
2:B:95:TRP:CH2	2:B:161:GLN:HB3	2.40	0.55
24:2:191:ARG:HB3	24:2:196:THR:HG23	1.88	0.55
25:3:1103:VAL:HB	26:4:639:VAL:HG11	1.89	0.55
26:4:156:ARG:NH2	26:4:191:SER:OG	2.39	0.55
26:4:558:ASP:OD1	26:4:561:GLY:N	2.29	0.55
26:4:1177:ILE:HD12	26:4:1186:TYR:HE2	1.69	0.55
28:Z:162:VAL:HG23	28:Z:164:ILE:HG12	1.86	0.55
30:7:20:DC:H2'	30:7:21:DG:C8	2.41	0.55
1:A:413:G:H1'	1:A:428:G:H21	1.72	0.55
1:A:1266:G:N2	1:A:1269:A:OP2	2.33	0.55
1:A:1393:U:H2'	1:A:1394:A:O4'	2.07	0.55
11:K:25:ILE:HD12	28:Z:165:PHE:CZ	2.41	0.55
25:3:1282:GLY:HA3	27:5:17:PHE:HE1	1.71	0.55
1:A:1481:U:C2'	1:A:1482:G:H5'	2.37	0.55
1:A:1483:A:OP2	1:A:1483:A:C8	2.60	0.55
2:B:148:GLU:HG3	2:B:148:GLU:O	2.05	0.55
8:H:37:SER:HB3	10:J:41:ARG:NH2	2.21	0.55
25:3:119:GLU:HB2	25:3:489:PRO:HG2	1.89	0.55
25:3:458:GLU:O	25:3:462:ASN:ND2	2.38	0.55
2:B:157:ILE:O	2:B:157:ILE:CG2	2.54	0.55
3:C:68:LEU:HD13	3:C:154:MET:HE1	1.87	0.55
26:4:275:ARG:HD2	26:4:302:ALA:CB	2.37	0.55
26:4:317:THR:HG21	26:4:321:LYS:HA	1.88	0.55
1:A:380:G:N2	1:A:383:A:OP2	2.39	0.55
3:C:151:ILE:O	3:C:151:ILE:HG12	2.07	0.55
4:D:68:ILE:HB	4:D:103:ILE:HD13	1.89	0.55
5:E:58:LYS:HD2	5:E:204:TYR:OH	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:100:ASN:O	5:E:104:ARG:HG2	2.06	0.55
5:E:106:GLY:O	5:E:108:GLY:N	2.40	0.55
1:A:362:G:N2	1:A:365:U:OP2	2.39	0.55
1:A:691:G:H2'	1:A:692:U:C6	2.41	0.55
2:B:132:PRO:CB	2:B:135:LEU:HD12	2.37	0.55
5:E:159:LEU:O	5:E:163:GLU:HG2	2.07	0.55
6:F:157:ARG:HH22	9:I:43:GLU:HG3	1.71	0.55
1:A:401:C:O2'	1:A:621:A:N3	2.34	0.55
28:Z:42:VAL:O	28:Z:42:VAL:HG22	2.06	0.55
29:6:15:DA:H2''	29:6:16:DT:C4	2.42	0.55
1:A:736:C:OP1	19:S:61:ARG:NH1	2.40	0.55
1:A:1025:U:H4'	1:A:1026:G:H5'	1.89	0.55
26:4:371:LYS:H	26:4:371:LYS:HD2	1.72	0.55
1:A:1490:U:H2'	1:A:1491:G:H5''	1.90	0.54
13:M:56:ARG:NH2	13:M:62:GLU:OE1	2.40	0.54
14:N:19:LEU:HD12	14:N:22:ILE:HD12	1.89	0.54
19:S:70:TYR:H	19:S:74:HIS:HE1	1.53	0.54
25:3:196:VAL:HG11	25:3:209:ILE:HD11	1.88	0.54
26:4:746:LEU:HD23	26:4:758:PRO:HB3	1.88	0.54
1:A:475:C:H2'	1:A:476:U:H6	1.72	0.54
1:A:662:U:H2'	1:A:663:A:C8	2.42	0.54
5:E:29:ASP:N	5:E:29:ASP:OD1	2.38	0.54
26:4:1172:LYS:HE3	26:4:1191:PRO:HA	1.88	0.54
1:A:1366:C:O2'	11:K:62:ARG:NH2	2.40	0.54
1:A:1519:MA6:O2'	1:A:1542:A:O3'	2.25	0.54
2:B:95:TRP:HH2	2:B:161:GLN:HB3	1.73	0.54
2:B:146:HIS:ND1	2:B:146:HIS:N	2.50	0.54
26:4:479:GLU:HG3	27:5:20:VAL:HG11	1.89	0.54
1:A:191:G:H2'	1:A:192:A:C8	2.42	0.54
1:A:202:G:O2'	1:A:468:A:H8	1.91	0.54
1:A:686:U:O4	1:A:703:G:O2'	2.17	0.54
1:A:951:G:OP2	14:N:101:ARG:NH2	2.40	0.54
1:A:1397:C:H2'	1:A:1398:A:H8	1.70	0.54
2:B:156:VAL:HA	2:B:168:VAL:CG2	2.37	0.54
17:Q:18:GLN:HE21	17:Q:35:ARG:HE	1.55	0.54
25:3:1109:ILE:CD1	26:4:644:MET:HG3	2.38	0.54
26:4:968:ASN:HB3	26:4:1118:GLY:HA3	1.89	0.54
5:E:102:VAL:CG1	5:E:114:ALA:HB1	2.38	0.54
9:I:41:LYS:HD2	9:I:48:ASP:HA	1.90	0.54
26:4:425:ARG:CB	26:4:466:MET:HE2	2.31	0.54
1:A:56:U:H2'	1:A:57:G:H8	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:7:VAL:HG22	7:G:61:LEU:HD12	1.89	0.54
11:K:50:THR:HG23	11:K:62:ARG:HB3	1.89	0.54
15:O:39:GLU:OE2	15:O:43:ASN:ND2	2.40	0.54
16:P:17:ARG:HG3	16:P:21:ASP:HB2	1.89	0.54
25:3:1327:LEU:O	25:3:1331:ARG:HG3	2.08	0.54
26:4:205:LEU:HD13	26:4:217:LEU:HD22	1.89	0.54
26:4:975:ILE:HG22	26:4:999:TYR:HA	1.89	0.54
29:6:18:DG:H5''	29:6:18:DG:C8	2.42	0.54
1:A:1538:C:H2'	1:A:1539:C:C6	2.43	0.54
17:Q:4:ILE:HB	17:Q:67:ILE:HD13	1.88	0.54
24:1:135:ASP:HB3	24:1:138:ALA:HB2	1.90	0.54
25:3:1119:MET:HG3	25:3:1204:LEU:HD13	1.90	0.54
1:A:1084:G:P	1:A:1086:U:H3	2.30	0.54
1:A:1486:G:C8	1:A:1486:G:OP2	2.60	0.54
3:C:89:GLN:NE2	3:C:225:ARG:HH21	2.06	0.54
24:2:124:VAL:HG23	24:2:125:LYS:HG2	1.90	0.54
25:3:119:GLU:HG2	25:3:122:VAL:HB	1.90	0.54
25:3:237:LEU:HB3	25:3:292:ILE:HD13	1.88	0.54
26:4:967:VAL:N	26:4:974:VAL:HB	2.22	0.54
1:A:575:G:H4'	1:A:576:C:H5''	1.89	0.54
1:A:1427:C:H2'	1:A:1428:A:H8	1.73	0.54
20:T:23:VAL:HG13	20:T:24:GLU:N	2.22	0.54
24:2:66:HIS:O	24:2:69:SER:OG	2.26	0.54
26:4:416:ILE:HG12	26:4:439:PRO:HG2	1.90	0.54
26:4:527:LEU:HD22	26:4:548:VAL:HG21	1.90	0.54
26:4:964:LYS:HB3	26:4:977:SER:HB2	1.88	0.54
1:A:1323:G:H2'	1:A:1324:A:C8	2.43	0.54
2:B:142:ARG:H	2:B:142:ARG:NE	2.06	0.54
8:H:88:PRO:HD2	8:H:152:ALA:HB2	1.90	0.54
8:H:113:ASP:HB2	8:H:119:ARG:HG3	1.90	0.54
24:1:27:THR:HB	24:1:202:VAL:HG22	1.90	0.54
24:2:109:PRO:HA	24:2:132:HIS:HA	1.90	0.54
25:3:595:THR:HG1	25:3:600:THR:HG1	1.56	0.54
26:4:987:GLU:CD	26:4:987:GLU:H	2.16	0.54
30:7:26:DA:H2''	30:7:27:DG:C8	2.43	0.54
1:A:579:A:H5'	1:A:728:A:H1'	1.89	0.53
1:A:997:U:H2'	1:A:998:C:H6	1.74	0.53
2:B:42:LEU:HB3	2:B:82:THR:HG21	1.90	0.53
2:B:157:ILE:N	2:B:167:VAL:O	2.38	0.53
4:D:79:LYS:O	4:D:82:GLU:HG2	2.08	0.53
25:3:615:VAL:HG22	25:3:650:VAL:HG23	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:5:7:GLN:NE2	27:5:11:GLU:OE2	2.42	0.53
1:A:1137:C:O2	1:A:1138:G:N2	2.41	0.53
2:B:12:SER:O	2:B:16:ILE:HG12	2.08	0.53
22:V:12:PHE:CZ	22:V:16:LEU:HD22	2.44	0.53
24:1:62:ASP:OD1	24:1:63:GLY:N	2.41	0.53
26:4:355:ILE:HG12	26:4:464:ASP:O	2.08	0.53
28:Z:104:SER:HB2	28:Z:107:GLU:HB2	1.89	0.53
1:A:1522:U:H2'	1:A:1523:G:H8	1.73	0.53
2:B:131:LEU:CD1	2:B:136:VAL:HA	2.36	0.53
5:E:78:GLU:OE2	5:E:81:ARG:NH2	2.34	0.53
7:G:43:GLY:HA2	7:G:58:HIS:CE1	2.43	0.53
17:Q:19:VAL:HG22	17:Q:36:VAL:HG23	1.91	0.53
26:4:646:ILE:HD12	26:4:762:ASN:HD21	1.73	0.53
26:4:1181:ASP:OD1	26:4:1181:ASP:N	2.33	0.53
1:A:1130:A:H2'	1:A:1131:G:H8	1.73	0.53
3:C:102:THR:HG23	3:C:175:GLU:HG3	1.90	0.53
19:S:70:TYR:N	19:S:74:HIS:HE1	2.07	0.53
25:3:941:LYS:HB2	25:3:946:LEU:HD21	1.91	0.53
28:Z:136:VAL:HB	28:Z:142:ALA:HA	1.89	0.53
1:A:525:C:OP1	13:M:86:ARG:NH2	2.41	0.53
1:A:559:A:H4'	1:A:560:A:H3'	1.91	0.53
1:A:1418:A:H2'	1:A:1418:A:N3	2.23	0.53
16:P:55:GLY:O	16:P:59:MET:HG3	2.09	0.53
24:1:62:ASP:OD1	24:1:71:LYS:NZ	2.39	0.53
24:2:135:ASP:HB2	24:2:138:ALA:HB2	1.89	0.53
1:A:613:C:H2'	1:A:614:C:C6	2.43	0.53
1:A:1487:G:C8	1:A:1487:G:OP2	2.61	0.53
2:B:112:ILE:HG21	2:B:120:PHE:HD2	1.73	0.53
5:E:110:THR:HG23	5:E:113:GLU:H	1.73	0.53
16:P:71:LYS:HE3	16:P:78:TYR:CE2	2.44	0.53
25:3:53:PHE:O	25:3:57:PHE:N	2.41	0.53
26:4:208:THR:O	26:4:214:ARG:NE	2.42	0.53
26:4:308:ASP:OD2	26:4:311:ARG:NE	2.40	0.53
1:A:1503:A:C8	1:A:1503:A:H5''	2.44	0.53
14:N:41:GLU:OE1	14:N:41:GLU:N	2.42	0.53
24:1:104:LYS:HG2	24:1:110:VAL:HG22	1.91	0.53
24:2:18:GLN:HG3	24:2:20:SER:O	2.09	0.53
24:2:47:LEU:HD22	24:2:180:VAL:HG21	1.91	0.53
26:4:242:LEU:HD21	26:4:306:LEU:HD22	1.91	0.53
26:4:952:VAL:HG13	26:4:1014:GLY:H	1.72	0.53
28:Z:12:VAL:HB	28:Z:69:VAL:HG23	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:5:PHE:CG	3:C:44:GLU:HG2	2.44	0.53
14:N:16:VAL:HG13	14:N:17:ILE:HD12	1.90	0.53
25:3:237:LEU:HD22	25:3:292:ILE:HG21	1.91	0.53
25:3:870:ILE:HB	25:3:944:ARG:HD2	1.90	0.53
26:4:888:CYS:SG	26:4:895:CYS:HB3	2.49	0.53
26:4:959:LYS:HA	26:4:959:LYS:CE	2.39	0.53
1:A:275:G:H5'	18:R:16:LYS:HD3	1.91	0.53
2:B:6:ALA:HA	2:B:9:PHE:HB2	1.91	0.53
2:B:53:PHE:CD1	2:B:62:ILE:HD13	2.44	0.53
5:E:105:MET:HG2	5:E:173:VAL:CG2	2.39	0.53
12:L:17:SER:HA	12:L:79:ILE:HA	1.91	0.53
26:4:312:ARG:NH1	26:4:314:ARG:O	2.42	0.53
26:4:1169:THR:HG23	26:4:1173:ARG:N	2.24	0.53
1:A:216:U:H2'	1:A:217:C:C6	2.44	0.52
1:A:390:U:H2'	1:A:391:G:H8	1.74	0.52
1:A:1393:U:H2'	1:A:1394:A:C8	2.44	0.52
2:B:154:PHE:CD1	2:B:169:SER:HA	2.44	0.52
4:D:34:ASP:O	4:D:38:LYS:HG2	2.09	0.52
7:G:4:TYR:CE2	7:G:71:ILE:HG13	2.44	0.52
24:2:16:ILE:HG22	24:2:26:VAL:HG22	1.90	0.52
25:3:436:ARG:NH1	25:3:436:ARG:O	2.42	0.52
25:3:705:GLU:HB3	25:3:794:LEU:H	1.73	0.52
25:3:726:TYR:HB3	25:3:733:VAL:HG13	1.90	0.52
25:3:812:PHE:CZ	26:4:503:SER:HB2	2.44	0.52
26:4:275:ARG:HD2	26:4:302:ALA:HB2	1.91	0.52
26:4:572:THR:OG1	26:4:573:THR:N	2.42	0.52
26:4:809:VAL:HA	26:4:894:VAL:HG13	1.91	0.52
1:A:136:C:H1'	17:Q:1:MET:HG2	1.91	0.52
2:B:131:LEU:HB2	2:B:168:VAL:O	2.09	0.52
26:4:312:ARG:HG2	26:4:313:GLY:H	1.74	0.52
26:4:973:LEU:CB	26:4:1003:LEU:HD12	2.39	0.52
26:4:977:SER:HB3	26:4:980:THR:HG22	1.91	0.52
26:4:1158:GLU:HG3	26:4:1159:ILE:HG13	1.91	0.52
1:A:511:C:O3'	5:E:44:ARG:NH2	2.41	0.52
1:A:692:U:O2'	1:A:694:A:N7	2.40	0.52
1:A:1507:A:H5''	1:A:1507:A:C8	2.43	0.52
2:B:5:PHE:CE1	3:C:43:LEU:HB2	2.44	0.52
9:I:78:VAL:HG22	9:I:127:CYS:HA	1.91	0.52
14:N:78:LYS:HE2	14:N:82:ASP:OD1	2.09	0.52
25:3:555:TYR:O	25:3:557:ARG:NH1	2.43	0.52
26:4:1178:THR:HA	26:4:1184:ASP:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:Z:90:MET:HB2	29:6:18:DG:O4'	2.09	0.52
1:A:1029:U:O2'	1:A:1032:G:O6	2.24	0.52
1:A:1180:A:P	10:J:99:ARG:HH22	2.33	0.52
1:A:1347:G:H2'	10:J:110:GLN:O	2.10	0.52
2:B:115:LYS:HG2	2:B:144:THR:N	2.19	0.52
5:E:74:ASN:O	5:E:77:LYS:HG2	2.09	0.52
12:L:16:VAL:HG13	12:L:79:ILE:HG12	1.91	0.52
25:3:228:VAL:HG13	25:3:335:THR:OG1	2.10	0.52
25:3:845:LEU:CB	25:3:890:LYS:CD	2.68	0.52
26:4:992:LYS:HE2	26:4:992:LYS:C	2.34	0.52
1:A:555:U:H2'	1:A:556:C:C6	2.43	0.52
1:A:1332:A:H2'	1:A:1333:A:O4'	2.10	0.52
3:C:21:ARG:HG3	3:C:22:TYR:CD2	2.45	0.52
23:X:44:A:N6	25:3:1264:GLN:OE1	2.43	0.52
24:2:224:LEU:O	24:2:228:LEU:HG	2.09	0.52
25:3:1138:VAL:HG11	25:3:1166:ASP:OD1	2.08	0.52
26:4:850:LYS:C	26:4:850:LYS:CD	2.80	0.52
1:A:1084:G:OP1	1:A:1086:U:N3	2.43	0.52
1:A:1239:A:O2'	8:H:114:LYS:O	2.26	0.52
1:A:1411:C:O5'	1:A:1411:C:H6	1.92	0.52
1:A:1422:G:H1	1:A:1478:U:H3	1.58	0.52
1:A:1504:G:H3'	1:A:1505:G:C2	2.44	0.52
1:A:1536:C:H2'	1:A:1537:U:C6	2.44	0.52
6:F:48:PHE:HZ	6:F:138:ARG:NH2	2.07	0.52
8:H:45:SER:O	8:H:49:THR:HG22	2.10	0.52
24:1:102:LEU:O	24:1:141:SER:HA	2.10	0.52
1:A:712:A:H2'	1:A:713:G:C8	2.44	0.52
1:A:745:G:H2'	1:A:746:A:C8	2.44	0.52
1:A:1079:G:H5''	6:F:50:TYR:HE2	1.74	0.52
1:A:1228:C:H5'	14:N:114:LYS:O	2.09	0.52
2:B:122:VAL:HG11	2:B:154:PHE:HD2	1.73	0.52
2:B:163:ARG:HD2	2:B:163:ARG:N	2.22	0.52
4:D:20:SER:OG	4:D:22:TRP:NE1	2.42	0.52
22:V:12:PHE:CG	22:V:12:PHE:O	2.62	0.52
25:3:1325:VAL:HG13	26:4:249:LEU:HD13	1.92	0.52
26:4:44:ILE:HG22	26:4:51:PRO:HA	1.91	0.52
4:D:110:GLU:HB2	4:D:144:LEU:HD12	1.92	0.52
11:K:15:HIS:O	11:K:18:ILE:HG22	2.10	0.52
12:L:106:ARG:NH2	22:V:6:VAL:HG11	2.25	0.52
16:P:2:SER:OG	16:P:3:LEU:N	2.43	0.52
1:A:539:A:H2'	1:A:540:G:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:728:A:H2'	1:A:729:A:C8	2.45	0.52
3:C:66:LYS:H	3:C:159:ASP:CG	2.18	0.52
3:C:203:ASN:O	3:C:213:TYR:OH	2.13	0.52
6:F:111:MET:HA	6:F:114:VAL:HG12	1.91	0.52
12:L:97:ILE:HG22	22:V:12:PHE:CZ	2.45	0.52
26:4:709:ARG:NH1	26:4:710:ASP:OD2	2.43	0.52
26:4:964:LYS:HD3	26:4:977:SER:HA	1.90	0.52
30:7:10:DT:H2''	30:7:11:DC:H5'	1.92	0.52
2:B:131:LEU:HD13	2:B:169:SER:HB3	1.90	0.52
14:N:27:LYS:HE2	14:N:31:LYS:NZ	2.25	0.52
17:Q:56:ARG:HA	17:Q:56:ARG:NE	2.24	0.52
18:R:23:VAL:HG21	18:R:61:ILE:HD13	1.92	0.52
25:3:210:LEU:HA	25:3:213:LEU:HB2	1.92	0.52
30:7:15:DC:H2''	30:7:16:DC:H5'	1.92	0.52
1:A:3:A:H5''	1:A:4:U:H5'	1.91	0.51
1:A:56:U:H2'	1:A:57:G:C8	2.45	0.51
1:A:390:U:H2'	1:A:391:G:C8	2.44	0.51
1:A:1017:U:O2'	1:A:1018:G:O4'	2.28	0.51
1:A:1026:G:N2	1:A:1035:A:N1	2.57	0.51
1:A:1120:C:H2'	1:A:1121:U:H6	1.76	0.51
1:A:1535:C:H2'	1:A:1536:C:H6	1.75	0.51
2:B:100:LYS:O	2:B:104:ASP:N	2.43	0.51
3:C:187:VAL:HG23	3:C:191:SER:HB2	1.93	0.51
12:L:98:ARG:HH11	12:L:98:ARG:HG2	1.72	0.51
13:M:46:ASN:HD22	13:M:46:ASN:N	2.07	0.51
25:3:730:SER:O	25:3:753:LEU:N	2.43	0.51
26:4:370:LYS:NZ	26:4:443:GLU:OE2	2.42	0.51
1:A:279:A:H5''	1:A:280:C:H3'	1.92	0.51
1:A:429:U:H2'	5:E:31:LYS:HE2	1.92	0.51
1:A:575:G:O2'	1:A:821:G:OP2	2.18	0.51
1:A:1062:U:H2'	1:A:1063:C:C6	2.45	0.51
1:A:1273:C:H2'	1:A:1274:A:O4'	2.10	0.51
2:B:135:LEU:O	2:B:171:ARG:HB2	2.11	0.51
6:F:45:ARG:HD3	6:F:71:MET:HE3	1.92	0.51
24:1:29:GLU:OE1	24:1:200:LYS:HE2	2.11	0.51
1:A:41:G:H2'	1:A:42:G:H8	1.75	0.51
1:A:1408:A:H1'	1:A:1491:G:C6	2.46	0.51
24:2:14:VAL:HG12	24:2:27:THR:HB	1.92	0.51
26:4:1175:LEU:HD13	26:4:1190:ILE:HD12	1.92	0.51
1:A:744:C:H2'	1:A:745:G:C8	2.44	0.51
1:A:925:G:N2	1:A:1506:U:OP1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1518:MA6:H2'	1:A:1519:MA6:C8	2.40	0.51
11:K:66:GLU:HB3	15:O:99:ALA:HB2	1.92	0.51
1:A:166:U:H2'	1:A:167:A:C8	2.45	0.51
1:A:1038:C:H2'	1:A:1039:G:H8	1.75	0.51
7:G:41:ASP:OD1	7:G:58:HIS:NE2	2.23	0.51
11:K:67:ILE:HG13	15:O:96:LEU:HD13	1.91	0.51
14:N:60:VAL:CG1	14:N:65:VAL:HG21	2.40	0.51
24:2:62:ASP:OD2	24:2:71:LYS:NZ	2.43	0.51
25:3:309:LEU:HD21	25:3:312:ALA:HB2	1.92	0.51
25:3:394:ARG:NH2	29:6:21:DC:OP2	2.43	0.51
25:3:848:GLU:HG2	25:3:889:PRO:HD3	1.92	0.51
25:3:1120:ALA:HB1	25:3:1198:LEU:HG	1.91	0.51
1:A:215:C:H2'	1:A:216:U:C6	2.45	0.51
2:B:121:THR:O	2:B:121:THR:CG2	2.59	0.51
4:D:77:ILE:HA	4:D:84:VAL:CG2	2.40	0.51
24:2:61:ILE:HG23	24:2:64:VAL:HB	1.91	0.51
26:4:956:GLY:HA3	26:4:984:LEU:HD23	1.93	0.51
1:A:299:G:H2'	1:A:300:A:C8	2.46	0.51
1:A:1418:A:N6	1:A:1482:G:O2'	2.44	0.51
2:B:154:PHE:HB3	2:B:168:VAL:CG1	2.39	0.51
4:D:207:ILE:HD13	4:D:207:ILE:N	2.26	0.51
5:E:23:SER:O	5:E:165:ARG:NH1	2.25	0.51
5:E:203:LEU:HA	5:E:206:LYS:HE3	1.93	0.51
15:O:67:THR:HG23	15:O:83:LYS:HD2	1.93	0.51
24:2:218:ARG:O	24:2:222:THR:OG1	2.23	0.51
26:4:822:MET:SD	26:4:838:ARG:NH2	2.81	0.51
26:4:1058:SER:OG	26:4:1108:GLN:NE2	2.43	0.51
28:Z:77:ASP:O	28:Z:81:HIS:ND1	2.28	0.51
1:A:511:C:H4'	5:E:44:ARG:HH22	1.75	0.51
1:A:1427:C:H2'	1:A:1428:A:C8	2.46	0.51
2:B:23:ILE:HD11	2:B:92:HIS:HD2	1.75	0.51
24:1:102:LEU:HB3	24:1:142:MET:HG2	1.91	0.51
25:3:119:GLU:HB2	25:3:489:PRO:HB2	1.93	0.51
25:3:812:PHE:HZ	26:4:503:SER:HB2	1.76	0.51
25:3:1340:GLU:OE2	26:4:1341:ARG:NH2	2.44	0.51
26:4:253:VAL:O	26:4:261:ALA:N	2.36	0.51
28:Z:128:PHE:CE2	28:Z:151:VAL:HG13	2.46	0.51
1:A:8:A:N6	5:E:206:LYS:HE2	2.26	0.51
1:A:1099:G:H4'	22:V:69:ARG:HH21	1.75	0.51
2:B:138:VAL:O	2:B:138:VAL:HG12	2.11	0.51
21:U:5:LYS:HG3	21:U:6:SER:N	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:1256:GLN:CG	25:3:1321:GLU:OE1	2.59	0.51
2:B:5:PHE:HE1	3:C:43:LEU:HB2	1.76	0.51
8:H:27:VAL:O	8:H:30:LEU:N	2.43	0.51
8:H:60:GLU:O	8:H:64:VAL:HG23	2.10	0.51
14:N:11:ASP:HA	14:N:45:ILE:HG13	1.93	0.51
26:4:964:LYS:O	26:4:964:LYS:CG	2.54	0.51
29:6:15:DA:H2''	29:6:16:DT:C5	2.46	0.51
2:B:122:VAL:O	2:B:129:ALA:N	2.40	0.50
3:C:217:VAL:O	3:C:221:VAL:HG23	2.10	0.50
17:Q:52:LEU:HD21	17:Q:57:ILE:CG1	2.38	0.50
25:3:314:ASN:O	25:3:352:ARG:NH2	2.30	0.50
25:3:1246:ARG:NE	26:4:348:ASP:OD1	2.29	0.50
26:4:978:ARG:HD3	26:4:999:TYR:HB2	1.93	0.50
1:A:844:G:N3	1:A:844:G:H3'	2.27	0.50
1:A:855:U:OP2	1:A:871:U:N3	2.42	0.50
1:A:1480:A:H2'	1:A:1481:U:C6	2.46	0.50
2:B:38:VAL:O	2:B:45:GLU:HA	2.12	0.50
2:B:170:ARG:O	2:B:170:ARG:CG	2.58	0.50
3:C:116:ASP:OD1	3:C:120:GLN:NE2	2.44	0.50
8:H:23:LEU:O	8:H:27:VAL:HG23	2.11	0.50
14:N:12:HIS:O	14:N:44:LYS:HD3	2.11	0.50
26:4:958:ILE:O	26:4:1008:GLY:HA2	2.11	0.50
1:A:704:A:H3'	1:A:705:G:H8	1.76	0.50
17:Q:52:LEU:HD22	17:Q:75:ILE:HD13	1.93	0.50
25:3:657:THR:HB	25:3:1187:PHE:HB2	1.93	0.50
25:3:1043:ALA:HB3	25:3:1044:PRO:HD3	1.92	0.50
26:4:982:LEU:CD2	26:4:982:LEU:N	2.74	0.50
29:6:31:DG:H2''	29:6:32:DA:C8	2.47	0.50
1:A:339:C:H2'	1:A:340:U:C6	2.46	0.50
1:A:1130:A:H2'	1:A:1131:G:C8	2.47	0.50
4:D:150:LYS:HD3	4:D:169:ARG:HD3	1.94	0.50
8:H:93:PRO:HA	8:H:96:ARG:HD2	1.93	0.50
25:3:800:MET:HE1	25:3:822:VAL:HB	1.93	0.50
25:3:820:GLU:HA	25:3:1079:ILE:HD11	1.92	0.50
1:A:1034:G:H2'	1:A:1035:A:H8	1.75	0.50
2:B:115:LYS:HD2	2:B:143:ASP:HA	1.92	0.50
4:D:82:GLU:HG3	4:D:83:ASP:N	2.26	0.50
25:3:382:GLU:O	25:3:386:GLU:HG2	2.12	0.50
25:3:629:PHE:HB2	25:3:647:ARG:HG3	1.94	0.50
26:4:388:ARG:NH2	26:4:414:GLU:OE1	2.45	0.50
28:Z:7:LYS:HG2	28:Z:74:VAL:HG13	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:G:H2'	1:A:192:A:H8	1.75	0.50
1:A:268:U:H2'	1:A:269:C:H6	1.77	0.50
1:A:1481:U:C5	1:A:1481:U:OP2	2.65	0.50
1:A:1504:G:H5''	1:A:1504:G:H8	1.76	0.50
8:H:135:VAL:O	8:H:139:GLU:HG2	2.12	0.50
11:K:65:TYR:HB3	15:O:96:LEU:HD11	1.94	0.50
11:K:88:MET:O	11:K:89:ARG:HD2	2.11	0.50
12:L:92:GLY:C	12:L:94:GLU:H	2.19	0.50
25:3:1256:GLN:HG2	25:3:1321:GLU:OE1	2.11	0.50
5:E:58:LYS:HD3	5:E:203:LEU:HD23	1.94	0.50
9:I:11:LEU:HD22	9:I:75:ILE:HD11	1.93	0.50
12:L:96:THR:O	12:L:100:LEU:HB2	2.11	0.50
13:M:107:VAL:HG12	13:M:117:TYR:HB3	1.92	0.50
15:O:57:PRO:O	15:O:60:GLN:HG2	2.12	0.50
24:1:11:PRO:HB3	24:1:31:LEU:HD21	1.94	0.50
25:3:667:LEU:HD23	25:3:704:MET:HB3	1.92	0.50
25:3:808:ASN:H	26:4:633:ALA:HB2	1.77	0.50
25:3:1109:ILE:HG13	25:3:1112:ILE:CD1	2.38	0.50
25:3:1109:ILE:HD12	26:4:644:MET:HG3	1.93	0.50
26:4:926:PRO:HG3	26:4:1248:ILE:HD11	1.92	0.50
