



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 01:19 AM UTC

PDB ID : 6AWD / pdb_00006awd
EMDB ID : EMD-7016
Title : Structure of 30S (S1 depleted) ribosomal subunit and RNA polymerase complex
Authors : Demo, G.; Rasouly, A.; Vasilyev, N.; Loveland, A.B.; Diaz-Avalos, R.; Grigorieff, N.; Nudler, E.; Korostelev, A.A.
Deposited on : 2017-09-05
Resolution : 8.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

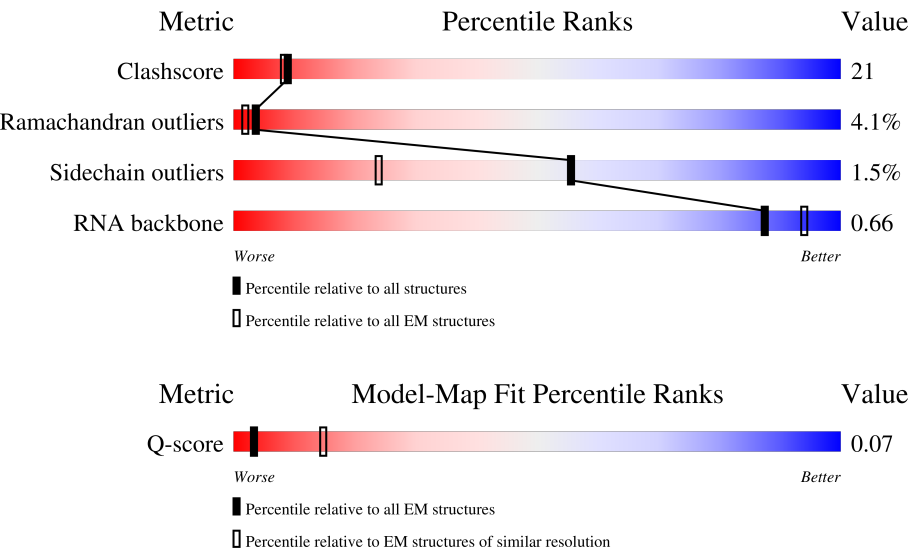
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 8.10 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	342 (7.60 - 8.60)

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	1539	
2	01	229	
2	02	229	

Continued on next page...

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Mol	Chain	Length	Quality of chain
3	03	1340	
4	04	1369	
5	05	59	
6	E	218	
7	F	206	
8	G	205	
9	H	157	
10	I	100	
11	J	151	
12	K	129	
13	L	127	
14	M	98	
15	N	116	
16	O	123	
17	P	114	
18	Q	100	
19	R	88	
20	S	82	
21	T	80	
22	U	65	
23	V	79	
24	W	85	
25	X	65	

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 76452 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	01	227	Total	C	N	O	S	0	0
			1753	1091	311	345	6		
2	02	227	Total	C	N	O	S	0	0
			1757	1094	311	346	6		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	03	1327	Total	C	N	O	S	0	0
			10272	6441	1787	2001	43		

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	04	1345	Total	C	N	O	S	0	0
			10372	6508	1853	1962	49		

- Molecule 5 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	05	59	Total	C	N	O	S	0	0
			458	283	86	88	1		

- Molecule 6 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 7 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 8 is a protein called 30S ribosomal protein S4.

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

- Molecule 9 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 10 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 11 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 12 is a protein called 30S ribosomal protein S8.

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

- Molecule 13 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 14 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 15 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 16 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 17 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 18 is a protein called 30S ribosomal protein S14.

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

- Molecule 19 is a protein called 30S ribosomal protein S15.

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

- Molecule 20 is a protein called 30S ribosomal protein S16.