26:4:964:LYS:N	26:4:977:SER:HB2	2.27	0.50
1:A:1329:A:OP1	14:N:26:GLY:HA3	2.12	0.50
2:B:134:SER:C	2:B:135:LEU:HD23	2.37	0.50
3:C:30:PHE:HE1	3:C:49:MET:HE1	1.76	0.50
10:J:58:VAL:HG13	10:J:59:GLU:H	1.77	0.50
25:3:232:ILE:HG12	25:3:331:LYS:O	2.12	0.50
25:3:750:ILE:HD13	25:3:963:GLU:OE2	2.12	0.50
26:4:252:LEU:HG	26:4:260:PHE:HB2	1.94	0.50
26:4:1109:LEU:HD12	26:4:1113:VAL:HG11	1.94	0.50
1:A:1086:U:H3'	1:A:1086:U:C6	2.47	0.50
3:C:77:SER:O	3:C:80:VAL:HG12	2.12	0.50
12:L:92:GLY:O	12:L:94:GLU:N	2.38	0.50
14:N:42:ASP:N	14:N:42:ASP:OD1	2.45	0.50
25:3:192:ASP:HB3	25:3:346:TYR:HD1	1.76	0.50
26:4:807:LEU:HD11	26:4:1258:ARG:HG2	1.94	0.50
26:4:972:LYS:HD3	26:4:972:LYS:N	2.26	0.50
1:A:698:G:H2'	1:A:699:C:C6	2.47	0.49
1:A:1072:G:H2'	1:A:1073:U:C6	2.47	0.49
1:A:1471:U:H2'	1:A:1472:U:C6	2.47	0.49
2:B:115:LYS:HD3	2:B:143:ASP:HA	1.94	0.49
2:B:132:PRO:HB2	2:B:135:LEU:CG	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:90:THR:OG1	6:F:91:GLY:N	2.45	0.49
24:1:102:LEU:HG	24:1:115:ILE:HG12	1.94	0.49
25:3:859:GLU:HA	25:3:862:LEU:HB2	1.94	0.49
26:4:965:SER:CB	26:4:976:THR:H	2.24	0.49
1:A:1539:C:H2'	1:A:1540:U:C6	2.47	0.49
2:B:138:VAL:HB	2:B:139:ARG:HH21	1.76	0.49
5:E:132:ILE:HG23	5:E:135:TYR:HB2	1.94	0.49
23:X:46:G:H2'	23:X:47:G:H8	1.75	0.49
26:4:960:LEU:CA	26:4:982:LEU:HA	2.40	0.49
26:4:1266:ILE:HD13	26:4:1274:PHE:HB3	1.93	0.49
28:Z:45:PRO:HB2	28:Z:64:PHE:CZ	2.47	0.49
1:A:696:A:H2'	1:A:697:U:H6	1.77	0.49
14:N:53:ILE:O	14:N:57:ARG:HG3	2.12	0.49
24:1:31:LEU:HB2	24:1:199:ASP:O	2.12	0.49
26:4:960:LEU:HG	26:4:982:LEU:HB3	1.94	0.49
26:4:976:THR:HA	26:4:999:TYR:CD1	2.47	0.49
26:4:1353:VAL:HG23	26:4:1355:ARG:HG2	1.93	0.49
28:Z:26:LEU:HD23	28:Z:42:VAL:HG11	1.94	0.49
1:A:719:C:H1'	19:S:38:LYS:HB2	1.94	0.49
1:A:1368:A:OP2	10:J:114:LYS:HD2	2.13	0.49
2:B:146:HIS:HB2	2:B:147:LEU:HD12	1.93	0.49
3:C:111:ILE:HD13	3:C:148:LEU:HD21	1.94	0.49
14:N:7:ILE:HD12	14:N:22:ILE:HG23	1.94	0.49
26:4:393:THR:OG1	26:4:394:ILE:N	2.45	0.49
26:4:884:SER:OG	26:4:1254:GLU:OE1	2.23	0.49
1:A:501:C:H2'	1:A:502:A:C8	2.48	0.49
1:A:1471:U:H2'	1:A:1472:U:H6	1.75	0.49
1:A:1489:G:H8	1:A:1489:G:H3'	1.76	0.49
23:X:50:C:OP2	25:3:540:ARG:NH2	2.45	0.49
25:3:1307:ASN:HB3	25:3:1312:ASN:HB3	1.94	0.49
26:4:964:LYS:HB3	26:4:977:SER:CB	2.42	0.49
26:4:968:ASN:CB	26:4:974:VAL:HG23	2.39	0.49
22:V:12:PHE:O	22:V:12:PHE:CD2	2.66	0.49
25:3:80:PHE:HE1	25:3:1035:LYS:HD2	1.77	0.49
1:A:1120:C:H2'	1:A:1121:U:C6	2.48	0.49
4:D:47:LEU:HB3	4:D:50:ALA:HB3	1.94	0.49
6:F:115:LEU:HD13	6:F:123:VAL:HG11	1.94	0.49
10:J:118:LEU:HD22	10:J:124:ARG:HG3	1.95	0.49
24:2:72:GLU:OE1	24:2:73:GLY:N	2.40	0.49
25:3:208:ILE:HD11	25:3:365:GLU:HB3	1.93	0.49
25:3:478:ARG:O	25:3:482:GLY:N	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:646:SER:O	25:3:649:GLN:HB3	2.13	0.49
1:A:1305:G:N2	1:A:1331:G:H1'	2.28	0.49
6:F:162:GLU:H	6:F:162:GLU:CD	2.20	0.49
10:J:91:ASP:O	10:J:92:GLU:HB2	2.11	0.49
25:3:1107:MET:HG2	26:4:763:PHE:CD2	2.48	0.49
25:3:1154:ASP:OD1	25:3:1154:ASP:N	2.44	0.49
1:A:792:A:H1'	1:A:794:A:N7	2.28	0.49
1:A:1481:U:OP2	1:A:1481:U:H5	1.95	0.49
2:B:157:ILE:HG22	2:B:167:VAL:CG1	2.43	0.49
4:D:46:GLU:HG3	4:D:47:LEU:HG	1.95	0.49
8:H:14:PRO:HB3	8:H:21:GLU:OE1	2.13	0.49
25:3:559:CYS:HB2	25:3:662:SER:HB3	1.94	0.49
26:4:659:ALA:O	26:4:662:ALA:HB3	2.13	0.49
26:4:1079:LYS:HE3	26:4:1081:VAL:HG12	1.95	0.49
1:A:1479:C:H2'	1:A:1480:A:H8	1.78	0.49
2:B:112:ILE:HD11	2:B:147:LEU:HB3	1.95	0.49
10:J:88:MET:SD	10:J:95:ARG:NH2	2.86	0.49
12:L:89:PRO:HG3	22:V:32:VAL:HG11	1.94	0.49
25:3:1109:ILE:HD11	26:4:641:ILE:HD12	1.95	0.49
25:3:1138:VAL:HG11	25:3:1166:ASP:CG	2.38	0.49
25:3:1293:VAL:O	25:3:1301:ARG:HB3	2.13	0.49
26:4:271:ARG:HH11	26:4:275:ARG:NH2	2.02	0.48
26:4:1109:LEU:HD23	26:4:1121:LEU:HA	1.95	0.48
11:K:77:VAL:C	11:K:78:GLU:HG2	2.38	0.48
12:L:86:VAL:HG11	12:L:97:ILE:HD11	1.95	0.48
13:M:25:GLU:CD	13:M:59:ASN:HD22	2.21	0.48
25:3:251:ALA:N	25:3:267:ARG:O	2.27	0.48
25:3:1293:VAL:HG21	25:3:1315:MET:HB2	1.95	0.48
26:4:1163:VAL:HG23	26:4:1177:ILE:HG12	1.94	0.48
30:7:19:DG:H2'	30:7:20:DC:C6	2.48	0.48
1:A:1479:C:H2'	1:A:1480:A:C8	2.48	0.48
1:A:1482:G:H2'	1:A:1483:A:C8	2.48	0.48
1:A:1528:U:O3'	1:A:1529:G:H3'	2.14	0.48
4:D:121:THR:O	4:D:125:GLU:HG3	2.13	0.48
4:D:179:ARG:HG3	4:D:206:GLU:HG2	1.95	0.48
4:D:180:ALA:HB1	4:D:203:PHE:HE1	1.79	0.48
25:3:549:ASP:OD1	25:3:550:VAL:N	2.46	0.48
26:4:865:HIS:NE2	26:4:867:GLN:HB2	2.28	0.48
29:6:31:DG:H2''	29:6:32:DA:H5'	1.96	0.48
1:A:501:C:H2'	1:A:502:A:H8	1.77	0.48
5:E:8:LYS:N	5:E:8:LYS:HD2	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:69:VAL:HG21	8:H:104:ILE:HD11	1.96	0.48
9:I:49:PHE:HB3	9:I:61:LEU:HD23	1.96	0.48
19:S:26:ILE:HG22	19:S:30:LYS:HG3	1.93	0.48
25:3:83:GLN:OE1	25:3:83:GLN:N	2.40	0.48
25:3:247:ARG:HE	25:3:274:ILE:HD11	1.77	0.48
25:3:929:ILE:HD13	25:3:1055:ALA:HB2	1.94	0.48
25:3:1132:LEU:HD11	25:3:1173:ALA:HB1	1.95	0.48
26:4:794:GLY:O	26:4:797:THR:OG1	2.26	0.48
26:4:982:LEU:HD23	26:4:982:LEU:N	2.28	0.48
2:B:102:TYR:HB2	2:B:156:VAL:HG12	1.95	0.48
5:E:196:ASN:OD1	5:E:197:GLU:N	2.47	0.48
25:3:678:ARG:NE	25:3:1106:ARG:HB3	2.29	0.48
26:4:1292:LEU:HD23	26:4:1299:GLY:HA2	1.95	0.48
1:A:17:U:H2'	1:A:18:C:C6	2.49	0.48
1:A:408:A:OP1	5:E:110:THR:HG21	2.13	0.48
1:A:591:U:H2'	1:A:592:G:H8	1.77	0.48
1:A:837:U:H2'	1:A:838:G:H8	1.79	0.48
6:F:80:THR:HG22	6:F:81:LEU:H	1.79	0.48
9:I:48:ASP:OD1	9:I:49:PHE:N	2.42	0.48
15:O:46:LEU:O	15:O:50:THR:HG23	2.14	0.48
25:3:845:LEU:HB3	25:3:890:LYS:HZ2	1.77	0.48
25:3:1111:GLN:HG3	25:3:1112:ILE:HG23	1.94	0.48
25:3:1319:MET:HE3	25:3:1324:ASN:HD21	1.78	0.48
1:A:294:U:OP1	1:A:610:U:O2'	2.28	0.48
1:A:343:U:O2'	1:A:344:A:H2'	2.13	0.48
1:A:1141:C:O2'	1:A:1142:G:H8	1.95	0.48
2:B:109:THR:HB	2:B:151:GLU:OE1	2.13	0.48
11:K:80:THR:HB	11:K:83:THR:HG23	1.94	0.48
25:3:262:TYR:HE2	25:3:285:ILE:HD11	1.79	0.48
25:3:314:ASN:HD21	25:3:348:SER:CB	2.27	0.48
25:3:976:ARG:HG3	25:3:989:LEU:HD21	1.95	0.48
28:Z:96:THR:HG23	28:Z:99:ARG:H	1.78	0.48
1:A:613:C:H2'	1:A:614:C:H6	1.79	0.48
1:A:1079:G:H5''	6:F:50:TYR:CE2	2.48	0.48
1:A:1388:C:H2'	1:A:1389:C:C6	2.49	0.48
12:L:85:MET:SD	12:L:111:THR:OG1	2.71	0.48
13:M:110:ARG:NH2	13:M:113:ALA:HB3	2.29	0.48
17:Q:45:GLU:C	17:Q:47:GLU:H	2.21	0.48
18:R:7:THR:O	18:R:8:LEU:HD23	2.13	0.48
21:U:35:VAL:HG22	21:U:50:ALA:HB1	1.95	0.48
24:1:231:PHE:HE2	24:2:39:LEU:HD13	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:247:ARG:HH21	25:3:274:ILE:HD12	1.78	0.48
26:4:93:THR:OG1	26:4:94:GLN:N	2.46	0.48
26:4:960:LEU:CD1	26:4:1003:LEU:HD13	2.43	0.48
1:A:674:G:H2'	1:A:675:A:C8	2.47	0.48
1:A:928:G:C5	1:A:929:G:C8	3.02	0.48
5:E:104:ARG:HB2	5:E:171:LEU:HD21	1.96	0.48
25:3:1103:VAL:N	25:3:1104:PRO:HD2	2.28	0.48
26:4:366:CYS:O	26:4:439:PRO:HA	2.14	0.48
28:Z:128:PHE:HZ	28:Z:153:TYR:HA	1.79	0.48
30:7:13:DT:H2'	30:7:14:DC:C6	2.49	0.48
1:A:1490:U:H2'	1:A:1490:U:O2	2.13	0.48
2:B:170:ARG:NH1	2:B:170:ARG:CB	2.77	0.48
5:E:107:PHE:CD1	5:E:107:PHE:N	2.78	0.48
15:O:67:THR:CG2	15:O:83:LYS:HD2	2.44	0.48
25:3:1107:MET:HE2	25:3:1107:MET:HB2	1.63	0.48
26:4:830:ASP:OD1	26:4:830:ASP:N	2.47	0.48
26:4:962:ASN:HB3	26:4:979:ASN:CG	2.39	0.48
27:5:26:ARG:HH21	27:5:37:PRO:HA	1.78	0.48
28:Z:35:MET:HE1	28:Z:78:ALA:HB1	1.96	0.48
1:A:416:G:H2'	1:A:417:G:H8	1.79	0.47
8:H:28:ASN:HA	8:H:31:MET:HE2	1.96	0.47
13:M:86:ARG:HG2	13:M:88:LYS:H	1.78	0.47
25:3:10:ARG:NH2	25:3:793:GLU:OE1	2.47	0.47
25:3:696:ASP:OD1	25:3:696:ASP:N	2.39	0.47
26:4:604:MET:O	26:4:607:THR:OG1	2.28	0.47
26:4:976:THR:HA	26:4:999:TYR:CE1	2.48	0.47
26:4:978:ARG:HD2	26:4:1197:ASN:OD1	2.13	0.47
29:6:10:DG:H2''	29:6:11:DT:C6	2.49	0.47
1:A:415:A:H2'	1:A:416:G:H8	1.79	0.47
1:A:1472:U:H2'	1:A:1473:G:H8	1.79	0.47
2:B:131:LEU:HD11	2:B:136:VAL:N	2.29	0.47
14:N:66:GLU:O	14:N:67:GLY:C	2.56	0.47
24:1:89:ALA:O	24:1:124:VAL:HG22	2.13	0.47
26:4:601:ILE:O	26:4:604:MET:HB3	2.14	0.47
26:4:676:GLY:O	26:4:680:ASN:ND2	2.47	0.47
29:6:30:DA:H2''	29:6:31:DG:H8	1.78	0.47
1:A:193:C:H4'	21:U:56:PRO:HG3	1.96	0.47
1:A:197:A:N1	1:A:220:G:O2'	2.43	0.47
1:A:1413:A:H2	1:A:1487:G:N2	2.10	0.47
3:C:88:ASP:HB3	3:C:225:ARG:NH2	2.29	0.47
10:J:23:PRO:HA	10:J:61:LEU:HD23	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:51:PHE:HA	21:U:54:MET:HG3	1.96	0.47
21:U:54:MET:O	21:U:57:ILE:HG12	2.14	0.47
25:3:987:GLU:O	25:3:991:LYS:HB2	2.13	0.47
26:4:66:LYS:HB3	26:4:69:GLU:OE1	2.14	0.47
26:4:846:GLU:C	26:4:860:ARG:HA	2.40	0.47
1:A:2:A:H3'	1:A:2:A:OP2	2.14	0.47
1:A:1202:U:O4'	15:O:69:ARG:NH1	2.47	0.47
1:A:1539:C:O5'	1:A:1539:C:H6	1.98	0.47
2:B:141:VAL:HG23	2:B:141:VAL:O	2.14	0.47
4:D:37:PHE:HB3	4:D:38:LYS:HZ2	1.79	0.47
6:F:77:ASN:HB2	6:F:82:GLN:NE2	2.29	0.47
14:N:107:ARG:NH2	14:N:110:LYS:HD2	2.30	0.47
25:3:859:GLU:HA	25:3:862:LEU:HD12	1.95	0.47
25:3:1328:LYS:HZ3	25:3:1331:ARG:NH1	2.13	0.47
26:4:1179:PRO:HD2	26:4:1183:SER:C	2.39	0.47
1:A:126:G:OP1	1:A:605:U:O2'	2.19	0.47
1:A:339:C:H2'	1:A:340:U:H6	1.80	0.47
1:A:500:G:H5''	13:M:121:ARG:NH1	2.29	0.47
1:A:1006:G:N1	1:A:1024:G:H1'	2.30	0.47
2:B:112:ILE:CG1	2:B:148:GLU:HA	2.39	0.47
2:B:147:LEU:HD12	2:B:147:LEU:N	2.29	0.47
5:E:198:HIS:O	5:E:201:VAL:HG12	2.15	0.47
6:F:137:VAL:HA	6:F:140:THR:HG22	1.96	0.47
8:H:66:LEU:O	8:H:70:ARG:HD2	2.14	0.47
14:N:14:HIS:HA	14:N:44:LYS:HA	1.95	0.47
25:3:696:ASP:O	25:3:790:ASP:HB3	2.15	0.47
25:3:1138:VAL:HG11	25:3:1166:ASP:OD2	2.14	0.47
26:4:516:ASP:HB3	26:4:573:THR:HG21	1.97	0.47
26:4:978:ARG:H	26:4:978:ARG:HG2	1.38	0.47
1:A:1107:C:C4	1:A:1108:G:C8	3.02	0.47
23:X:51:G:H1	30:7:18:DC:H42	1.63	0.47
25:3:267:ARG:NE	25:3:268:ARG:O	2.44	0.47
25:3:689:ALA:HB2	25:3:1233:LEU:HD23	1.96	0.47
25:3:975:ILE:HG23	25:3:1011:LEU:HD22	1.97	0.47
26:4:290:ILE:HG23	28:Z:93:ILE:HG21	1.96	0.47
26:4:558:ASP:OD1	26:4:562:GLU:N	2.37	0.47
26:4:1197:ASN:HD22	26:4:1209:VAL:HG23	1.80	0.47
1:A:371:A:H2'	1:A:372:C:O4'	2.15	0.47
1:A:1236:A:H2'	1:A:1237:C:C6	2.50	0.47
1:A:1392:G:C2	1:A:1504:G:H1'	2.50	0.47
1:A:1519:MA6:H8	1:A:1519:MA6:O5'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1537:U:H2'	1:A:1538:C:H6	1.75	0.47
2:B:159:LEU:HA	2:B:166:VAL:CG2	2.45	0.47
11:K:37:ARG:N	11:K:75:ASP:O	2.47	0.47
12:L:22:HIS:HB2	12:L:33:THR:CG2	2.43	0.47
17:Q:4:ILE:HD12	17:Q:67:ILE:HD11	1.97	0.47
18:R:28:PHE:CE1	18:R:39:LYS:HG3	2.49	0.47
26:4:975:ILE:HG22	26:4:1000:GLY:H	1.80	0.47
26:4:980:THR:O	26:4:997:VAL:HG23	2.15	0.47
26:4:1237:VAL:HG11	26:4:1253:ILE:HG21	1.96	0.47
1:A:477:C:H2'	1:A:478:A:C8	2.50	0.47
2:B:43:LYS:HB2	2:B:82:THR:CG2	2.44	0.47
25:3:820:GLU:N	25:3:1080:ASN:O	2.47	0.47
25:3:840:SER:O	25:3:1046:VAL:HG13	2.15	0.47
26:4:308:ASP:OD2	26:4:311:ARG:HB2	2.14	0.47
26:4:515:ARG:HH21	26:4:717:VAL:HB	1.80	0.47
1:A:235:C:H2'	1:A:236:A:C8	2.49	0.47
1:A:825:A:H2'	1:A:826:C:C6	2.50	0.47
2:B:132:PRO:HB2	2:B:135:LEU:HD12	1.96	0.47
5:E:104:ARG:HB2	5:E:171:LEU:CD2	2.44	0.47
7:G:2:ARG:HG3	7:G:4:TYR:CZ	2.49	0.47
11:K:22:THR:O	11:K:26:VAL:HG12	2.15	0.47
24:1:78:ILE:HD13	24:1:81:ILE:HD12	1.97	0.47
26:4:425:ARG:HH11	26:4:459:ALA:HA	1.80	0.47
26:4:1072:LYS:HD2	26:4:1168:GLU:HB3	1.97	0.47
1:A:1316:G:N1	1:A:1319:A:OP2	2.45	0.47
1:A:1490:U:P	22:V:21:ARG:HH12	2.38	0.47
2:B:130:PHE:HB3	2:B:167:VAL:CG2	2.39	0.47
21:U:21:ASN:O	21:U:25:ARG:HG3	2.15	0.47
25:3:187:GLU:O	25:3:194:LEU:HD12	2.15	0.47
25:3:255:ILE:O	25:3:261:VAL:HG23	2.15	0.47
25:3:560:PRO:HG2	25:3:561:ILE:HD12	1.96	0.47
25:3:745:GLU:CD	25:3:746:ALA:H	2.23	0.47
1:A:494:G:H2'	1:A:496:A:H8	1.78	0.46
1:A:521:G:OP1	13:M:51:LYS:NZ	2.46	0.46
1:A:958:A:N7	20:T:55:ARG:NH1	2.63	0.46
1:A:1297:G:N2	8:H:114:LYS:HB3	2.31	0.46
1:A:1413:A:H2	1:A:1487:G:N1	2.08	0.46
1:A:1501:C:H2'	1:A:1502:A:C8	2.50	0.46
25:3:196:VAL:HG21	25:3:209:ILE:HD11	1.97	0.46
25:3:1282:GLY:HA3	27:5:17:PHE:CE1	2.49	0.46
26:4:891:ASP:OD1	26:4:1286:LYS:NZ	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:4:952:VAL:HG13	26:4:1014:GLY:N	2.30	0.46
26:4:1029:THR:HA	26:4:1099:TYR:CZ	2.49	0.46
1:A:384:G:H2'	1:A:385:C:C6	2.50	0.46
1:A:728:A:H2'	1:A:729:A:H8	1.80	0.46
6:F:35:ALA:HB1	6:F:60:ILE:HD13	1.98	0.46
7:G:6:ILE:HG12	7:G:89:VAL:HG12	1.97	0.46
8:H:75:VAL:HG11	8:H:144:MET:HG2	1.95	0.46
1:A:8:A:C6	5:E:206:LYS:HB3	2.50	0.46
1:A:704:A:C4	1:A:705:G:C8	3.03	0.46
1:A:908:A:H2'	1:A:909:A:H8	1.81	0.46
1:A:1489:G:H3'	1:A:1489:G:C8	2.50	0.46
2:B:131:LEU:HD22	2:B:169:SER:HB2	1.96	0.46
4:D:111:LEU:HB3	4:D:204:LYS:HE2	1.96	0.46
16:P:14:GLU:HB3	16:P:15:PHE:CD1	2.50	0.46
25:3:106:GLU:HB2	25:3:114:VAL:HG23	1.98	0.46
25:3:845:LEU:HB3	25:3:890:LYS:HD2	1.88	0.46
26:4:1282:TYR:HA	26:4:1285:VAL:HG12	1.96	0.46
1:A:841:C:N4	1:A:846:G:H21	2.12	0.46
1:A:1000:A:H2'	1:A:1001:C:C6	2.50	0.46
1:A:1487:G:H8	1:A:1487:G:P	2.37	0.46
3:C:135:LEU:O	3:C:138:THR:HG22	2.15	0.46
6:F:12:GLN:HB3	6:F:117:VAL:HG23	1.97	0.46
10:J:129:LYS:HE2	10:J:129:LYS:HB3	1.80	0.46
14:N:33:ILE:HD11	14:N:63:PHE:HE2	1.80	0.46
15:O:24:ARG:NH2	15:O:56:SER:HB2	2.31	0.46
24:1:180:VAL:HB	24:1:183:ILE:HD11	1.97	0.46
26:4:959:LYS:CE	26:4:959:LYS:CA	2.94	0.46
26:4:1160:SER:HB2	26:4:1203:ARG:NH1	2.28	0.46
1:A:1228:C:H5''	14:N:113:ARG:CG	2.46	0.46
1:A:1368:A:OP1	10:J:113:ARG:NH2	2.49	0.46
1:A:1486:G:H8	1:A:1486:G:P	2.37	0.46
12:L:52:PHE:O	12:L:57:LYS:HB2	2.15	0.46
24:1:231:PHE:HD1	24:2:217:ILE:HD11	1.81	0.46
25:3:99:LYS:HG2	25:3:121:GLU:H	1.80	0.46
25:3:256:GLU:HB2	25:3:261:VAL:HB	1.96	0.46
26:4:977:SER:C	26:4:979:ASN:H	2.23	0.46
28:Z:23:ALA:O	28:Z:27:ARG:HG3	2.16	0.46
30:7:22:DC:H2''	30:7:23:DC:H5'	1.97	0.46
1:A:1034:G:H2'	1:A:1035:A:C8	2.51	0.46
1:A:1329:A:P	14:N:26:GLY:HA3	2.55	0.46
6:F:45:ARG:HA	6:F:72:ILE:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:158:GLY:C	6:F:159:LYS:HG2	2.40	0.46
7:G:47:LEU:HD12	7:G:56:LYS:N	2.31	0.46
15:O:27:LEU:O	15:O:31:ILE:HG13	2.16	0.46
26:4:72:CYS:SG	26:4:87:LYS:HB3	2.56	0.46
26:4:1238:GLN:NE2	26:4:1250:ASP:OD1	2.49	0.46
1:A:171:A:H2'	1:A:172:A:C8	2.50	0.46
1:A:268:U:H2'	1:A:269:C:C6	2.51	0.46
1:A:1007:U:H2'	1:A:1008:U:C6	2.51	0.46
1:A:1038:C:H2'	1:A:1039:G:C8	2.51	0.46
4:D:151:VAL:HG12	4:D:200:VAL:HG22	1.97	0.46
8:H:138:ARG:HD3	8:H:142:HIS:CE1	2.51	0.46
25:3:358:ASP:O	25:3:361:SER:OG	2.16	0.46
25:3:802:VAL:HG21	25:3:1098:LEU:HD22	1.98	0.46
25:3:819:SER:HB2	25:3:1085:MET:SD	2.55	0.46
26:4:399:LYS:O	26:4:403:ARG:HG2	2.15	0.46
26:4:442:ILE:HG13	26:4:448:GLN:HG3	1.97	0.46
26:4:1172:LYS:HE3	26:4:1192:LYS:H	1.79	0.46
1:A:454:G:H2'	1:A:455:G:H8	1.81	0.46
1:A:868:C:H2'	1:A:869:G:O4'	2.16	0.46
1:A:1381:U:H2'	1:A:1382:C:H6	1.81	0.46
2:B:116:VAL:HG12	2:B:117:LYS:N	2.30	0.46
9:I:113:ASP:OD1	9:I:114:ARG:N	2.49	0.46
25:3:406:ASN:HD22	25:3:414:ILE:HA	1.79	0.46
1:A:76:G:H2'	1:A:77:A:C8	2.51	0.46
1:A:376:G:H5''	17:Q:5:ARG:HD2	1.98	0.46
1:A:579:A:H2'	1:A:580:C:C6	2.51	0.46
1:A:620:C:H2'	1:A:621:A:C8	2.50	0.46
1:A:1029:U:H2'	1:A:1031:C:O2	2.15	0.46
6:F:156:LYS:HG2	9:I:71:VAL:HG13	1.97	0.46
10:J:67:VAL:HG21	10:J:79:ILE:HD11	1.98	0.46
12:L:94:GLU:O	12:L:98:ARG:HG3	2.15	0.46
14:N:9:ILE:CG2	14:N:18:ALA:HB1	2.46	0.46
17:Q:72:ALA:O	17:Q:75:ILE:HG22	2.16	0.46
25:3:24:VAL:HG21	25:3:704:MET:HE1	1.98	0.46
25:3:354:ASP:OD1	25:3:356:THR:OG1	2.31	0.46
25:3:1176:LEU:HD22	25:3:1180:MET:HA	1.97	0.46
26:4:342:LEU:HD23	26:4:1352:ILE:HG23	1.98	0.46
29:6:13:DC:O2	30:7:28:DG:N2	2.49	0.46
1:A:219:U:H2'	1:A:220:G:H8	1.80	0.46
1:A:1041:G:H2'	1:A:1042:A:C8	2.51	0.46
1:A:1430:A:H2'	1:A:1431:A:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:7:LYS:O	15:O:11:VAL:HG23	2.15	0.46
15:O:10:GLU:HG3	15:O:63:ARG:HD2	1.96	0.46
15:O:28:LYS:HE2	15:O:28:LYS:HB2	1.78	0.46
25:3:314:ASN:OD1	25:3:352:ARG:NH1	2.49	0.46
25:3:841:ARG:N	25:3:848:GLU:OE1	2.38	0.46
26:4:257:GLY:HA3	26:4:259:ARG:HH22	1.80	0.46
26:4:982:LEU:O	26:4:994:SER:HA	2.15	0.46
26:4:1167:LYS:HD2	26:4:1174:ARG:HD3	1.98	0.46
28:Z:136:VAL:HG13	28:Z:177:GLN:HB3	1.98	0.46
1:A:376:G:H2'	1:A:377:G:H8	1.81	0.45
1:A:474:G:H2'	1:A:475:C:C6	2.51	0.45
1:A:846:G:C2	1:A:847:G:C4	3.04	0.45
2:B:142:ARG:NE	2:B:142:ARG:N	2.64	0.45
5:E:99:ASP:OD2	5:E:115:ARG:HB2	2.17	0.45
24:2:214:GLU:O	24:2:218:ARG:HG3	2.16	0.45
25:3:727:VAL:HG22	25:3:732:ILE:HG12	1.98	0.45
26:4:312:ARG:HG2	26:4:313:GLY:N	2.31	0.45
26:4:337:ARG:HD3	26:4:341:ASN:HD22	1.81	0.45
26:4:814:CYS:HB2	26:4:889:ASP:OD1	2.16	0.45
26:4:825:VAL:HG12	26:4:833:GLU:HG2	1.98	0.45
26:4:1158:GLU:HA	26:4:1206:ARG:HA	1.98	0.45
27:5:13:ILE:O	27:5:15:ASN:N	2.43	0.45
1:A:187:G:N2	1:A:190:A:OP2	2.50	0.45
3:C:73:LYS:HE3	3:C:73:LYS:HB3	1.83	0.45
3:C:124:GLY:O	3:C:125:THR:HG22	2.16	0.45
25:3:27:LEU:O	25:3:528:ARG:NH1	2.49	0.45
25:3:1130:ALA:O	25:3:1134:GLN:N	2.43	0.45
1:A:690:G:H2'	1:A:691:G:H8	1.81	0.45
1:A:857:C:H2'	1:A:858:G:O4'	2.16	0.45
1:A:1106:G:O2'	4:D:169:ARG:NH1	2.35	0.45
1:A:1395:C:H3'	1:A:1396:A:C8	2.51	0.45
2:B:157:ILE:HB	2:B:168:VAL:HA	1.97	0.45
3:C:207:ILE:HA	3:C:210:VAL:HG22	1.97	0.45
7:G:2:ARG:HG3	7:G:4:TYR:OH	2.16	0.45
26:4:1198:VAL:HB	26:4:1202:GLU:HB2	1.99	0.45
29:6:26:DG:C2	29:6:27:DA:C5	3.05	0.45
1:A:967:5MC:OP1	1:A:969:A:H5'	2.15	0.45
1:A:1000:A:H2'	1:A:1001:C:H6	1.80	0.45
1:A:1064:G:H1'	1:A:1190:G:N2	2.32	0.45
1:A:1086:U:H3'	1:A:1086:U:H6	1.80	0.45
1:A:1425:U:H2'	1:A:1426:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:126:LYS:HE2	6:F:128:TYR:CE1	2.51	0.45
16:P:10:LYS:O	16:P:13:SER:OG	2.30	0.45
25:3:699:LEU:HG	25:3:799:ASN:HD22	1.81	0.45
25:3:1158:LYS:HE3	25:3:1158:LYS:HB3	1.71	0.45
26:4:1030:GLU:O	26:4:1117:SER:OG	2.31	0.45
26:4:1105:ALA:HA	26:4:1124:ILE:HG13	1.98	0.45
1:A:490:C:H2'	1:A:491:G:H8	1.81	0.45
1:A:1360:A:OP2	15:O:75:ARG:NH2	2.50	0.45
2:B:155:LYS:O	2:B:168:VAL:HG22	2.15	0.45
24:1:213:PRO:O	24:1:217:ILE:HG22	2.16	0.45
25:3:150:HIS:CE1	25:3:454:ARG:HG3	2.51	0.45
25:3:228:VAL:HB	25:3:245:ARG:NH1	2.30	0.45
25:3:288:PRO:O	25:3:292:ILE:HG13	2.16	0.45
25:3:488:MET:N	25:3:491:ASP:OD2	2.38	0.45
25:3:611:GLU:OE2	25:3:637:ARG:NH2	2.46	0.45
26:4:117:LEU:HG	26:4:118:LYS:HG3	1.98	0.45
26:4:851:PRO:HG2	26:4:875:ASN:HB3	1.98	0.45
26:4:960:LEU:CD2	26:4:982:LEU:HB3	2.46	0.45
26:4:974:VAL:CG2	26:4:1118:GLY:HA2	2.47	0.45
1:A:2:A:H2'	1:A:3:A:C4	2.51	0.45
1:A:323:U:H2'	1:A:324:G:O4'	2.17	0.45
3:C:153:ASP:OD1	3:C:153:ASP:N	2.50	0.45
4:D:136:ARG:NH1	4:D:136:ARG:HB2	2.32	0.45
4:D:180:ALA:HB1	4:D:203:PHE:CE1	2.52	0.45
15:O:34:VAL:O	15:O:36:ALA:N	2.49	0.45
24:2:74:VAL:HG21	24:2:81:ILE:HD11	1.99	0.45
25:3:301:TYR:O	25:3:310:ILE:HG22	2.17	0.45
25:3:1106:ARG:O	25:3:1107:MET:C	2.60	0.45
25:3:1290:MET:HG3	26:4:347:VAL:HG11	1.99	0.45
26:4:432:LEU:HD13	26:4:499:ILE:HG12	1.98	0.45
26:4:850:LYS:O	26:4:850:LYS:CD	2.64	0.45
26:4:1075:ARG:HD2	26:4:1075:ARG:HA	1.82	0.45
27:5:27:ALA:HA	27:5:30:MET:HE2	1.99	0.45
28:Z:47:GLU:HG3	28:Z:64:PHE:CE1	2.52	0.45
1:A:407:U:H2'	1:A:408:A:C8	2.52	0.45
1:A:407:U:H2'	1:A:408:A:H8	1.82	0.45
1:A:515:G:H2'	1:A:516:PSU:H6	1.82	0.45
1:A:625:U:H2'	1:A:626:G:H8	1.80	0.45
1:A:1484:C:H2'	1:A:1485:U:C6	2.49	0.45
25:3:935:THR:HA	25:3:1048:LYS:HA	1.98	0.45
25:3:1321:GLU:OE2	26:4:99:ARG:CZ	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:4:865:HIS:CD2	26:4:867:GLN:H	2.30	0.45
1:A:210:C:O2	1:A:211:G:N2	2.50	0.45
1:A:212:G:C4	1:A:213:G:C8	3.05	0.45
1:A:795:C:O2'	12:L:128:ARG:O	2.28	0.45
1:A:908:A:H2'	1:A:909:A:C8	2.52	0.45
1:A:1390:U:O2'	1:A:1391:U:H5'	2.17	0.45
1:A:1503:A:OP1	1:A:1503:A:H4'	2.17	0.45
1:A:1533:C:O2	1:A:1533:C:H2'	2.15	0.45
4:D:97:VAL:HB	4:D:98:PRO:HD2	1.99	0.45
8:H:6:VAL:O	8:H:6:VAL:HG12	2.17	0.45
13:M:44:LYS:HD2	23:X:7:G:H5'	1.99	0.45
25:3:243:PRO:HB2	25:3:274:ILE:HG23	1.99	0.45
25:3:270:THR:HG1	25:3:273:HIS:CE1	2.35	0.45
25:3:994:ARG:HA	25:3:997:TRP:NE1	2.32	0.45
27:5:21:LEU:HA	27:5:21:LEU:HD12	1.75	0.45
1:A:1:A:N3	1:A:1:A:H2'	2.31	0.45
2:B:158:LYS:CG	2:B:159:LEU:N	2.80	0.45
3:C:73:LYS:HD2	3:C:165:ASP:OD2	2.17	0.45
5:E:83:LYS:HE3	5:E:83:LYS:HB3	1.85	0.45
6:F:99:ALA:HB1	6:F:103:THR:HG21	1.99	0.45
10:J:60:LYS:HE2	10:J:60:LYS:HB3	1.76	0.45
14:N:14:HIS:HB2	14:N:17:ILE:HD13	1.98	0.45
24:2:86:LYS:HD2	24:2:174:ASP:HB2	1.99	0.45
25:3:14:ASP:HA	25:3:1183:ALA:HB3	1.99	0.45
25:3:56:VAL:HG13	25:3:472:GLU:OE1	2.17	0.45
25:3:240:GLU:HA	25:3:283:LYS:O	2.17	0.45
25:3:333:ILE:HD12	25:3:333:ILE:HA	1.70	0.45
25:3:1085:MET:HE2	25:3:1085:MET:HA	1.99	0.45
26:4:40:LYS:O	26:4:55:GLY:HA2	2.17	0.45
26:4:424:ASN:ND2	26:4:424:ASN:C	2.74	0.45
26:4:1108:GLN:O	26:4:1110:GLU:HG3	2.17	0.45
28:Z:18:PHE:HB3	28:Z:88:ARG:HD3	1.99	0.45
1:A:409:U:H3	1:A:433:G:H1	1.65	0.45
1:A:736:C:H2'	1:A:737:C:C6	2.52	0.45
1:A:1037:C:H2'	1:A:1038:C:H6	1.82	0.45
1:A:1414:U:H2'	1:A:1415:G:C8	2.51	0.45
1:A:1492:A:H5''	1:A:1492:A:H8	1.81	0.45
2:B:198:ILE:O	2:B:210:ASP:N	2.33	0.45
4:D:46:GLU:HG2	4:D:87:LEU:HD21	1.98	0.45
13:M:99:ARG:NH2	13:M:105:SER:O	2.49	0.45
14:N:3:ARG:HE	14:N:6:GLY:HA2	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:44:SER:OG	17:Q:47:GLU:OE2	2.25	0.45
24:1:182:ARG:HG2	24:1:206:GLU:HB3	1.98	0.45
25:3:139:ASN:C	25:3:141:THR:H	2.25	0.45
25:3:349:GLU:O	25:3:353:VAL:HG23	2.17	0.45
26:4:212:THR:OG1	30:7:4:DT:H71	2.17	0.45
26:4:423:LEU:HG	26:4:468:VAL:HG12	1.99	0.45
26:4:502:PRO:HG2	26:4:601:ILE:HD13	1.99	0.45
26:4:982:LEU:H	26:4:982:LEU:HD22	1.82	0.45
28:Z:18:PHE:O	28:Z:22:VAL:HG23	2.17	0.45
1:A:632:U:H5'	1:A:633:G:C8	2.52	0.44
1:A:900:A:H2'	1:A:901:A:C8	2.51	0.44
1:A:944:G:N2	1:A:1338:G:H8	2.15	0.44
1:A:1086:U:C6	1:A:1086:U:OP1	2.70	0.44
1:A:1134:G:O6	1:A:1141:C:N4	2.50	0.44
2:B:200:LYS:N	2:B:208:PHE:O	2.47	0.44
6:F:164:ILE:O	6:F:165:LEU:HB2	2.17	0.44
9:I:92:LEU:O	9:I:117:ARG:NH1	2.50	0.44
10:J:17:ALA:CB	10:J:67:VAL:HG13	2.48	0.44
14:N:90:ARG:HB2	14:N:97:VAL:HG23	1.99	0.44
17:Q:1:MET:CG	17:Q:2:VAL:H	2.19	0.44
24:1:23:HIS:HE1	24:1:25:LYS:NZ	2.15	0.44
24:2:52:PRO:HA	24:2:150:ARG:HA	1.98	0.44
24:2:207:THR:OG1	24:2:208:ASN:N	2.50	0.44
25:3:729:ALA:HA	25:3:769:PRO:CG	2.48	0.44
26:4:26:SER:HB3	26:4:236:TRP:CZ2	2.52	0.44
26:4:113:HIS:HB3	26:4:116:PHE:HD2	1.82	0.44
26:4:481:ARG:HA	26:4:485:MET:HE2	2.00	0.44
26:4:1185:PRO:O	26:4:1187:GLU:N	2.49	0.44
27:5:52:ARG:O	27:5:56:GLU:HG2	2.17	0.44
28:Z:137:ASN:HB3	28:Z:177:GLN:HA	2.00	0.44
1:A:1503:A:H2'	1:A:1503:A:N3	2.32	0.44
3:C:188:ASP:OD1	3:C:189:THR:N	2.50	0.44
7:G:86:ARG:NH1	19:S:64:TYR:O	2.50	0.44
14:N:83:LEU:HG	20:T:74:PHE:HE1	1.83	0.44
17:Q:19:VAL:HG13	17:Q:37:GLY:C	2.42	0.44
25:3:1058:ARG:HE	25:3:1238:LEU:HD11	1.82	0.44
25:3:1340:GLU:OE1	25:3:1341:ASP:N	2.43	0.44
26:4:1183:SER:C	26:4:1185:PRO:HD2	2.43	0.44
1:A:690:G:H2'	1:A:691:G:C8	2.51	0.44
1:A:1079:G:H2'	1:A:1080:A:C8	2.52	0.44
1:A:1513:A:H2'	1:A:1514:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1517:G:H2'	1:A:1518:MA6:O4'	2.17	0.44
25:3:1115:THR:HG23	25:3:1228:GLY:HA3	2.00	0.44
1:A:34:C:H2'	1:A:35:G:H8	1.82	0.44
1:A:338:A:H2'	1:A:339:C:H6	1.82	0.44
1:A:763:G:H2'	1:A:764:C:C6	2.52	0.44
1:A:1513:A:H2'	1:A:1514:G:H8	1.82	0.44
5:E:146:ARG:HG2	5:E:147:GLU:N	2.33	0.44
12:L:64:GLN:HG2	12:L:99:ALA:HB2	2.00	0.44
24:1:79:LEU:HD13	25:3:693:LEU:HD11	2.00	0.44
25:3:242:VAL:HB	25:3:245:ARG:HG3	2.00	0.44
26:4:968:ASN:H	26:4:971:GLY:HA2	1.82	0.44
30:7:20:DC:H2'	30:7:21:DG:H8	1.82	0.44
1:A:350:G:H2'	1:A:351:G:C8	2.53	0.44
1:A:1228:C:OP1	14:N:113:ARG:HG3	2.17	0.44
1:A:1322:C:OP1	20:T:78:ARG:NH2	2.42	0.44
4:D:131:ARG:HA	4:D:134:MET:HE2	1.99	0.44
6:F:50:TYR:O	6:F:66:LYS:HD3	2.17	0.44
15:O:24:ARG:HE	15:O:48:LEU:HD11	1.82	0.44
24:1:192:VAL:HG12	24:1:193:GLU:HG3	1.99	0.44
25:3:515:MET:O	25:3:760:ASN:ND2	2.43	0.44
28:Z:162:VAL:O	28:Z:168:ALA:HA	2.17	0.44
1:A:338:A:H2'	1:A:339:C:C6	2.53	0.44
1:A:414:A:C4	1:A:415:A:C8	3.06	0.44
1:A:460:A:H2'	1:A:461:A:H8	1.83	0.44
1:A:1086:U:C6	1:A:1086:U:C3'	3.00	0.44
1:A:1140:C:O2'	1:A:1141:C:O5'	2.31	0.44
1:A:1346:A:N1	1:A:1374:A:H5''	2.32	0.44
1:A:1541:U:N3	23:X:5:A:C6	2.86	0.44
4:D:90:VAL:O	4:D:93:ASP:HB3	2.18	0.44
5:E:37:ALA:HB3	5:E:42:GLY:HA2	1.98	0.44
5:E:61:VAL:HG21	5:E:200:ILE:HD11	1.99	0.44
7:G:9:MET:CG	7:G:86:ARG:HB2	2.47	0.44
8:H:51:ALA:O	8:H:55:GLY:N	2.46	0.44
16:P:12:VAL:HG21	16:P:22:THR:HG22	1.99	0.44
23:X:48:C:H2'	23:X:49:G:H8	1.82	0.44
25:3:105:TYR:CD1	25:3:113:THR:HG22	2.52	0.44
25:3:135:THR:HG22	25:3:144:VAL:HG22	2.00	0.44
25:3:297:VAL:HG11	25:3:311:CYS:SG	2.57	0.44
25:3:299:LYS:HB2	25:3:301:TYR:CE2	2.52	0.44
26:4:813:ASP:OD2	26:4:897:HIS:ND1	2.50	0.44
26:4:996:LYS:HB2	26:4:996:LYS:HZ3	1.78	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:Z:26:LEU:HA	28:Z:86:VAL:HG21	1.99	0.44
1:A:509:A:H5'	5:E:52:GLY:HA2	2.00	0.44
1:A:1134:G:N1	1:A:1141:C:C4	2.86	0.44
1:A:1305:G:H22	1:A:1331:G:H1'	1.83	0.44
1:A:1490:U:H1'	1:A:1491:G:C2	2.52	0.44
7:G:42:TRP:CZ2	7:G:102:MET:HG3	2.53	0.44
11:K:40:ILE:HD12	11:K:73:LEU:O	2.18	0.44
21:U:5:LYS:HE2	21:U:5:LYS:HB2	1.84	0.44
26:4:213:LYS:HE2	26:4:216:LYS:HB3	2.00	0.44
26:4:1076:PRO:HG2	26:4:1101:LEU:O	2.18	0.44
26:4:1173:ARG:HG3	26:4:1190:ILE:HB	2.00	0.44
1:A:41:G:H2'	1:A:42:G:C8	2.53	0.44
1:A:254:G:OP1	18:R:70:THR:HG22	2.17	0.44
1:A:312:C:H2'	1:A:313:A:C8	2.53	0.44
1:A:352:C:H4'	1:A:354:G:OP1	2.18	0.44
1:A:1083:U:H3'	1:A:1084:G:C8	2.53	0.44
1:A:1175:G:H2'	1:A:1176:A:H8	1.83	0.44
1:A:1219:A:H2'	1:A:1220:G:C8	2.53	0.44
1:A:1530:G:H4'	1:A:1531:A:OP1	2.17	0.44
3:C:164:ILE:O	3:C:165:ASP:HB3	2.16	0.44
10:J:42:GLU:HA	10:J:45:ARG:HE	1.83	0.44
23:X:49:G:H2'	23:X:50:C:C6	2.53	0.44
24:2:58:GLU:HG2	24:2:172:LEU:HD23	1.99	0.44
24:2:205:MET:HE1	24:2:217:ILE:HB	1.99	0.44
25:3:41:GLN:CD	25:3:41:GLN:H	2.25	0.44
25:3:565:GLU:HA	25:3:569:ILE:HG12	2.00	0.44
25:3:1272:GLU:HG2	25:3:1276:TRP:NE1	2.33	0.44
25:3:1339:LEU:HD22	26:4:17:PHE:CG	2.52	0.44
26:4:518:VAL:HG23	26:4:716:GLN:OE1	2.18	0.44
26:4:865:HIS:CE1	26:4:868:TRP:HD1	2.35	0.44
26:4:959:LYS:HA	26:4:959:LYS:HD2	1.76	0.44
26:4:1115:ILE:HG23	26:4:1119:ASP:HB2	2.00	0.44
28:Z:13:GLN:HG2	29:6:18:DG:N2	2.33	0.44
1:A:17:U:O2'	1:A:1079:G:H1'	2.18	0.44
1:A:98:A:H2'	1:A:99:C:C6	2.52	0.44
1:A:409:U:H2'	1:A:410:G:O4'	2.18	0.44
1:A:1120:C:C2	1:A:1121:U:C5	3.06	0.44
2:B:142:ARG:N	2:B:142:ARG:HE	2.16	0.44
3:C:127:ASP:N	3:C:127:ASP:OD1	2.50	0.44
5:E:74:ASN:HA	5:E:77:LYS:HE3	2.00	0.44
6:F:86:LYS:HB2	6:F:86:LYS:HE3	1.73	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:42:LEU:HD23	11:K:42:LEU:HA	1.81	0.44
22:V:13:ASP:O	22:V:16:LEU:N	2.51	0.44
24:2:58:GLU:HA	24:2:171:LEU:O	2.17	0.44
25:3:757:THR:O	25:3:765:ILE:HG12	2.18	0.44
26:4:179:LYS:HB2	26:4:184:ALA:HB2	1.99	0.44
26:4:210:SER:O	26:4:214:ARG:N	2.44	0.44
26:4:641:ILE:HD12	26:4:641:ILE:HA	1.86	0.44
27:5:50:ALA:O	27:5:54:ILE:HG12	2.17	0.44
28:Z:92:PHE:HB2	28:Z:100:PRO:HB3	2.00	0.44
1:A:946:A:O2'	1:A:1333:A:N3	2.49	0.43
1:A:1367:C:OP2	10:J:114:LYS:NZ	2.48	0.43
1:A:1391:U:H4'	1:A:1392:G:C5'	2.47	0.43
1:A:1394:A:H2	1:A:1502:A:C2	2.36	0.43
2:B:157:ILE:CG2	2:B:167:VAL:HG12	2.43	0.43
5:E:145:ILE:HD13	5:E:150:LYS:HA	1.99	0.43
10:J:3:GLU:OE2	10:J:4:ASN:ND2	2.51	0.43
22:V:4:ILE:HG22	22:V:5:LYS:N	2.33	0.43
24:1:120:ASP:OD1	24:1:120:ASP:N	2.43	0.43
24:2:12:ARG:N	24:2:29:GLU:O	2.51	0.43
25:3:270:THR:O	25:3:274:ILE:HG13	2.18	0.43
30:7:19:DG:H2'	30:7:20:DC:H6	1.83	0.43
1:A:36:C:O2'	13:M:114:ARG:NH2	2.47	0.43
1:A:628:G:H3'	1:A:629:A:H8	1.83	0.43
2:B:165:ASN:O	2:B:166:VAL:HG23	2.17	0.43
9:I:96:MET:HE3	9:I:99:LEU:HB2	1.99	0.43
21:U:28:MET:HE2	21:U:67:ILE:HD12	1.99	0.43
24:1:31:LEU:HD23	24:1:31:LEU:HA	1.79	0.43
26:4:209:ASN:HD22	26:4:209:ASN:C	2.25	0.43
26:4:850:LYS:N	26:4:855:ASP:O	2.44	0.43
26:4:1108:GLN:HE21	26:4:1108:GLN:HB2	1.64	0.43
26:4:1169:THR:OG1	26:4:1173:ARG:HB3	2.18	0.43
1:A:1390:U:H2'	1:A:1391:U:H6	1.80	0.43
4:D:33:LEU:HD23	4:D:33:LEU:HA	1.86	0.43
9:I:36:ILE:O	9:I:39:VAL:HG12	2.17	0.43
11:K:32:THR:OG1	11:K:82:LYS:NZ	2.47	0.43
12:L:64:GLN:CG	12:L:99:ALA:HB2	2.48	0.43
14:N:62:LYS:HE2	14:N:62:LYS:HB2	1.90	0.43
25:3:98:VAL:C	25:3:121:GLU:HA	2.43	0.43
25:3:162:GLY:HA2	25:3:166:SER:HA	2.00	0.43
26:4:39:LYS:NZ	26:4:54:ASP:OD2	2.46	0.43
1:A:688:G:H2'	1:A:689:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1004:A:C6	1:A:1026:G:H1'	2.52	0.43
1:A:1495:U:O5'	1:A:1495:U:H6	2.00	0.43
1:A:1517:G:H2'	1:A:1518:MA6:H8	1.99	0.43
2:B:132:PRO:HB2	2:B:135:LEU:HG	2.00	0.43
5:E:57:GLU:CD	5:E:199:LEU:HB2	2.43	0.43
5:E:99:ASP:O	5:E:102:VAL:HG12	2.18	0.43
9:I:96:MET:HE2	9:I:130:ALA:HB1	2.01	0.43
18:R:25:ILE:HD11	18:R:61:ILE:HD11	2.00	0.43
19:S:26:ILE:O	19:S:30:LYS:HG3	2.18	0.43
19:S:71:THR:H	19:S:74:HIS:CE1	2.36	0.43
20:T:28:LYS:HD2	20:T:28:LYS:HA	1.46	0.43
25:3:116:ASP:N	25:3:116:ASP:OD1	2.51	0.43
26:4:264:ASP:N	26:4:264:ASP:OD1	2.50	0.43
26:4:847:ASP:N	26:4:847:ASP:OD1	2.50	0.43
26:4:959:LYS:C	26:4:983:LYS:H	2.27	0.43
30:7:21:DG:H2'	30:7:22:DC:C6	2.54	0.43
1:A:460:A:H2'	1:A:461:A:C8	2.54	0.43
1:A:524:G:H2'	1:A:525:C:C6	2.54	0.43
2:B:103:GLU:C	2:B:105:ALA:H	2.26	0.43
6:F:138:ARG:HH11	6:F:138:ARG:HD3	1.65	0.43
14:N:40:ALA:O	14:N:43:VAL:HG12	2.18	0.43
21:U:24:ARG:HB2	21:U:66:LEU:HD11	2.00	0.43
24:1:231:PHE:CD1	24:2:217:ILE:HD11	2.54	0.43
24:2:66:HIS:ND1	24:2:68:TYR:HB3	2.33	0.43
25:3:845:LEU:HD13	25:3:889:PRO:HB2	2.01	0.43
25:3:1327:LEU:HD23	25:3:1327:LEU:HA	1.75	0.43
26:4:145:VAL:HG23	26:4:157:GLN:O	2.18	0.43
26:4:971:GLY:C	26:4:973:LEU:H	2.26	0.43
26:4:982:LEU:HD23	26:4:982:LEU:H	1.84	0.43
1:A:838:G:H2'	1:A:839:C:C6	2.53	0.43
1:A:939:G:H2'	1:A:940:C:C6	2.53	0.43
1:A:988:G:H1'	1:A:1015:G:H22	1.84	0.43
2:B:44:SER:OG	2:B:80:GLY:O	2.30	0.43
3:C:78:GLU:H	3:C:78:GLU:CD	2.26	0.43
8:H:15:ASP:OD2	8:H:23:LEU:HB3	2.18	0.43
12:L:100:LEU:HD23	12:L:100:LEU:HA	1.77	0.43
21:U:3:ASN:OD1	21:U:3:ASN:N	2.51	0.43
26:4:126:LEU:HD23	26:4:223:LEU:HD22	2.01	0.43
26:4:417:ARG:HG3	26:4:418:GLU:HG2	2.01	0.43
26:4:557:LYS:HA	26:4:563:LEU:HA	2.01	0.43
26:4:709:ARG:C	26:4:711:GLY:H	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:5:76:GLU:O	27:5:79:GLU:HB2	2.19	0.43
1:A:745:G:C2	1:A:746:A:C5	3.07	0.43
1:A:1121:U:C2	1:A:1122:U:C5	3.06	0.43
2:B:141:VAL:HB	2:B:142:ARG:HH21	1.84	0.43
7:G:55:HIS:ND1	7:G:55:HIS:N	2.67	0.43
11:K:7:ARG:HG2	11:K:75:ASP:OD1	2.19	0.43
15:O:10:GLU:O	15:O:14:VAL:HG23	2.19	0.43
16:P:12:VAL:HG23	16:P:27:VAL:HG11	2.01	0.43
24:1:167:PRO:HD2	24:1:170:ARG:HD2	2.01	0.43
26:4:271:ARG:CB	26:4:275:ARG:NH1	2.61	0.43
26:4:1266:ILE:HD12	26:4:1278:GLU:HB3	2.01	0.43
1:A:415:A:C4	1:A:416:G:C8	3.07	0.43
1:A:1409:C:H2'	1:A:1410:A:N9	2.34	0.43
2:B:16:ILE:HD13	2:B:16:ILE:N	2.34	0.43
4:D:26:THR:HG23	4:D:27:LYS:HD2	1.99	0.43
15:O:42:TRP:O	15:O:46:LEU:HG	2.19	0.43
26:4:259:ARG:CZ	26:4:259:ARG:HB2	2.48	0.43
26:4:983:LYS:HA	26:4:994:SER:HB3	2.00	0.43
1:A:787:A:H2'	1:A:788:U:C6	2.54	0.43
1:A:1388:C:H2'	1:A:1389:C:H6	1.83	0.43
2:B:50:ALA:O	2:B:54:LYS:HG3	2.18	0.43
2:B:156:VAL:HG22	2:B:166:VAL:HG11	2.00	0.43
2:B:158:LYS:HG2	2:B:167:VAL:HG23	2.01	0.43
5:E:59:GLN:OE1	5:E:62:ARG:NH1	2.51	0.43
24:2:82:LEU:HD12	24:2:82:LEU:HA	1.92	0.43
25:3:232:ILE:HB	25:3:331:LYS:HD2	2.01	0.43
25:3:246:LEU:HB3	25:3:269:ILE:HD13	2.00	0.43
25:3:672:GLU:HG3	25:3:673:HIS:CE1	2.53	0.43
26:4:30:ILE:HD13	26:4:243:PRO:HD3	2.01	0.43
26:4:132:LEU:HA	26:4:135:ILE:HG12	2.01	0.43
26:4:275:ARG:CD	26:4:302:ALA:HB2	2.49	0.43
28:Z:47:GLU:HG3	28:Z:64:PHE:HE1	1.84	0.43
1:A:872:A:C5	1:A:874:G:C8	3.07	0.43
1:A:1487:G:C8	1:A:1487:G:P	3.12	0.43
2:B:131:LEU:HD22	2:B:169:SER:CB	2.49	0.43
6:F:157:ARG:NH2	9:I:43:GLU:HG3	2.33	0.43
17:Q:2:VAL:HG13	17:Q:65:ALA:CA	2.47	0.43
24:2:18:GLN:O	24:2:20:SER:N	2.51	0.43
25:3:209:ILE:O	25:3:213:LEU:N	2.45	0.43
25:3:453:ILE:HD12	25:3:587:LEU:HD21	2.00	0.43
25:3:729:ALA:HA	25:3:769:PRO:HG2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:812:PHE:HB3	26:4:357:VAL:HG11	2.01	0.43
25:3:935:THR:HB	25:3:941:LYS:HZ3	1.84	0.43
26:4:1369:ARG:HH12	26:4:1373:ARG:HD2	1.84	0.43
1:A:592:G:H2'	1:A:593:U:C6	2.54	0.42
1:A:1367:C:H5''	10:J:116:VAL:HG22	2.00	0.42
4:D:21:THR:OG1	4:D:58:GLU:HG2	2.19	0.42
7:G:61:LEU:HG	7:G:62:MET:N	2.34	0.42
11:K:92:LEU:HD23	11:K:92:LEU:HA	1.81	0.42
18:R:59:VAL:HG12	18:R:78:VAL:HG22	2.01	0.42
25:3:720:ARG:NH2	25:3:736:VAL:HG11	2.35	0.42
25:3:799:ASN:OD1	25:3:799:ASN:N	2.35	0.42
26:4:583:VAL:HG13	26:4:587:LEU:HD12	2.01	0.42
26:4:975:ILE:HG22	26:4:975:ILE:O	2.19	0.42
30:7:6:DA:H2''	30:7:7:DA:C8	2.53	0.42
1:A:737:C:H2'	1:A:738:C:C6	2.54	0.42
1:A:816:A:OP1	1:A:1526:G:O2'	2.30	0.42
1:A:1489:G:C8	1:A:1489:G:O5'	2.72	0.42
2:B:23:ILE:HG12	2:B:71:ALA:HB2	2.01	0.42
5:E:15:GLU:OE1	5:E:56:ARG:NH2	2.52	0.42
8:H:79:ARG:NH2	8:H:82:GLY:HA2	2.34	0.42
14:N:3:ARG:O	14:N:57:ARG:NH2	2.52	0.42
24:2:103:ASN:HA	24:2:140:ILE:O	2.20	0.42
24:2:104:LYS:HZ2	24:2:110:VAL:HA	1.83	0.42
25:3:475:VAL:HG21	25:3:492:MET:HB3	2.00	0.42
25:3:930:ASP:HB3	25:3:1053:TYR:HD2	1.84	0.42
26:4:232:ASN:HA	26:4:236:TRP:CZ3	2.54	0.42
26:4:460:ASP:OD1	26:4:460:ASP:N	2.47	0.42
26:4:822:MET:O	26:4:879:ALA:HA	2.19	0.42
30:7:22:DC:C2	30:7:23:DC:C5	3.07	0.42
1:A:154:U:H2'	1:A:155:A:H8	1.84	0.42
1:A:204:U:C2	1:A:205:A:C8	3.08	0.42
1:A:500:G:H5''	13:M:121:ARG:HH12	1.85	0.42
1:A:806:C:H2'	1:A:807:A:H8	1.83	0.42
1:A:1121:U:H2'	1:A:1122:U:H6	1.85	0.42
1:A:1180:A:OP2	10:J:99:ARG:NH2	2.47	0.42
1:A:1248:A:H4'	10:J:33:ARG:HH12	1.84	0.42
3:C:133:GLU:HA	3:C:133:GLU:OE1	2.19	0.42
13:M:39:THR:HB	13:M:49:LEU:HG	2.00	0.42
18:R:16:LYS:HZ3	18:R:16:LYS:HB2	1.84	0.42
19:S:69:PRO:HB2	19:S:71:THR:O	2.19	0.42
22:V:68:THR:HG22	22:V:69:ARG:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:930:ASP:HB3	25:3:1053:TYR:CD2	2.54	0.42
26:4:452:LEU:HB3	26:4:500:ILE:HG23	2.01	0.42
26:4:773:PHE:O	26:4:776:THR:OG1	2.37	0.42
26:4:1067:ARG:NE	26:4:1070:GLY:O	2.30	0.42
27:5:68:GLU:O	27:5:72:GLN:HG3	2.19	0.42
29:6:27:DA:C2	29:6:28:DA:C4	3.07	0.42
1:A:553:A:H2'	1:A:554:A:H8	1.84	0.42
10:J:68:LYS:HB2	10:J:68:LYS:HE3	1.80	0.42
14:N:65:VAL:HG23	14:N:65:VAL:O	2.19	0.42
16:P:3:LEU:HD12	16:P:3:LEU:HA	1.72	0.42
23:X:39:C:H2'	23:X:40:A:O4'	2.19	0.42
24:1:185:TYR:HB2	24:1:201:LEU:HD11	2.02	0.42
24:1:234:LEU:HB2	24:2:218:ARG:HE	1.84	0.42
25:3:119:GLU:OE1	25:3:489:PRO:HD2	2.19	0.42
25:3:935:THR:HB	25:3:941:LYS:NZ	2.34	0.42
25:3:1038:GLN:O	25:3:1038:GLN:NE2	2.46	0.42
25:3:1106:ARG:HE	25:3:1106:ARG:HB2	1.72	0.42
25:3:1280:ALA:HB1	26:4:431:ARG:HD2	2.02	0.42
26:4:157:GLN:H	26:4:157:GLN:HG2	1.70	0.42
26:4:959:LYS:C	26:4:959:LYS:HE3	2.45	0.42
1:A:459:A:H2'	1:A:460:A:C8	2.55	0.42
1:A:538:G:H2'	1:A:539:A:H8	1.84	0.42
1:A:601:G:H2'	1:A:602:A:H8	1.84	0.42
1:A:1086:U:P	1:A:1086:U:O4'	2.77	0.42
1:A:1117:A:H4'	10:J:106:ARG:NH1	2.33	0.42
1:A:1119:C:H2'	1:A:1120:C:H6	1.84	0.42
2:B:128:ARG:O	2:B:165:ASN:HA	2.19	0.42
3:C:22:TYR:OH	22:V:67:ARG:NH1	2.52	0.42
7:G:85:ILE:O	7:G:86:ARG:HG2	2.19	0.42
9:I:77:ARG:NH1	9:I:126:ILE:O	2.48	0.42
10:J:45:ARG:O	10:J:49:ARG:HG2	2.20	0.42
13:M:90:LEU:HD12	13:M:90:LEU:HA	1.78	0.42
24:2:18:GLN:O	24:2:19:VAL:C	2.62	0.42
24:2:102:LEU:O	24:2:141:SER:HA	2.19	0.42
25:3:16:GLY:HA3	25:3:1156:ARG:HH21	1.84	0.42
25:3:1304:MET:HE2	25:3:1308:ILE:HG12	2.01	0.42
26:4:47:ARG:NH1	26:4:47:ARG:HA	2.34	0.42
26:4:118:LYS:HB2	26:4:311:ARG:HD3	2.02	0.42
26:4:251:PRO:HB2	26:4:253:VAL:HG13	2.01	0.42
26:4:956:GLY:O	26:4:1010:GLN:HA	2.19	0.42
26:4:1173:ARG:HG2	26:4:1190:ILE:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:4:1184:ASP:N	26:4:1185:PRO:CD	2.82	0.42
28:Z:92:PHE:CD2	28:Z:100:PRO:HG3	2.54	0.42
2:B:137:ASP:HB2	2:B:139:ARG:CZ	2.50	0.42
3:C:163:VAL:HG21	3:C:173:ILE:HD11	2.02	0.42
14:N:64:VAL:HG13	14:N:68:ASP:HB2	2.02	0.42
17:Q:56:ARG:N	17:Q:56:ARG:HD2	2.30	0.42
18:R:28:PHE:HE1	18:R:39:LYS:HG3	1.85	0.42
25:3:632:ASP:N	25:3:632:ASP:OD1	2.52	0.42
25:3:873:ILE:HG13	25:3:944:ARG:NH2	2.34	0.42
26:4:71:LEU:HD23	26:4:88:CYS:SG	2.59	0.42
26:4:527:LEU:HD23	26:4:533:ALA:HB2	2.01	0.42
26:4:823:THR:HA	26:4:878:ASP:O	2.20	0.42
26:4:883:ARG:NH2	26:4:895:CYS:SG	2.92	0.42
29:6:29:DG:C6	29:6:30:DA:C6	3.07	0.42
1:A:79:G:H2'	1:A:80:A:C8	2.54	0.42
1:A:166:U:C2	1:A:167:A:C8	3.07	0.42
1:A:376:G:H4'	17:Q:5:ARG:HD2	2.01	0.42
1:A:1229:A:P	14:N:113:ARG:HD3	2.60	0.42
5:E:27:ALA:HB3	5:E:30:THR:HG23	2.02	0.42
14:N:29:ARG:O	14:N:33:ILE:HG13	2.20	0.42
22:V:2:PRO:HB3	22:V:22:SER:OG	2.19	0.42
24:1:47:LEU:HA	24:1:51:MET:HG2	2.01	0.42
24:2:18:GLN:C	24:2:20:SER:N	2.77	0.42
25:3:119:GLU:HB2	25:3:489:PRO:CG	2.49	0.42
25:3:672:GLU:OE1	25:3:1187:PHE:HA	2.19	0.42
26:4:209:ASN:O	26:4:211:GLU:N	2.53	0.42
26:4:591:ILE:HG13	26:4:592:VAL:HG13	2.02	0.42
1:A:309:A:H2'	1:A:310:G:H8	1.85	0.42
1:A:1219:A:H2'	1:A:1220:G:H8	1.85	0.42
1:A:1507:A:OP1	1:A:1507:A:H4'	2.18	0.42
7:G:55:HIS:O	7:G:56:LYS:HB2	2.19	0.42
17:Q:58:ALA:O	17:Q:59:HIS:C	2.60	0.42
22:V:9:ASN:O	22:V:9:ASN:CG	2.58	0.42
25:3:363:LEU:HD23	25:3:363:LEU:HA	1.82	0.42
26:4:1350:ASN:ND2	26:4:1358:PRO:CG	2.83	0.42
1:A:838:G:H2'	1:A:839:C:H6	1.85	0.42
1:A:1243:C:H2'	1:A:1244:G:H8	1.84	0.42
1:A:1414:U:H2'	1:A:1415:G:H8	1.84	0.42
2:B:141:VAL:O	2:B:141:VAL:CG2	2.67	0.42
5:E:50:ASP:O	5:E:53:VAL:HG22	2.19	0.42
8:H:2:PRO:C	8:H:4:ARG:H	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:56:LYS:HB2	9:I:56:LYS:HE3	1.85	0.42
10:J:123:ARG:HD3	10:J:123:ARG:C	2.44	0.42
26:4:793:SER:O	26:4:797:THR:HG23	2.19	0.42
26:4:919:ALA:HA	26:4:1252:HIS:HD2	1.85	0.42
26:4:979:ASN:O	26:4:981:GLU:HG3	2.20	0.42
1:A:415:A:H2'	1:A:416:G:C8	2.54	0.42
2:B:17:GLU:CG	2:B:19:ARG:HG3	2.50	0.42
3:C:91:PHE:O	3:C:150:GLY:HA3	2.20	0.42
11:K:25:ILE:HD12	28:Z:165:PHE:CE1	2.53	0.42
22:V:7:ARG:HB3	22:V:8:GLU:H	1.63	0.42
25:3:1334:GLY:H	26:4:113:HIS:CE1	2.38	0.42
26:4:128:LEU:HD11	26:4:185:ILE:HG23	2.01	0.42
26:4:138:VAL:O	26:4:181:GLY:HA2	2.20	0.42
26:4:720:ASN:HD21	26:4:722:ILE:HB	1.84	0.42
26:4:804:ALA:HA	26:4:1259:GLN:NE2	2.29	0.42
26:4:872:LEU:HD22	26:4:877:VAL:HG21	2.01	0.42
27:5:3:ARG:HD3	27:5:3:ARG:HA	1.76	0.42
1:A:223:A:H2'	1:A:224:U:C6	2.55	0.41
1:A:782:A:H62	1:A:800:G:N2	2.18	0.41
1:A:1151:A:O2'	1:A:1152:A:O4'	2.38	0.41
1:A:1410:A:OP2	1:A:1410:A:C8	2.73	0.41
3:C:126:PHE:CG	3:C:127:ASP:N	2.88	0.41
5:E:197:GLU:HG2	5:E:198:HIS:CD2	2.55	0.41
6:F:99:ALA:CB	6:F:103:THR:HG21	2.48	0.41
20:T:45:ILE:HD12	20:T:63:THR:C	2.45	0.41
23:X:48:C:H2'	23:X:49:G:C8	2.55	0.41
26:4:1032:SER:HA	26:4:1115:ILE:O	2.19	0.41
1:A:93:U:H6	1:A:93:U:O5'	2.02	0.41
1:A:131:A:H2'	1:A:132:C:C6	2.55	0.41
1:A:698:G:H2'	1:A:699:C:H6	1.84	0.41
1:A:1048:G:H5''	15:O:3:LYS:HG2	2.01	0.41
1:A:1060:U:H4'	11:K:53:ILE:HG13	2.02	0.41
1:A:1169:A:H2'	1:A:1170:A:H8	1.85	0.41
2:B:112:ILE:HG13	2:B:148:GLU:CA	2.39	0.41
9:I:2:SER:OG	9:I:3:MET:N	2.51	0.41
12:L:44:TRP:HZ3	12:L:46:THR:HG23	1.84	0.41
12:L:123:PRO:HG2	22:V:38:TYR:HB2	2.02	0.41
16:P:9:ALA:O	16:P:12:VAL:HG12	2.20	0.41
24:2:64:VAL:HG13	24:2:69:SER:OG	2.20	0.41
25:3:178:PRO:HB3	25:3:395:TYR:CZ	2.55	0.41
25:3:742:TYR:HB2	25:3:745:GLU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:C:C2	17:Q:1:MET:SD	3.13	0.41
1:A:310:G:H5''	17:Q:31:ARG:HB2	2.01	0.41
1:A:1422:G:C2	1:A:1479:C:C2	3.08	0.41
14:N:83:LEU:HD11	20:T:66:MET:HG2	2.02	0.41
25:3:806:PRO:CD	25:3:1100:PRO:HG3	2.44	0.41
29:6:23:DT:H6	29:6:23:DT:H2'	1.70	0.41
1:A:35:G:H2'	1:A:36:C:C6	2.55	0.41
1:A:88:U:C4	1:A:89:U:C4	3.08	0.41
1:A:147:G:H2'	1:A:148:G:H8	1.83	0.41
1:A:204:U:H2'	1:A:205:A:C8	2.55	0.41
1:A:413:G:H4'	1:A:414:A:H5''	2.01	0.41
1:A:704:A:H3'	1:A:705:G:C8	2.55	0.41
1:A:1487:G:OP2	1:A:1487:G:N7	2.54	0.41
2:B:43:LYS:HG3	2:B:76:GLU:OE2	2.20	0.41
2:B:101:ALA:CB	2:B:156:VAL:HB	2.51	0.41
3:C:196:VAL:HB	3:C:199:VAL:HG23	2.02	0.41
6:F:48:PHE:HZ	6:F:138:ARG:HH21	1.68	0.41
25:3:820:GLU:O	25:3:823:VAL:HG12	2.20	0.41
26:4:152:THR:HG22	26:4:172:PHE:CD1	2.55	0.41
26:4:984:LEU:O	26:4:991:THR:HA	2.20	0.41
28:Z:12:VAL:HA	28:Z:92:PHE:HA	2.01	0.41
1:A:95:C:H2'	1:A:96:U:C6	2.56	0.41
1:A:412:A:N1	1:A:414:A:H1'	2.35	0.41
1:A:523:A:N6	13:M:89:D2T:OD1	2.43	0.41
1:A:1073:U:C2	1:A:1074:G:C8	3.08	0.41
1:A:1140:C:O2'	1:A:1141:C:H6	2.03	0.41
1:A:1387:G:H2'	1:A:1388:C:C6	2.55	0.41
1:A:1393:U:H6	1:A:1393:U:O5'	2.03	0.41
3:C:45:LYS:O	3:C:49:MET:HG3	2.19	0.41
4:D:130:PHE:O	4:D:134:MET:HG2	2.20	0.41
24:1:25:LYS:HG2	24:1:204:GLU:HB3	2.02	0.41
24:2:104:LYS:HG2	24:2:110:VAL:HG22	2.03	0.41
25:3:15:PHE:CE1	25:3:1194:GLU:HB3	2.56	0.41
25:3:61:SER:HB3	25:3:479:LEU:HD22	2.02	0.41
25:3:1004:ASP:OD1	25:3:1004:ASP:N	2.44	0.41
25:3:1042:LEU:HD13	25:3:1042:LEU:HA	1.93	0.41
26:4:309:ASN:ND2	26:4:324:LEU:O	2.42	0.41
26:4:1052:GLU:CD	26:4:1052:GLU:H	2.28	0.41
1:A:26:A:H61	1:A:558:G:H1'	1.85	0.41
1:A:376:G:H5''	17:Q:5:ARG:HB2	2.02	0.41
1:A:455:G:H2'	1:A:456:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:468:A:H5'	1:A:469:C:OP2	2.20	0.41
1:A:539:A:H2'	1:A:540:G:H8	1.86	0.41
1:A:547:A:OP2	5:E:2:ALA:HA	2.20	0.41
1:A:839:C:H2'	1:A:840:C:C6	2.56	0.41
1:A:1472:U:H2'	1:A:1473:G:C8	2.56	0.41
5:E:71:GLN:O	5:E:75:TYR:HD1	2.03	0.41
20:T:23:VAL:CG1	20:T:24:GLU:N	2.84	0.41
23:X:5:A:H2'	23:X:6:G:C8	2.56	0.41
24:1:50:SER:HB3	24:2:8:PHE:CZ	2.56	0.41
25:3:388:LEU:HB3	25:3:389:PHE:CD2	2.55	0.41
25:3:1334:GLY:H	26:4:113:HIS:HE1	1.69	0.41
26:4:809:VAL:O	26:4:912:GLY:N	2.47	0.41
1:A:80:A:H2'	1:A:81:A:C8	2.55	0.41
1:A:459:A:H2'	1:A:460:A:H8	1.85	0.41
1:A:462:G:H2'	1:A:463:U:H6	1.86	0.41
1:A:509:A:H2'	1:A:510:A:C8	2.56	0.41
1:A:584:G:H2'	1:A:585:G:H8	1.84	0.41
1:A:931:C:H2'	1:A:932:C:H6	1.86	0.41
1:A:946:A:H2'	1:A:947:G:H8	1.82	0.41
1:A:1502:A:H2'	1:A:1503:A:O4'	2.19	0.41
2:B:102:TYR:CD1	2:B:103:GLU:HG3	2.56	0.41
2:B:158:LYS:HG3	2:B:159:LEU:H	1.84	0.41
3:C:6:MET:HE3	3:C:6:MET:HB2	1.83	0.41
8:H:47:LEU:HD23	8:H:47:LEU:HA	1.93	0.41
11:K:77:VAL:HG12	11:K:78:GLU:HG2	2.02	0.41
12:L:61:PHE:O	12:L:65:VAL:HG12	2.20	0.41
13:M:73:ASN:OD1	13:M:73:ASN:N	2.54	0.41
13:M:88:LYS:O	13:M:90:LEU:N	2.48	0.41
17:Q:1:MET:HE2	17:Q:2:VAL:HG12	2.01	0.41
24:2:152:TYR:HE2	26:4:536:LEU:HD21	1.86	0.41
25:3:297:VAL:HA	25:3:335:THR:HG22	2.03	0.41
25:3:1107:MET:SD	26:4:736:GLN:HG3	2.60	0.41
25:3:1273:MET:HE3	30:7:16:DC:H5''	2.01	0.41
25:3:1305:TYR:HE1	26:4:379:PRO:HB3	1.86	0.41
26:4:974:VAL:HG21	26:4:1118:GLY:HA2	2.03	0.41
26:4:979:ASN:O	26:4:980:THR:C	2.64	0.41
26:4:1281:GLU:HG2	26:4:1284:ARG:HB3	2.02	0.41
1:A:321:A:H2'	1:A:322:C:H6	1.85	0.41
1:A:555:U:H2'	1:A:556:C:H6	1.85	0.41
1:A:882:C:O2'	1:A:883:C:H5'	2.20	0.41
1:A:1125:U:HO2'	1:A:1126:U:P	2.44	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:155:LYS:C	2:B:168:VAL:HG22	2.46	0.41
2:B:158:LYS:CG	2:B:159:LEU:H	2.33	0.41
4:D:85:GLU:OE2	4:D:89:LYS:HE2	2.20	0.41
5:E:56:ARG:CZ	5:E:56:ARG:HB3	2.51	0.41
6:F:47:GLY:O	6:F:67:ALA:HB1	2.20	0.41
6:F:89:HIS:CD2	6:F:90:THR:H	2.38	0.41
8:H:111:ARG:NE	8:H:123:GLU:OE1	2.51	0.41
11:K:7:ARG:HB2	11:K:101:SER:OG	2.21	0.41
11:K:50:THR:CG2	11:K:62:ARG:HB3	2.51	0.41
25:3:1099:ASN:CG	25:3:1100:PRO:HD2	2.46	0.41
25:3:1238:LEU:HD23	25:3:1238:LEU:H	1.85	0.41
1:A:204:U:H2'	1:A:205:A:H8	1.84	0.41
1:A:820:U:H4'	1:A:821:G:OP2	2.21	0.41
1:A:844:G:H2'	1:A:845:A:H5''	2.02	0.41
1:A:997:U:H2'	1:A:998:C:C6	2.55	0.41
1:A:1171:A:H2'	1:A:1172:C:C6	2.56	0.41
1:A:1409:C:H6	1:A:1409:C:H3'	1.86	0.41
2:B:116:VAL:HG12	2:B:117:LYS:H	1.86	0.41
2:B:155:LYS:HB3	2:B:155:LYS:HE2	1.87	0.41
3:C:144:LEU:O	3:C:148:LEU:HB3	2.20	0.41
4:D:34:ASP:CG	4:D:38:LYS:HZ3	2.29	0.41
5:E:177:LYS:O	5:E:178:MET:HB2	2.20	0.41
6:F:159:LYS:HE3	6:F:159:LYS:HB3	1.79	0.41
7:G:53:LYS:N	7:G:53:LYS:HD3	2.36	0.41
9:I:39:VAL:HA	9:I:42:GLU:HG2	2.02	0.41
10:J:65:ILE:HG21	10:J:79:ILE:HG12	2.03	0.41
12:L:44:TRP:CZ3	12:L:46:THR:HG23	2.55	0.41
23:X:38:A:H2	26:4:77:ARG:NH1	2.18	0.41
23:X:49:G:H2'	23:X:50:C:H6	1.86	0.41
24:1:54:CYS:SG	24:1:148:ARG:HD2	2.60	0.41
25:3:870:ILE:HG21	25:3:931:VAL:HG21	2.02	0.41
26:4:201:LEU:HD22	26:4:220:ARG:HH11	1.86	0.41
26:4:846:GLU:HA	26:4:860:ARG:HB2	2.03	0.41
26:4:849:LEU:HG	26:4:856:ILE:HA	2.03	0.41
28:Z:65:PHE:O	28:Z:67:GLY:N	2.53	0.41
30:7:27:DG:H2''	30:7:28:DG:C8	2.56	0.41
1:A:322:C:H2'	1:A:323:U:C6	2.56	0.41
1:A:657:U:H2'	1:A:658:C:H6	1.85	0.41
1:A:1408:A:H8	1:A:1408:A:O5'	2.04	0.41
5:E:50:ASP:O	5:E:54:GLN:HG3	2.20	0.41
8:H:74:GLU:O	8:H:88:PRO:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:43:LYS:HB2	13:M:43:LYS:HE2	1.83	0.41
19:S:32:TYR:O	19:S:40:VAL:HG12	2.21	0.41
24:2:23:HIS:HB3	24:2:206:GLU:HG2	2.02	0.41
26:4:102:MET:HG2	26:4:246:PRO:HD3	2.02	0.41
26:4:189:LEU:HB3	26:4:234:PRO:HB2	2.03	0.41
26:4:536:LEU:HD22	26:4:541:LEU:HB2	2.03	0.41
26:4:634:ARG:HD2	26:4:634:ARG:HA	1.80	0.41
26:4:894:VAL:HG11	26:4:915:ILE:HD13	2.02	0.41
26:4:960:LEU:HG	26:4:982:LEU:CB	2.50	0.41
1:A:209:U:OP2	1:A:210:C:N4	2.52	0.40
1:A:645:G:C2	1:A:646:G:C8	3.09	0.40
1:A:1001:C:C2	1:A:1002:G:C8	3.09	0.40
1:A:1394:A:H2	1:A:1502:A:H2	1.67	0.40
10:J:11:ARG:HA	10:J:15:SER:O	2.21	0.40
11:K:35:GLN:HG3	11:K:77:VAL:HB	2.03	0.40
11:K:39:PRO:HA	11:K:73:LEU:O	2.21	0.40
11:K:92:LEU:O	11:K:93:ALA:C	2.64	0.40
13:M:43:LYS:HE2	13:M:89:D2T:H4	2.02	0.40
18:R:15:ASP:HA	18:R:21:ILE:HG22	2.03	0.40
25:3:213:LEU:HD22	25:3:422:LYS:HG2	2.02	0.40
25:3:1140:LYS:HA	25:3:1140:LYS:HD3	1.82	0.40
26:4:473:THR:O	26:4:477:GLN:HG3	2.21	0.40
26:4:1178:THR:HG23	26:4:1184:ASP:HB3	2.02	0.40
1:A:154:U:H2'	1:A:155:A:C8	2.56	0.40
1:A:215:C:H2'	1:A:216:U:H6	1.86	0.40
1:A:692:U:N3	1:A:695:A:OP2	2.52	0.40
1:A:721:G:H4'	1:A:722:G:O4'	2.20	0.40
1:A:846:G:H2'	1:A:847:G:C8	2.57	0.40
1:A:864:A:H2'	1:A:865:A:C8	2.56	0.40
6:F:81:LEU:H	6:F:81:LEU:HD12	1.87	0.40
15:O:18:ASP:OD1	15:O:19:LYS:N	2.55	0.40
20:T:20:GLU:O	20:T:23:VAL:HG12	2.21	0.40
24:1:149:GLY:HA2	24:2:5:VAL:HG12	2.03	0.40
24:2:16:ILE:HD12	24:2:16:ILE:N	2.36	0.40
25:3:265:LYS:HE2	25:3:265:LYS:HB3	1.80	0.40
25:3:811:ASN:ND2	25:3:1097:VAL:HG12	2.36	0.40
26:4:422:LEU:O	26:4:468:VAL:HA	2.20	0.40
1:A:456:A:H2'	1:A:457:G:O4'	2.22	0.40
1:A:494:G:O2'	1:A:496:A:H1'	2.22	0.40
1:A:876:C:H2'	1:A:877:G:H8	1.85	0.40
1:A:996:A:H2'	1:A:997:U:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1392:G:H1	1:A:1504:G:H1'	1.84	0.40
2:B:98:LEU:HA	2:B:156:VAL:HG21	2.03	0.40
4:D:6:HIS:CE1	4:D:8:ASN:HB3	2.55	0.40
12:L:79:ILE:HG21	12:L:82:LEU:CD1	2.50	0.40
15:O:3:LYS:HB2	15:O:3:LYS:HE3	1.83	0.40
25:3:44:GLU:O	25:3:46:GLN:N	2.54	0.40
25:3:164:THR:C	25:3:166:SER:H	2.29	0.40
25:3:262:TYR:CE2	25:3:285:ILE:HD11	2.57	0.40
25:3:267:ARG:NH2	25:3:268:ARG:O	2.50	0.40
25:3:285:ILE:HD12	25:3:285:ILE:HA	1.80	0.40
25:3:503:LYS:HE3	25:3:503:LYS:HB2	1.86	0.40
25:3:1268:GLN:CD	26:4:352:ARG:HH11	2.28	0.40
26:4:697:MET:HE3	26:4:697:MET:HB3	2.00	0.40
26:4:960:LEU:CD2	26:4:997:VAL:HG21	2.52	0.40
26:4:1109:LEU:HB3	26:4:1115:ILE:HD11	2.03	0.40
26:4:1160:SER:HA	26:4:1205:GLU:HA	2.02	0.40
26:4:1172:LYS:HG3	26:4:1190:ILE:O	2.22	0.40
1:A:553:A:H2'	1:A:554:A:C8	2.57	0.40
1:A:705:G:C5	1:A:706:A:C8	3.09	0.40
1:A:1005:A:C6	1:A:1006:G:H1'	2.56	0.40
1:A:1171:A:H2'	1:A:1172:C:H6	1.86	0.40
1:A:1360:A:C8	15:O:58:SER:HB2	2.57	0.40
1:A:1419:G:C6	1:A:1420:U:C4	3.10	0.40
3:C:94:HIS:O	3:C:95:ARG:C	2.64	0.40
3:C:145:GLU:O	3:C:149:GLY:N	2.50	0.40
10:J:120:LYS:HB3	10:J:121:ALA:H	1.77	0.40
20:T:29:LYS:HE2	20:T:29:LYS:HB2	1.52	0.40
25:3:19:PRO:HA	25:3:1156:ARG:HD3	2.03	0.40
25:3:292:ILE:HG13	25:3:292:ILE:H	1.59	0.40
25:3:388:LEU:HD23	25:3:388:LEU:HA	1.93	0.40
25:3:845:LEU:HD22	25:3:890:LYS:HB2	2.03	0.40
26:4:312:ARG:NH1	26:4:314:ARG:H	2.19	0.40
26:4:1281:GLU:H	26:4:1281:GLU:CD	2.30	0.40
29:6:22:DT:OP1	29:6:23:DT:N3	2.50	0.40
1:A:9:G:H5'	6:F:108:GLY:HA3	2.03	0.40
1:A:454:G:H2'	1:A:455:G:C8	2.56	0.40
1:A:505:G:H2'	1:A:506:G:C8	2.56	0.40
1:A:563:A:H5'	1:A:566:G:N2	2.37	0.40
1:A:606:G:C6	1:A:631:C:H5	2.40	0.40
1:A:844:G:N3	1:A:844:G:C3'	2.85	0.40
14:N:43:VAL:HG11	14:N:48:LEU:HD21	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:55:THR:O	14:N:59:GLU:HG2	2.22	0.40
23:X:7:G:H2'	23:X:8:A:C8	2.51	0.40
24:1:8:PHE:O	24:1:10:LYS:NZ	2.55	0.40
25:3:997:TRP:HA	25:3:1000:LEU:HG	2.03	0.40
26:4:72:CYS:HB2	26:4:87:LYS:CD	2.47	0.40
26:4:504:GLN:HG3	26:4:505:ASP:N	2.37	0.40
26:4:1197:ASN:N	26:4:1210:ILE:O	2.42	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	B	258/557 (46%)	223 (86%)	25 (10%)	10 (4%)	2	16
3	C	224/241 (93%)	207 (92%)	16 (7%)	1 (0%)	30	60
4	D	209/233 (90%)	193 (92%)	14 (7%)	2 (1%)	12	40
5	E	203/206 (98%)	199 (98%)	3 (2%)	1 (0%)	24	55
6	F	154/157 (98%)	138 (90%)	15 (10%)	1 (1%)	21	52
7	G	102/131 (78%)	96 (94%)	6 (6%)	0	100	100
8	H	151/156 (97%)	137 (91%)	12 (8%)	2 (1%)	9	35
9	I	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
10	J	126/130 (97%)	109 (86%)	16 (13%)	1 (1%)	16	45
11	K	99/103 (96%)	90 (91%)	8 (8%)	1 (1%)	12	40
12	L	115/129 (89%)	102 (89%)	12 (10%)	1 (1%)	14	43
13	M	119/124 (96%)	106 (89%)	12 (10%)	1 (1%)	16	45
14	N	113/118 (96%)	102 (90%)	8 (7%)	3 (3%)	4	22
15	O	98/101 (97%)	94 (96%)	3 (3%)	1 (1%)	12	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	P	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
17	Q	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
18	R	78/84 (93%)	73 (94%)	5 (6%)	0	100	100
19	S	64/75 (85%)	61 (95%)	3 (5%)	0	100	100
20	T	81/92 (88%)	70 (86%)	9 (11%)	2 (2%)	4	23
21	U	84/87 (97%)	84 (100%)	0	0	100	100
22	V	68/71 (96%)	58 (85%)	10 (15%)	0	100	100
24	1	227/329 (69%)	223 (98%)	4 (2%)	0	100	100
24	2	215/329 (65%)	206 (96%)	6 (3%)	3 (1%)	9	33
25	3	1316/1342 (98%)	1235 (94%)	76 (6%)	5 (0%)	30	60
26	4	1327/1406 (94%)	1240 (93%)	75 (6%)	12 (1%)	14	43
27	5	88/91 (97%)	83 (94%)	5 (6%)	0	100	100
28	Z	147/180 (82%)	136 (92%)	10 (7%)	1 (1%)	18	49
All	All	5959/6773 (88%)	5539 (93%)	372 (6%)	48 (1%)	18	45

All (48) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	61	ALA
5	E	107	PHE
6	F	90	THR
13	M	88	LYS
24	2	16	ILE
25	3	1107	MET
26	4	210	SER
2	B	136	VAL
2	B	145	LEU
2	B	169	SER
4	D	127	ARG
8	H	28	ASN
14	N	44	LYS
14	N	110	LYS
20	T	28	LYS
24	2	17	GLU
25	3	1104	PRO
26	4	1159	ILE
2	B	20	PRO

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Mol	Chain	Res	Type
2	B	143	ASP
2	B	166	VAL
14	N	66	GLU
15	O	35	ASN
20	T	26	GLY
25	3	596	ASP
26	4	712	GLN
26	4	980	THR
26	4	994	SER
8	H	27	VAL
12	L	89	PRO
25	3	1105	SER
26	4	1186	TYR
28	Z	66	PRO
2	B	153	GLU
2	B	155	LYS
10	J	13	LYS
26	4	966	VAL
2	B	21	GLY
2	B	158	LYS
3	C	165	ASP
11	K	78	GLU
24	2	19	VAL
25	3	1223	ARG
26	4	974	VAL
26	4	427	PRO
26	4	1179	PRO
26	4	975	ILE
26	4	1185	PRO

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	B	143/461 (31%)	115 (80%)	28 (20%)	1	6
3	C	187/199 (94%)	169 (90%)	18 (10%)	8	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	172/190 (90%)	151 (88%)	21 (12%)	5	19
5	E	172/173 (99%)	153 (89%)	19 (11%)	6	23
6	F	119/119 (100%)	100 (84%)	19 (16%)	2	11
7	G	91/112 (81%)	72 (79%)	19 (21%)	1	5
8	H	126/129 (98%)	117 (93%)	9 (7%)	13	40
9	I	104/105 (99%)	96 (92%)	8 (8%)	12	37
10	J	106/107 (99%)	90 (85%)	16 (15%)	3	13
11	K	88/90 (98%)	79 (90%)	9 (10%)	7	26
12	L	90/99 (91%)	81 (90%)	9 (10%)	7	27
13	M	102/103 (99%)	90 (88%)	12 (12%)	5	20
14	N	93/96 (97%)	85 (91%)	8 (9%)	10	33
15	O	83/84 (99%)	81 (98%)	2 (2%)	43	65
16	P	76/77 (99%)	71 (93%)	5 (7%)	15	43
17	Q	65/65 (100%)	58 (89%)	7 (11%)	6	23
18	R	74/78 (95%)	72 (97%)	2 (3%)	39	63
19	S	57/65 (88%)	57 (100%)	0	100	100
20	T	72/79 (91%)	62 (86%)	10 (14%)	3	15
21	U	65/66 (98%)	61 (94%)	4 (6%)	16	45
22	V	60/61 (98%)	58 (97%)	2 (3%)	33	59
24	1	197/286 (69%)	189 (96%)	8 (4%)	27	55
24	2	187/286 (65%)	172 (92%)	15 (8%)	11	36
25	3	1139/1157 (98%)	1073 (94%)	66 (6%)	18	47
26	4	1118/1167 (96%)	1030 (92%)	88 (8%)	11	36
27	5	74/75 (99%)	73 (99%)	1 (1%)	59	73
28	Z	135/157 (86%)	119 (88%)	16 (12%)	5	20
All	All	4995/5686 (88%)	4574 (92%)	421 (8%)	12	34

All (421) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	3	GLU
2	B	15	GLU
2	B	16	ILE

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Mol	Chain	Res	Type
2	B	17	GLU
2	B	19	ARG
2	B	100	LYS
2	B	102	TYR
2	B	104	ASP
2	B	112	ILE
2	B	117	LYS
2	B	131	LEU
2	B	137	ASP
2	B	139	ARG
2	B	142	ARG
2	B	145	LEU
2	B	146	HIS
2	B	148	GLU
2	B	150	LYS
2	B	153	GLU
2	B	155	LYS
2	B	160	ASP
2	B	161	GLN
2	B	162	LYS
2	B	163	ARG
2	B	166	VAL
2	B	168	VAL
2	B	170	ARG
2	B	171	ARG
3	C	45	LYS
3	C	46	THR
3	C	54	LEU
3	C	88	ASP
3	C	101	LEU
3	C	117	LEU
3	C	127	ASP
3	C	141	LEU
3	C	148	LEU
3	C	151	ILE
3	C	152	LYS
3	C	159	ASP
3	C	163	VAL
3	C	164	ILE
3	C	183	VAL
3	C	199	VAL
3	C	212	LEU

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Mol	Chain	Res	Type
3	C	214	LEU
4	D	4	LYS
4	D	26	THR
4	D	27	LYS
4	D	31	ASP
4	D	36	ASP
4	D	38	LYS
4	D	46	GLU
4	D	52	VAL
4	D	62	LYS
4	D	64	ILE
4	D	72	ARG
4	D	85	GLU
4	D	121	THR
4	D	123	GLN
4	D	128	VAL
4	D	162	ILE
4	D	172	ARG
4	D	175	LEU
4	D	178	LEU
4	D	207	ILE
4	D	211	MET
5	E	29	ASP
5	E	34	ILE
5	E	56	ARG
5	E	83	LYS
5	E	107	PHE
5	E	125	VAL
5	E	129	VAL
5	E	132	ILE
5	E	137	VAL
5	E	142	VAL
5	E	143	VAL
5	E	155	VAL
5	E	164	GLN
5	E	171	LEU
5	E	178	MET
5	E	179	GLU
5	E	181	THR
5	E	183	LYS
5	E	194	ASP
6	F	13	GLU

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Mol	Chain	Res	Type
6	F	14	LYS
6	F	15	LEU
6	F	34	THR
6	F	36	LEU
6	F	39	VAL
6	F	45	ARG
6	F	46	VAL
6	F	48	PHE
6	F	50	TYR
6	F	52	LYS
6	F	54	ARG
6	F	94	VAL
6	F	116	GLU
6	F	117	VAL
6	F	138	ARG
6	F	153	VAL
6	F	157	ARG
6	F	159	LYS
7	G	1	MET
7	G	2	ARG
7	G	10	VAL
7	G	36	ILE
7	G	44	ARG
7	G	46	GLN
7	G	47	LEU
7	G	52	ASN
7	G	53	LYS
7	G	54	LEU
7	G	55	HIS
7	G	61	LEU
7	G	84	VAL
7	G	89	VAL
7	G	90	MET
7	G	93	LYS
7	G	97	THR
7	G	102	MET
7	G	103	VAL
8	H	21	GLU
8	H	22	LEU
8	H	58	GLU
8	H	75	VAL
8	H	83	SER

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Mol	Chain	Res	Type
8	H	87	VAL
8	H	90	GLU
8	H	130	ASN
8	H	143	ARG
9	I	3	MET
9	I	40	LEU
9	I	62	THR
9	I	78	VAL
9	I	87	LYS
9	I	90	ASP
9	I	107	SER
9	I	110	VAL
10	J	5	GLN
10	J	9	THR
10	J	22	LYS
10	J	29	VAL
10	J	32	GLN
10	J	57	MET
10	J	58	VAL
10	J	63	LEU
10	J	67	VAL
10	J	94	LEU
10	J	97	GLU
10	J	105	THR
10	J	116	VAL
10	J	119	ARG
10	J	123	ARG
10	J	130	ARG
11	K	36	VAL
11	K	40	ILE
11	K	47	GLU
11	K	52	LEU
11	K	78	GLU
11	K	80	THR
11	K	88	MET
11	K	92	LEU
11	K	98	VAL
12	L	16	VAL
12	L	69	ARG
12	L	82	LEU
12	L	86	VAL
12	L	98	ARG

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Mol	Chain	Res	Type
12	L	100	LEU
12	L	106	ARG
12	L	108	THR
12	L	113	VAL
13	M	12	ARG
13	M	16	VAL
13	M	18	LYS
13	M	24	LEU
13	M	34	CYS
13	M	35	THR
13	M	38	TYR
13	M	46	ASN
13	M	55	VAL
13	M	75	GLN
13	M	96	HIS
13	M	112	GLN
14	N	17	ILE
14	N	42	ASP
14	N	56	LEU
14	N	58	ASP
14	N	63	PHE
14	N	66	GLU
14	N	93	ARG
14	N	114	LYS
15	O	26	GLU
15	O	83	LYS
16	P	3	LEU
16	P	10	LYS
16	P	12	VAL
16	P	14	GLU
16	P	72	ARG
17	Q	18	GLN
17	Q	19	VAL
17	Q	21	VAL
17	Q	44	SER
17	Q	54	LEU
17	Q	56	ARG
17	Q	57	ILE
18	R	5	ILE
18	R	14	SER
20	T	24	GLU
20	T	28	LYS

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Mol	Chain	Res	Type
20	T	29	LYS
20	T	31	LEU
20	T	32	ARG
20	T	48	THR
20	T	51	VAL
20	T	58	VAL
20	T	63	THR
20	T	79	THR
21	U	3	ASN
21	U	40	GLU
21	U	59	ASP
21	U	67	ILE
22	V	6	VAL
22	V	42	THR
24	1	7	GLU
24	1	26	VAL
24	1	27	THR
24	1	100	LEU
24	1	129	VAL
24	1	204	GLU
24	1	224	LEU
24	1	228	LEU
24	2	6	THR
24	2	13	LEU
24	2	15	ASP
24	2	16	ILE
24	2	17	GLU
24	2	23	HIS
24	2	48	LEU
24	2	76	GLU
24	2	83	LEU
24	2	150	ARG
24	2	170	ARG
24	2	183	ILE
24	2	191	ARG
24	2	196	THR
24	2	207	THR
25	3	39	ILE
25	3	59	ILE
25	3	85	CYS
25	3	141	THR
25	3	150	HIS

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Mol	Chain	Res	Type
25	3	173	ASN
25	3	208	ILE
25	3	228	VAL
25	3	235	ASN
25	3	258	ASN
25	3	261	VAL
25	3	262	TYR
25	3	267	ARG
25	3	296	VAL
25	3	297	VAL
25	3	310	ILE
25	3	320	ASP
25	3	333	ILE
25	3	369	MET
25	3	412	GLU
25	3	423	ASP
25	3	468	LEU
25	3	491	ASP
25	3	498	ILE
25	3	518	ASN
25	3	565	GLU
25	3	569	ILE
25	3	595	THR
25	3	600	THR
25	3	615	VAL
25	3	623	LEU
25	3	633	LEU
25	3	680	LEU
25	3	731	ARG
25	3	733	VAL
25	3	736	VAL
25	3	748	ILE
25	3	754	THR
25	3	799	ASN
25	3	800	MET
25	3	813	GLU
25	3	822	VAL
25	3	845	LEU
25	3	854	ILE
25	3	856	ASN
25	3	888	THR
25	3	913	VAL

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Mol	Chain	Res	Type
25	3	931	VAL
25	3	933	VAL
25	3	950	GLU
25	3	979	LEU
25	3	992	LEU
25	3	1038	GLN
25	3	1047	LEU
25	3	1076	ILE
25	3	1085	MET
25	3	1098	LEU
25	3	1103	VAL
25	3	1106	ARG
25	3	1107	MET
25	3	1112	ILE
25	3	1159	VAL
25	3	1217	THR
25	3	1254	VAL
25	3	1304	MET
25	3	1340	GLU
26	4	68	TYR
26	4	83	VAL
26	4	92	VAL
26	4	145	VAL
26	4	146	VAL
26	4	157	GLN
26	4	158	GLN
26	4	159	ILE
26	4	161	THR
26	4	188	LEU
26	4	196	GLN
26	4	209	ASN
26	4	213	LYS
26	4	224	LEU
26	4	227	PHE
26	4	235	GLU
26	4	259	ARG
26	4	260	PHE
26	4	264	ASP
26	4	281	ARG
26	4	282	LEU
26	4	290	ILE
26	4	394	ILE

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Mol	Chain	Res	Type
26	4	418	GLU
26	4	424	ASN
26	4	427	PRO
26	4	428	THR
26	4	490	ILE
26	4	527	LEU
26	4	532	GLU
26	4	552	ILE
26	4	554	GLU
26	4	572	THR
26	4	592	VAL
26	4	624	ILE
26	4	634	ARG
26	4	658	GLU
26	4	700	ASN
26	4	736	GLN
26	4	789	LYS
26	4	800	LEU
26	4	816	THR
26	4	833	GLU
26	4	846	GLU
26	4	849	LEU
26	4	850	LYS
26	4	869	CYS
26	4	895	CYS
26	4	897	HIS
26	4	959	LYS
26	4	961	SER
26	4	963	VAL
26	4	964	LYS
26	4	966	VAL
26	4	967	VAL
26	4	968	ASN
26	4	972	LYS
26	4	973	LEU
26	4	974	VAL
26	4	975	ILE
26	4	978	ARG
26	4	982	LEU
26	4	983	LYS
26	4	984	LEU
26	4	985	ILE

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Mol	Chain	Res	Type
26	4	986	ASP
26	4	988	PHE
26	4	990	ARG
26	4	992	LYS
26	4	995	TYR
26	4	996	LYS
26	4	997	VAL
26	4	1028	ILE
26	4	1035	VAL
26	4	1046	ILE
26	4	1087	ASP
26	4	1141	VAL
26	4	1159	ILE
26	4	1167	LYS
26	4	1180	VAL
26	4	1181	ASP
26	4	1187	GLU
26	4	1204	VAL
26	4	1226	VAL
26	4	1258	ARG
26	4	1261	LEU
26	4	1306	LEU
26	4	1365	TYR
27	5	4	VAL
28	Z	15	PHE
28	Z	41	GLU
28	Z	42	VAL
28	Z	63	LYS
28	Z	64	PHE
28	Z	65	PHE
28	Z	69	VAL
28	Z	103	ILE
28	Z	109	ASP
28	Z	133	MET
28	Z	143	ASP
28	Z	147	VAL
28	Z	153	TYR
28	Z	155	LYS
28	Z	158	LEU
28	Z	179	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (86) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	7	GLN
2	B	92	HIS
2	B	165	ASN
3	C	18	HIS
3	C	89	GLN
3	C	168	HIS
4	D	8	ASN
4	D	123	GLN
5	E	40	GLN
6	F	89	HIS
6	F	135	ASN
7	G	17	GLN
7	G	68	GLN
8	H	86	GLN
8	H	142	HIS
10	J	32	GLN
10	J	37	GLN
10	J	75	GLN
12	L	15	GLN
12	L	22	HIS
12	L	24	HIS
12	L	81	ASN
13	M	96	HIS
15	O	66	GLN
16	P	35	GLN
17	Q	18	GLN
17	Q	59	HIS
19	S	54	GLN
19	S	74	HIS
21	U	13	GLN
21	U	48	GLN
21	U	78	ASN
22	V	64	ASN
24	1	18	GLN
24	1	23	HIS
24	1	41	ASN
24	1	132	HIS
24	2	84	ASN
24	2	93	GLN
24	2	117	HIS
25	3	69	GLN
25	3	238	GLN
25	3	327	GLN

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Mol	Chain	Res	Type
25	3	463	GLN
25	3	494	ASN
25	3	518	ASN
25	3	580	GLN
25	3	686	GLN
25	3	761	GLN
25	3	767	GLN
25	3	952	GLN
25	3	955	GLN
25	3	1111	GLN
25	3	1116	HIS
25	3	1209	GLN
25	3	1256	GLN
25	3	1288	GLN
25	3	1313	HIS
26	4	80	HIS
26	4	113	HIS
26	4	157	GLN
26	4	186	GLN
26	4	196	GLN
26	4	209	ASN
26	4	229	GLN
26	4	335	GLN
26	4	365	GLN
26	4	519	ASN
26	4	623	GLN
26	4	667	GLN
26	4	680	ASN
26	4	690	ASN
26	4	700	ASN
26	4	712	GLN
26	4	720	ASN
26	4	762	ASN
26	4	817	HIS
26	4	865	HIS
26	4	929	GLN
26	4	979	ASN
26	4	1108	GLN
26	4	1126	GLN
26	4	1259	GLN
26	4	1279	GLN
26	4	1350	ASN

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Mol	Chain	Res	Type
27	5	31	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1510/1542 (97%)	236 (15%)	17 (1%)
23	X	19/53 (35%)	3 (15%)	0
All	All	1529/1595 (95%)	239 (15%)	17 (1%)

All (239) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	A
1	A	3	A
1	A	4	U
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	51	A
1	A	54	C
1	A	71	A
1	A	72	A
1	A	77	A
1	A	83	C
1	A	85	U
1	A	86	G
1	A	94	G
1	A	95	C
1	A	121	U
1	A	130	A
1	A	131	A
1	A	141	G
1	A	144	G
1	A	160	A
1	A	164	G
1	A	181	A
1	A	189	A
1	A	197	A

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Mol	Chain	Res	Type
1	A	211	G
1	A	212	G
1	A	226	G
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C
1	A	279	A
1	A	280	C
1	A	281	G
1	A	289	G
1	A	306	A
1	A	328	C
1	A	332	G
1	A	351	G
1	A	352	C
1	A	354	G
1	A	367	U
1	A	372	C
1	A	373	A
1	A	406	G
1	A	411	A
1	A	413	G
1	A	414	A
1	A	421	U
1	A	422	C
1	A	428	G
1	A	429	U
1	A	430	A
1	A	457	G
1	A	458	U
1	A	463	U
1	A	466	A
1	A	467	U
1	A	468	A
1	A	474	G
1	A	479	U
1	A	481	G
1	A	484	G
1	A	486	U
1	A	495	A
1	A	496	A

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Mol	Chain	Res	Type
1	A	497	G
1	A	509	A
1	A	511	C
1	A	518	C
1	A	521	G
1	A	527	G7M
1	A	531	U
1	A	532	A
1	A	533	A
1	A	547	A
1	A	563	A
1	A	572	A
1	A	573	A
1	A	576	C
1	A	577	G
1	A	595	A
1	A	630	A
1	A	632	U
1	A	633	G
1	A	642	A
1	A	650	G
1	A	653	U
1	A	665	A
1	A	687	A
1	A	718	A
1	A	723	U
1	A	731	G
1	A	734	G
1	A	755	G
1	A	793	U
1	A	794	A
1	A	815	A
1	A	817	C
1	A	821	G
1	A	828	U
1	A	829	G
1	A	841	C
1	A	842	U
1	A	843	U
1	A	845	A
1	A	846	G
1	A	872	A

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Mol	Chain	Res	Type
1	A	873	A
1	A	876	C
1	A	887	G
1	A	914	A
1	A	925	G
1	A	926	G
1	A	927	G
1	A	929	G
1	A	933	G
1	A	934	C
1	A	935	A
1	A	960	U
1	A	966	2MG
1	A	967	5MC
1	A	969	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	992	U
1	A	993	G
1	A	994	A
1	A	996	A
1	A	1004	A
1	A	1009	U
1	A	1018	G
1	A	1020	G
1	A	1022	A
1	A	1024	G
1	A	1025	U
1	A	1028	C
1	A	1030	U
1	A	1031	C
1	A	1033	G
1	A	1044	A
1	A	1065	U
1	A	1066	C
1	A	1078	U
1	A	1079	G
1	A	1085	U
1	A	1086	U
1	A	1087	G
1	A	1094	G

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Mol	Chain	Res	Type
1	A	1095	U
1	A	1101	A
1	A	1108	G
1	A	1133	G
1	A	1136	C
1	A	1137	C
1	A	1139	G
1	A	1140	C
1	A	1141	C
1	A	1145	A
1	A	1151	A
1	A	1152	A
1	A	1158	C
1	A	1159	U
1	A	1184	G
1	A	1196	A
1	A	1197	A
1	A	1207	2MG
1	A	1213	A
1	A	1227	A
1	A	1238	A
1	A	1241	G
1	A	1257	A
1	A	1260	G
1	A	1278	G
1	A	1279	G
1	A	1280	A
1	A	1286	U
1	A	1287	A
1	A	1299	A
1	A	1300	G
1	A	1302	C
1	A	1305	G
1	A	1317	C
1	A	1318	A
1	A	1320	C
1	A	1338	G
1	A	1346	A
1	A	1363	A
1	A	1364	U
1	A	1370	G
1	A	1379	G

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Mol	Chain	Res	Type
1	A	1391	U
1	A	1392	G
1	A	1395	C
1	A	1396	A
1	A	1397	C
1	A	1406	U
1	A	1407	C
1	A	1409	C
1	A	1410	A
1	A	1411	C
1	A	1412	C
1	A	1419	G
1	A	1432	G
1	A	1476	A
1	A	1481	U
1	A	1482	G
1	A	1485	U
1	A	1486	G
1	A	1487	G
1	A	1488	G
1	A	1490	U
1	A	1491	G
1	A	1492	A
1	A	1495	U
1	A	1496	C
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1507	A
1	A	1517	G
1	A	1520	C
1	A	1529	G
1	A	1530	G
1	A	1531	A
1	A	1532	U
1	A	1533	C
1	A	1534	A
1	A	1535	C
23	X	44	A
23	X	45	C
23	X	46	G

All (17) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	429	U
1	A	641	U
1	A	1078	U
1	A	1086	U
1	A	1391	U
1	A	1396	A
1	A	1406	U
1	A	1485	U
1	A	1486	G
1	A	1489	G
1	A	1491	G
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1531	A
1	A	1533	C

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

9 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
13	D2T	M	89	13	8,9,10	1.72	1 (12%)	6,11,13	2.24	2 (33%)
1	5MC	A	967	1	19,22,23	4.14	8 (42%)	26,32,35	1.06	1 (3%)
1	PSU	A	516	1	18,21,22	1.10	3 (16%)	21,30,33	1.90	5 (23%)
1	2MG	A	1516	1	23,26,27	1.29	4 (17%)	33,38,41	2.28	8 (24%)
1	2MG	A	1207	31,1	23,26,27	2.83	8 (34%)	33,38,41	3.12	11 (33%)
1	2MG	A	966	1	23,26,27	2.92	9 (39%)	33,38,41	2.96	12 (36%)
1	MA6	A	1518	1	23,26,27	1.60	4 (17%)	33,38,41	3.83	12 (36%)
1	MA6	A	1519	1	23,26,27	1.57	5 (21%)	33,38,41	2.48	15 (45%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	G7M	A	527	1	23,26,27	0.74	1 (4%)	34,39,42	0.62	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	D2T	M	89	13	-	2/7/12/14	-
1	5MC	A	967	1	-	3/7/25/26	0/2/2/2
1	PSU	A	516	1	-	0/7/25/26	0/2/2/2
1	2MG	A	1516	1	-	0/9/27/28	0/3/3/3
1	2MG	A	1207	31,1	-	2/9/27/28	0/3/3/3
1	2MG	A	966	1	-	2/9/27/28	0/3/3/3
1	MA6	A	1518	1	-	3/11/29/30	0/3/3/3
1	MA6	A	1519	1	-	7/11/29/30	0/3/3/3
1	G7M	A	527	1	-	2/7/25/26	0/3/3/3

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	967	5MC	C6-C5	10.13	1.51	1.34
1	A	966	2MG	C2-N3	8.62	1.48	1.32
1	A	1207	2MG	C2-N3	8.43	1.48	1.32
1	A	967	5MC	C4-N3	7.47	1.46	1.34
1	A	967	5MC	C2-N3	6.71	1.49	1.36
1	A	967	5MC	C5-C4	6.17	1.48	1.44
1	A	966	2MG	C4-N3	5.90	1.47	1.34
1	A	1207	2MG	C4-N3	5.61	1.47	1.34
1	A	967	5MC	C4-N4	5.40	1.47	1.34
1	A	966	2MG	C2-N2	5.15	1.44	1.33
1	A	967	5MC	C6-N1	4.93	1.46	1.38
1	A	1207	2MG	C2-N2	4.84	1.43	1.33
1	A	1519	MA6	C5-C4	4.77	1.47	1.39
1	A	967	5MC	C2-N1	4.53	1.49	1.40
1	A	1518	MA6	C6-N6	4.46	1.49	1.36
13	M	89	D2T	CB-CA	-4.00	1.53	1.54
1	A	966	2MG	C2-N1	3.90	1.42	1.36
1	A	1207	2MG	O6-C6	-3.86	1.16	1.23
1	A	966	2MG	O6-C6	-3.79	1.16	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1207	2MG	C2-N1	3.54	1.42	1.36
1	A	1207	2MG	C5-N7	-3.51	1.32	1.39
1	A	966	2MG	C5-N7	-3.41	1.32	1.39
1	A	1518	MA6	C10-N6	3.40	1.53	1.45
1	A	516	PSU	C6-C5	3.19	1.38	1.35
1	A	1516	2MG	C5-C4	3.13	1.47	1.38
1	A	1519	MA6	C5-C6	2.95	1.49	1.41
1	A	1518	MA6	C5-C4	-2.74	1.34	1.39
1	A	527	G7M	C8-N7	2.61	1.37	1.33
1	A	1518	MA6	C8-N7	2.60	1.36	1.31
1	A	1519	MA6	C8-N7	2.52	1.36	1.31
1	A	1516	2MG	C6-N1	-2.46	1.34	1.38
1	A	966	2MG	C6-N1	2.42	1.43	1.38
1	A	1516	2MG	C2-N3	2.42	1.36	1.32
1	A	967	5MC	O2-C2	-2.41	1.19	1.23
1	A	1207	2MG	C6-N1	2.35	1.43	1.38
1	A	1519	MA6	C4-N9	-2.25	1.33	1.37
1	A	1207	2MG	C5-C6	2.25	1.52	1.44
1	A	966	2MG	C5-C6	2.21	1.52	1.44
1	A	1519	MA6	C5-N7	-2.17	1.35	1.39
1	A	516	PSU	C4-C5	-2.15	1.38	1.44
1	A	1516	2MG	C5-N7	-2.09	1.34	1.39
1	A	516	PSU	O4'-C1'	-2.06	1.41	1.43
1	A	966	2MG	C4-N9	-2.03	1.32	1.38

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1518	MA6	N1-C6-N6	-15.27	98.26	116.86
1	A	1518	MA6	C5-C6-N6	10.62	142.14	125.33
1	A	1207	2MG	C1'-N9-C8	-9.13	100.80	126.73
1	A	966	2MG	C1'-N9-C8	-8.86	101.56	126.73
1	A	1207	2MG	C1'-N9-C4	8.70	152.20	126.49
1	A	966	2MG	C1'-N9-C4	8.25	150.84	126.49
1	A	1516	2MG	C2-N3-C4	7.51	121.39	112.00
1	A	1207	2MG	C2-N3-C4	6.77	120.46	112.00
1	A	966	2MG	C2-N3-C4	6.33	119.92	112.00
1	A	1516	2MG	C5-C4-N3	-6.31	118.35	128.39
1	A	1207	2MG	C5-C4-N3	-5.65	119.39	128.39
1	A	1519	MA6	C5-C4-N3	-5.30	119.42	126.72
1	A	966	2MG	C5-C4-N3	-5.12	120.24	128.39
1	A	1518	MA6	C5-C4-N3	-5.08	119.72	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1516	2MG	N9-C4-N3	4.85	135.65	125.95
1	A	1518	MA6	N1-C2-N3	-4.79	121.33	128.58
1	A	1207	2MG	C2-N1-C6	-4.77	118.79	124.55
1	A	516	PSU	N1-C2-N3	4.72	120.14	115.17
1	A	1519	MA6	C9-N6-C6	-4.63	108.75	120.52
1	A	516	PSU	C4-N3-C2	-4.61	120.02	126.37
1	A	1518	MA6	C4-C5-C6	4.58	120.65	115.91
1	A	1519	MA6	C2-N1-C6	4.27	122.27	111.83
1	A	1519	MA6	C10-N6-C6	-4.23	109.75	120.52
1	A	966	2MG	C2-N1-C6	-4.10	119.59	124.55
1	A	1518	MA6	N9-C8-N7	-3.92	108.37	113.94
1	A	1519	MA6	C4-C5-N7	-3.88	106.15	110.58
1	A	1519	MA6	N3-C4-N9	3.80	133.63	127.17
13	M	89	D2T	CB1-SB-CB	3.75	109.10	102.36
1	A	1519	MA6	C2-N3-C4	3.69	120.84	111.83
1	A	1519	MA6	N1-C2-N3	-3.48	123.31	128.58
1	A	967	5MC	C5-C6-N1	-3.42	119.60	123.31
1	A	1518	MA6	C2-N3-C4	3.27	119.82	111.83
1	A	1516	2MG	C6-C5-N7	3.19	136.09	130.29
1	A	966	2MG	N1-C2-N2	3.10	119.73	116.56
1	A	1519	MA6	C2'-C1'-N9	-3.10	105.60	113.30
1	A	1207	2MG	N9-C4-N3	3.10	132.15	125.95
1	A	1207	2MG	N1-C2-N2	3.08	119.71	116.56
1	A	1518	MA6	N3-C4-N9	2.99	132.25	127.17
13	M	89	D2T	OD2-CG-CB	2.97	119.56	113.15
1	A	1518	MA6	C2-N1-C6	2.89	118.88	111.83
1	A	1207	2MG	C5-C6-N1	2.83	120.45	113.25
1	A	966	2MG	N9-C4-N3	2.82	131.59	125.95
1	A	516	PSU	O2-C2-N1	-2.78	119.92	122.79
1	A	1518	MA6	C5-N7-C8	2.74	107.76	103.45
1	A	966	2MG	C5-C6-N1	2.74	120.22	113.25
1	A	966	2MG	N9-C8-N7	-2.72	108.36	113.40
1	A	1519	MA6	N1-C6-N6	2.65	120.08	116.86
1	A	516	PSU	C6-N1-C2	-2.64	120.24	122.69
1	A	1519	MA6	C5-N7-C8	2.58	107.51	103.45
1	A	1516	2MG	C2'-C1'-N9	-2.57	106.09	113.25
1	A	1519	MA6	C10-N6-C9	-2.54	108.03	116.18
1	A	1519	MA6	C4-N9-C8	2.52	108.39	105.74
1	A	966	2MG	O6-C6-C5	-2.50	119.93	126.53
1	A	1207	2MG	N9-C8-N7	-2.47	108.83	113.40
1	A	1519	MA6	C6-C5-N7	2.46	137.36	133.43
1	A	1207	2MG	O6-C6-C5	-2.46	120.04	126.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1516	2MG	C4-C5-N7	-2.44	106.81	110.67
1	A	516	PSU	O4'-C1'-C2'	2.29	108.31	105.15
1	A	966	2MG	N1-C2-N3	-2.21	119.95	123.68
1	A	1516	2MG	O6-C6-C5	-2.16	120.82	126.53
1	A	1207	2MG	CM2-N2-C2	-2.11	119.12	123.65
1	A	1519	MA6	N9-C8-N7	-2.07	111.00	113.94
1	A	1516	2MG	C3'-C2'-C1'	2.06	105.36	101.46
1	A	1518	MA6	C4-C5-N7	-2.06	108.23	110.58
1	A	1518	MA6	C5-C4-N9	2.03	108.02	105.81
1	A	966	2MG	C8-N7-C5	2.03	107.88	104.26

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	967	5MC	O4'-C4'-C5'-O5'
1	A	967	5MC	C3'-C4'-C5'-O5'
1	A	1207	2MG	O4'-C4'-C5'-O5'
1	A	1207	2MG	C3'-C4'-C5'-O5'
1	A	1518	MA6	C5-C6-N6-C10
1	A	1518	MA6	N1-C6-N6-C10
1	A	1519	MA6	C5-C6-N6-C9
1	A	1519	MA6	C5-C6-N6-C10
1	A	1519	MA6	N1-C6-N6-C9
13	M	89	D2T	SB-CB-CG-OD2
1	A	527	G7M	C3'-C4'-C5'-O5'
1	A	1519	MA6	O4'-C4'-C5'-O5'
1	A	1519	MA6	C3'-C4'-C5'-O5'
1	A	1519	MA6	C4'-C5'-O5'-P
1	A	527	G7M	O4'-C4'-C5'-O5'
1	A	966	2MG	C3'-C4'-C5'-O5'
13	M	89	D2T	CG-CB-SB-CB1
1	A	1518	MA6	C5-C6-N6-C9
1	A	1519	MA6	N1-C6-N6-C10
1	A	966	2MG	O4'-C4'-C5'-O5'
1	A	967	5MC	C4'-C5'-O5'-P

There are no ring outliers.

5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	M	89	D2T	2	0
1	A	967	5MC	1	0
1	A	516	PSU	1	0
1	A	1518	MA6	3	0
1	A	1519	MA6	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 134 ligands modelled in this entry, 134 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

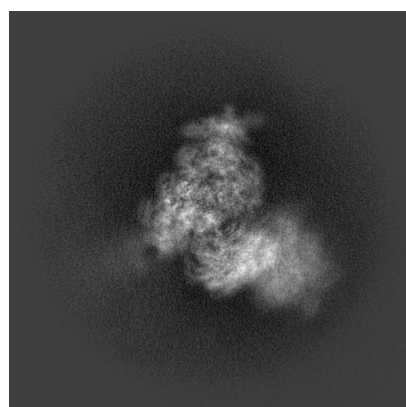
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51623. These allow visual inspection of the internal detail of the map and identification of artifacts.

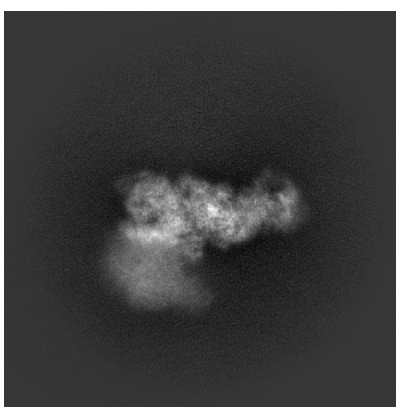
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

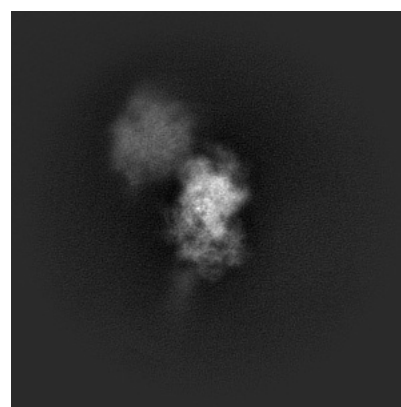
6.1.1 Primary map



X



Y

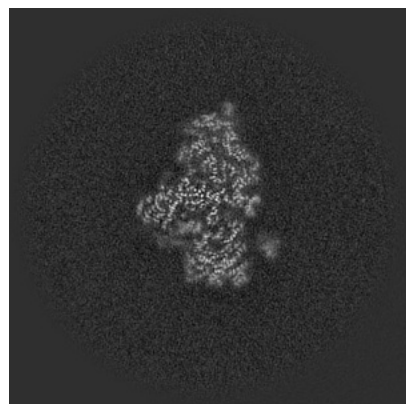


Z

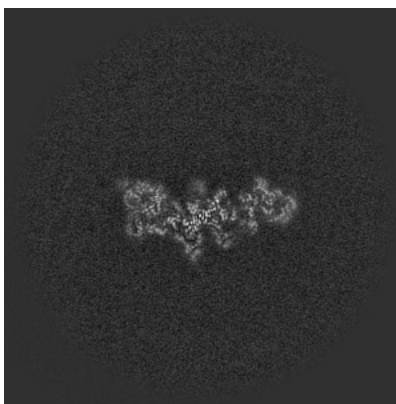
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

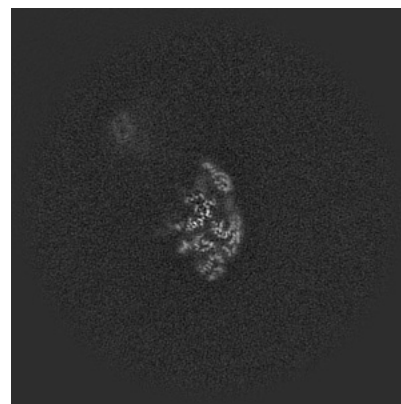
6.2.1 Primary map



X Index: 300



Y Index: 300

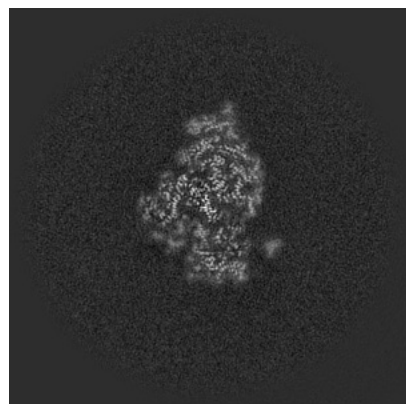


Z Index: 300

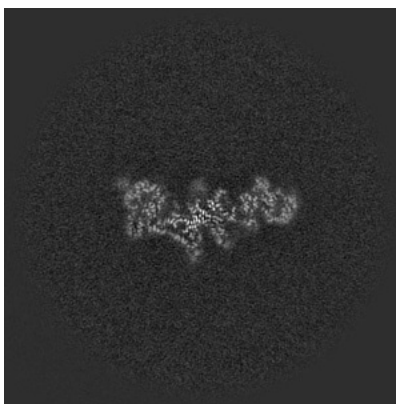
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

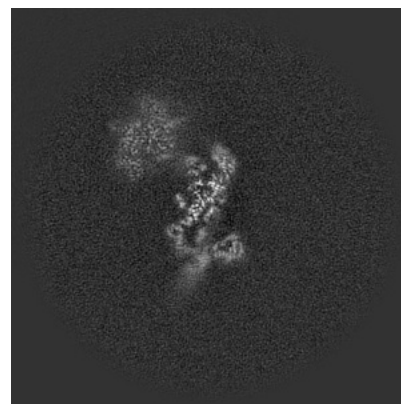
6.3.1 Primary map



X Index: 295



Y Index: 302

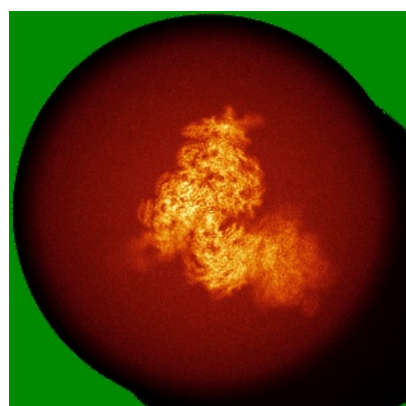


Z Index: 257

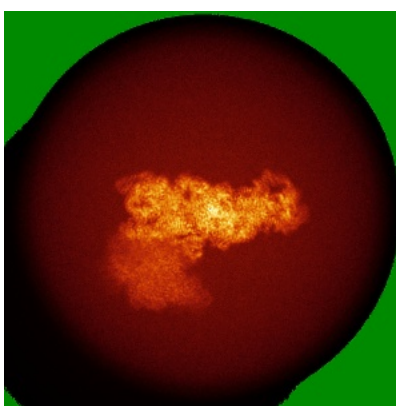
The images above show the largest variance slices of the map in three orthogonal directions.

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

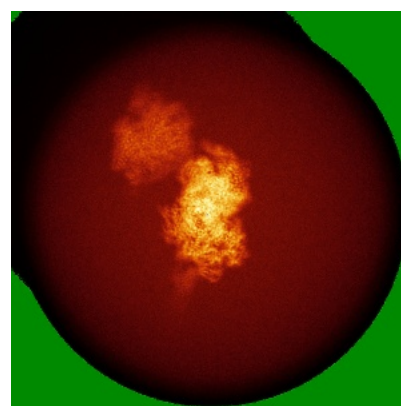
6.4.1 Primary map



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 [i](#)

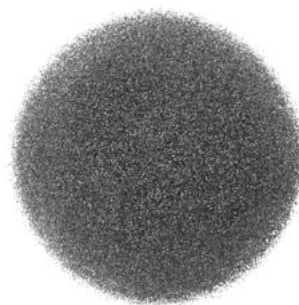
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.303. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

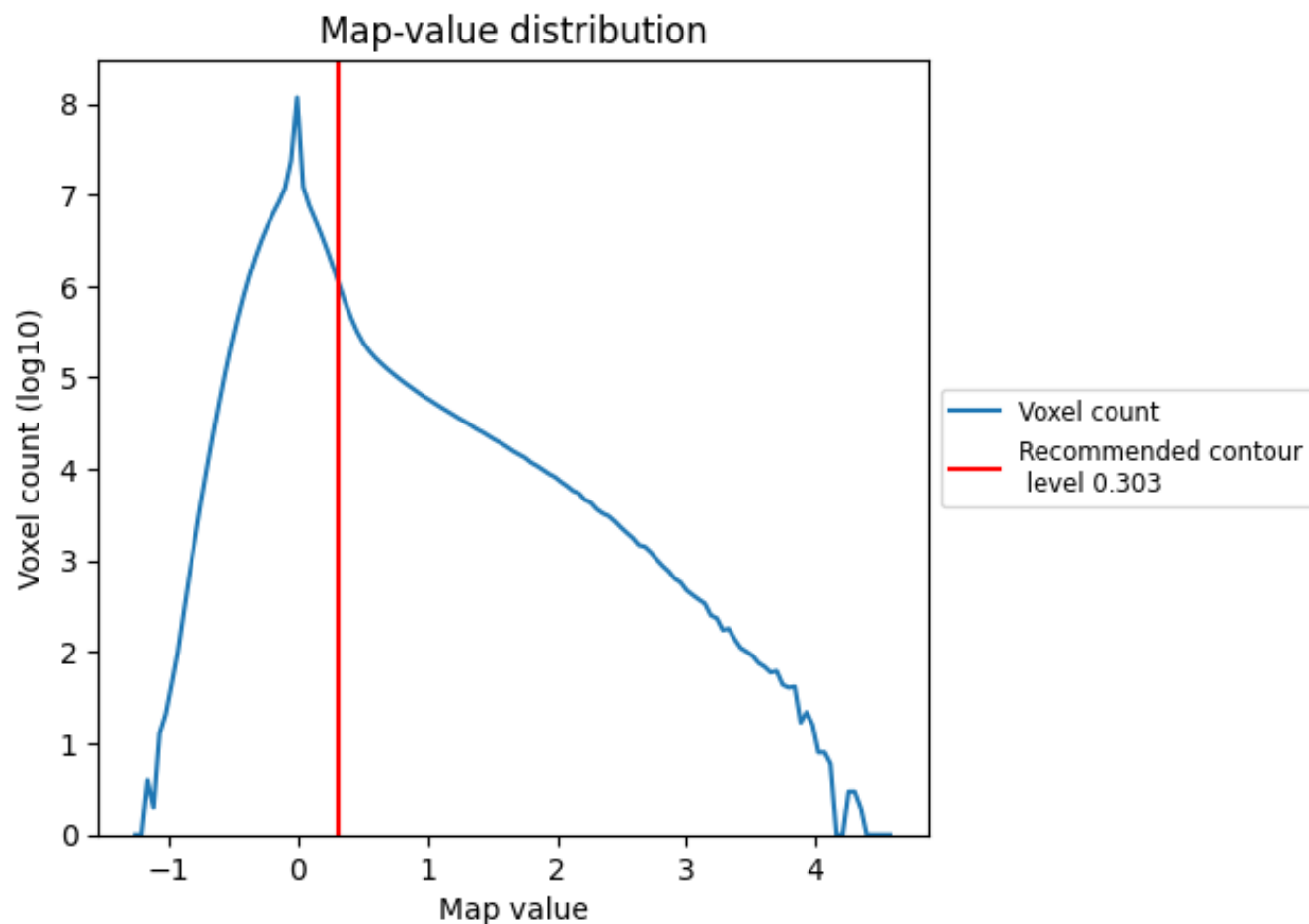
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

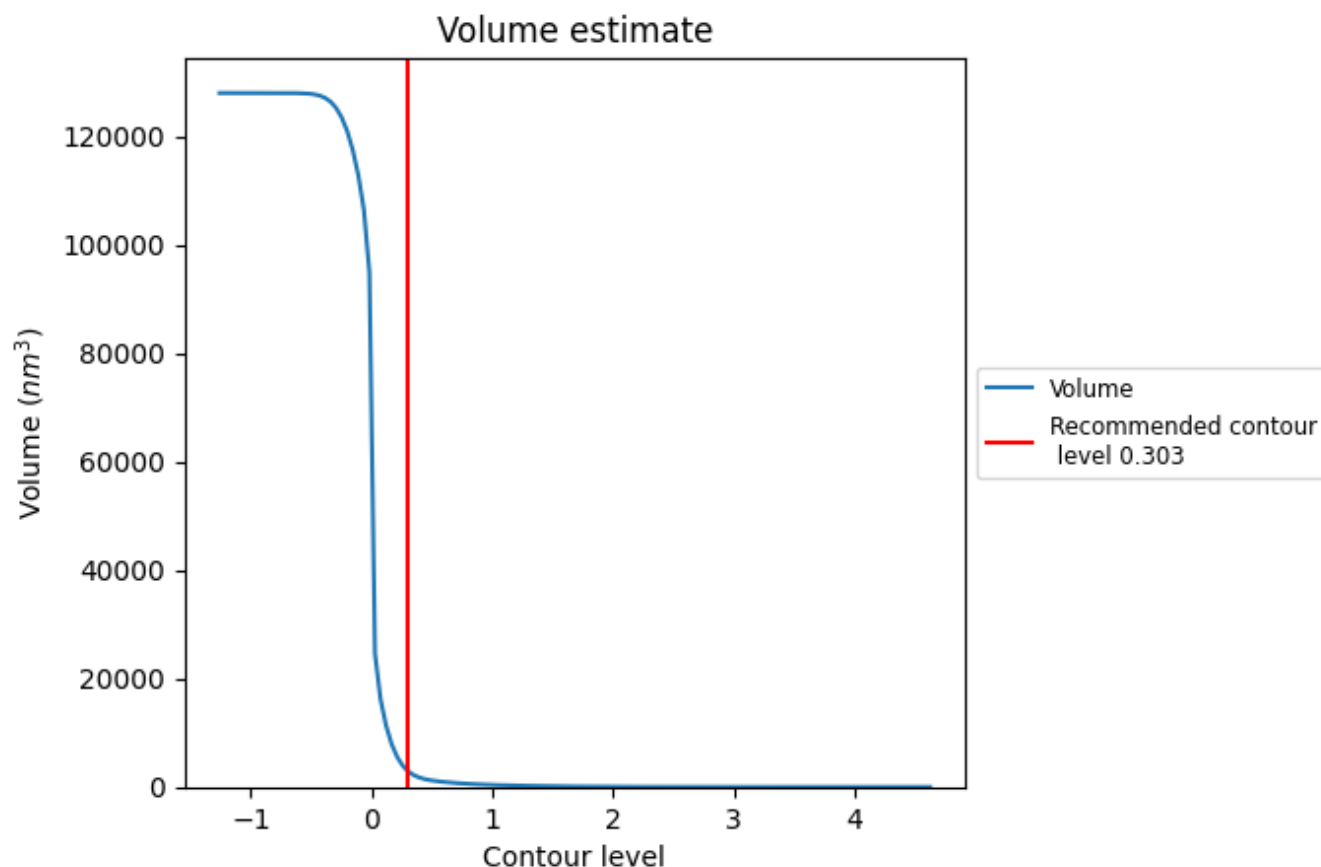
This section contains the results of statistical analysis of the map.

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.

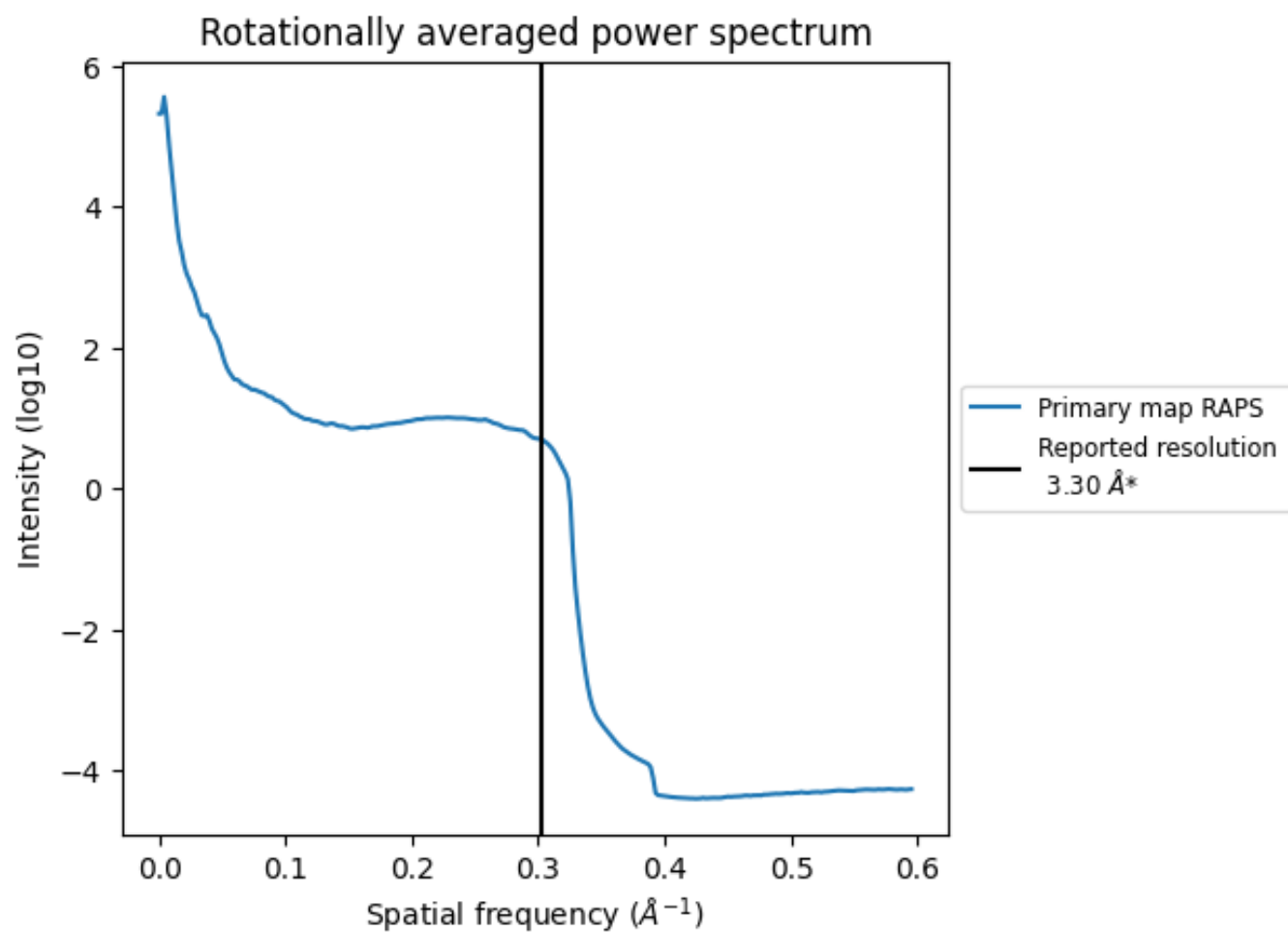
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2883 nm³; this corresponds to an approximate mass of 2604 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 0.303 Å⁻¹

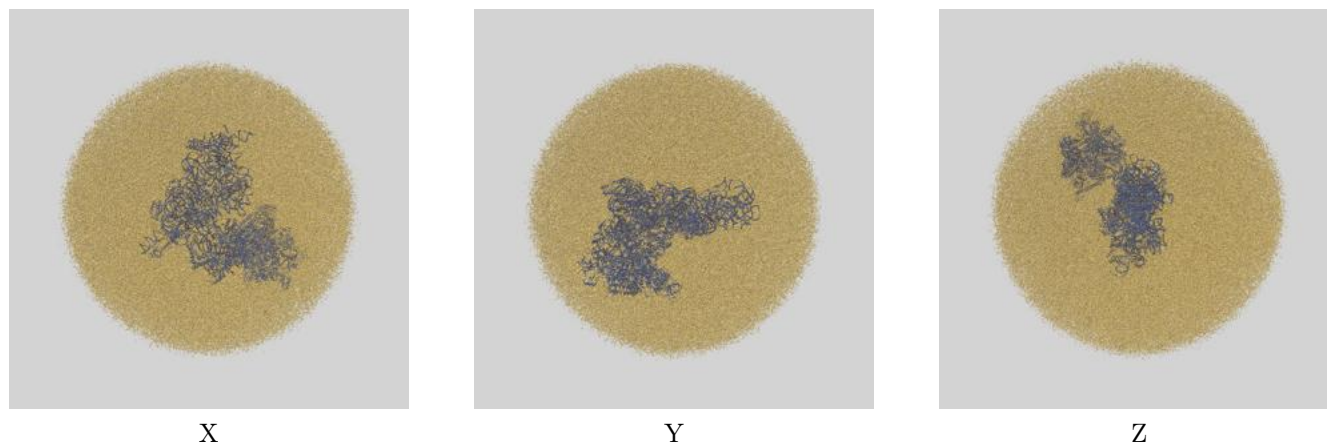
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

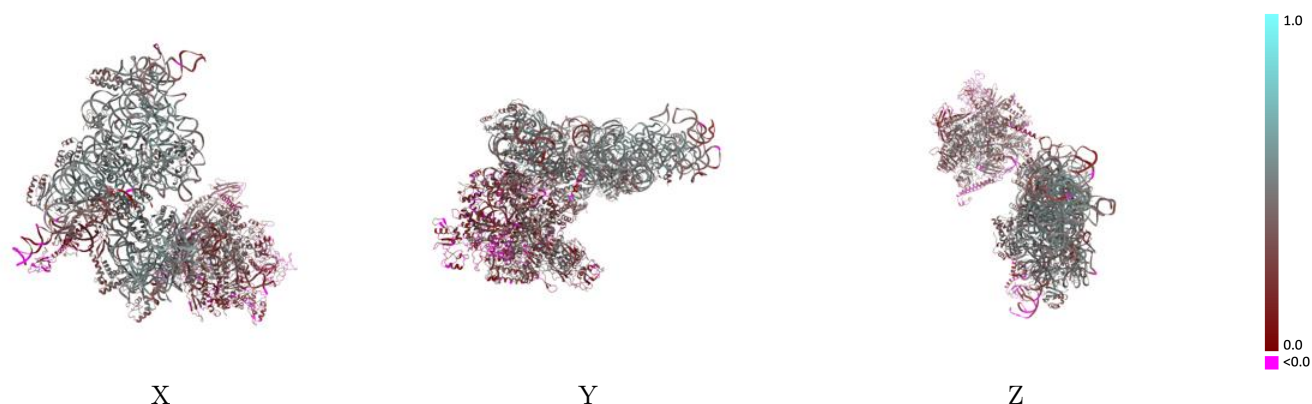
This section contains information regarding the fit between EMDB map EMD-51623 and PDB model 9GUX. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



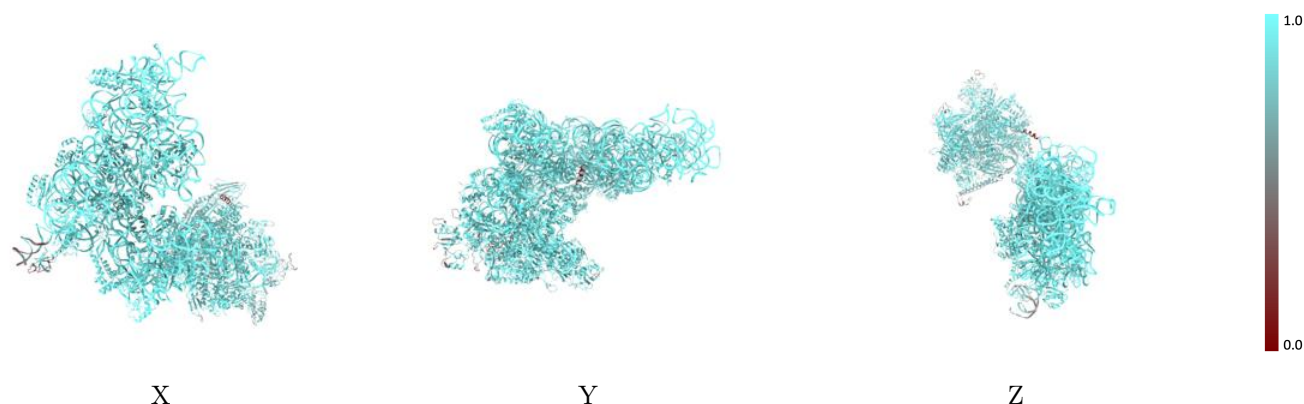
The images above show the 3D surface view of the map at the recommended contour level 0.303 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



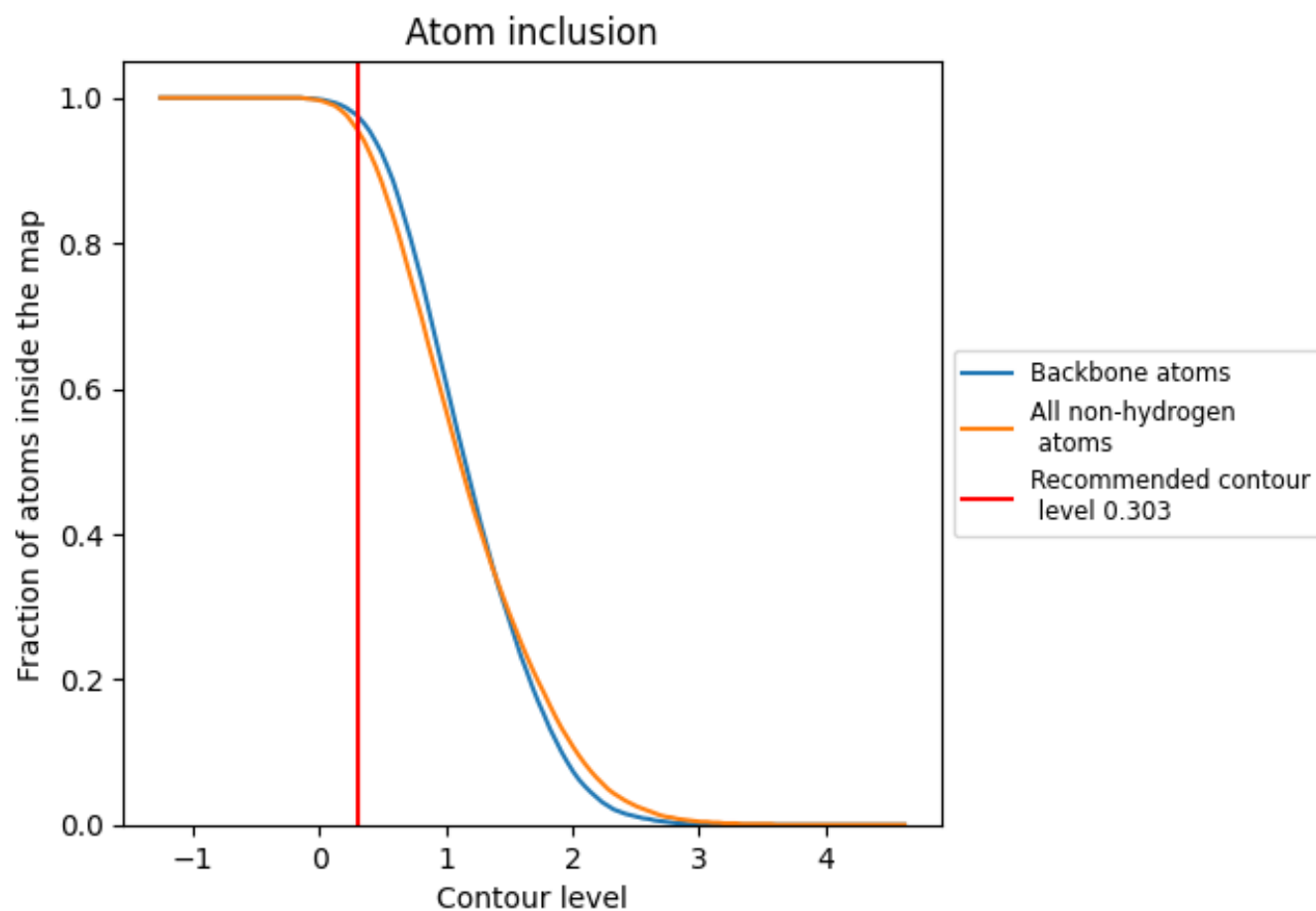
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.303).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.303) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9550	 0.3740
1	 0.8880	 0.3020
2	 0.8630	 0.2520
3	 0.9020	 0.2700
4	 0.9240	 0.2640
5	 0.8270	 0.2340
6	 0.9140	 0.1200
7	 0.9690	 0.2350
A	 0.9910	 0.4550
B	 0.8650	 0.1640
C	 0.9640	 0.4160
D	 0.9710	 0.4500
E	 0.9680	 0.4250
F	 0.9650	 0.4510
G	 0.9650	 0.4050
H	 0.9620	 0.3470
I	 0.9660	 0.4860
J	 0.9770	 0.4390
K	 0.9580	 0.3980
L	 0.9670	 0.3480
M	 0.9780	 0.4710
N	 0.9720	 0.3980
O	 0.9780	 0.4610
P	 0.9650	 0.4300
Q	 0.9710	 0.4670
R	 0.9700	 0.4280
S	 0.9750	 0.4600
T	 0.9820	 0.4590
U	 0.9760	 0.4110
V	 0.9550	 0.3820
X	 0.9410	 0.1920
Z	 0.9230	 0.1710