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

- Molecule 21 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 22 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 23 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 24 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

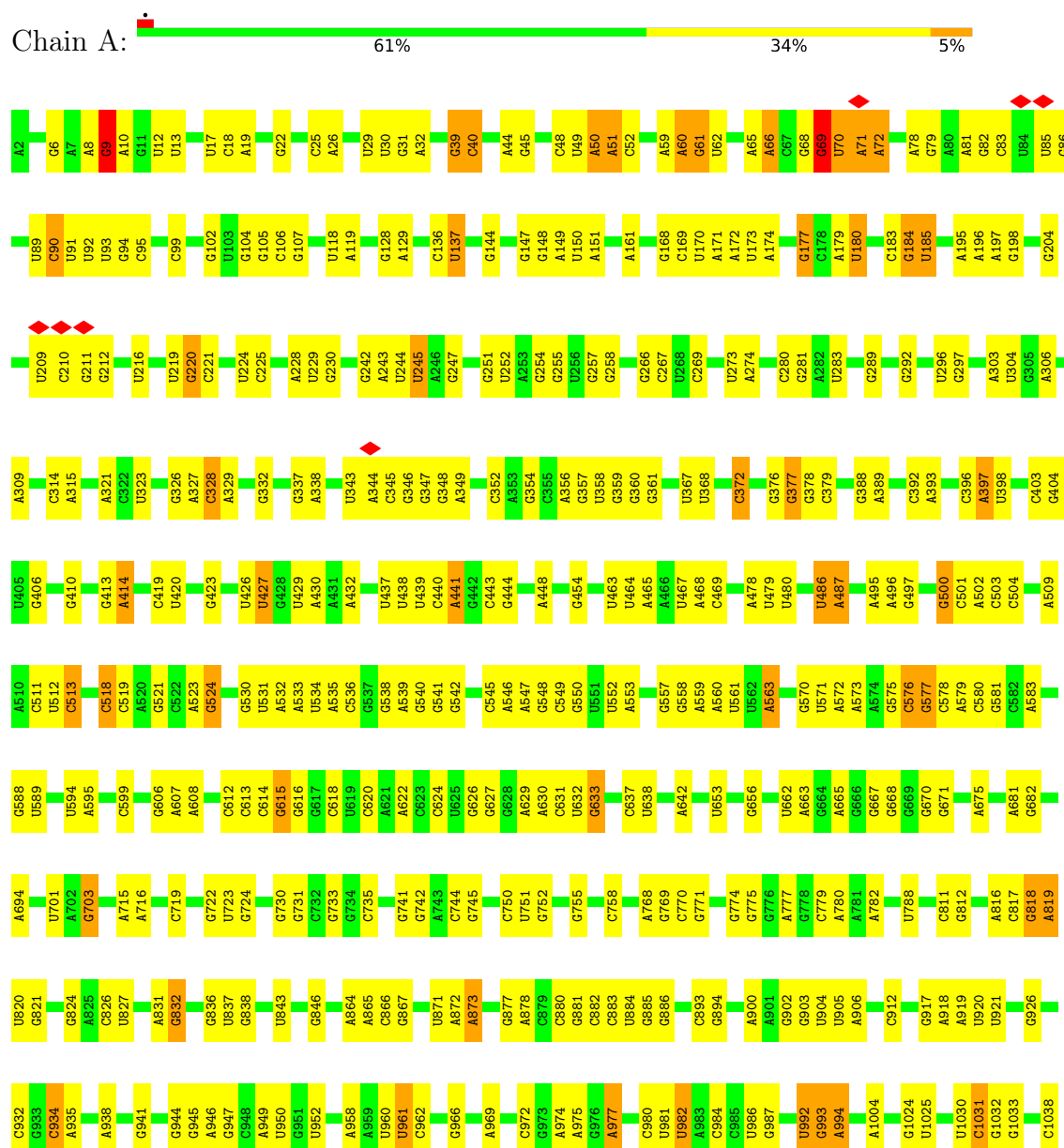
- Molecule 25 is a protein called 30S ribosomal protein S21.

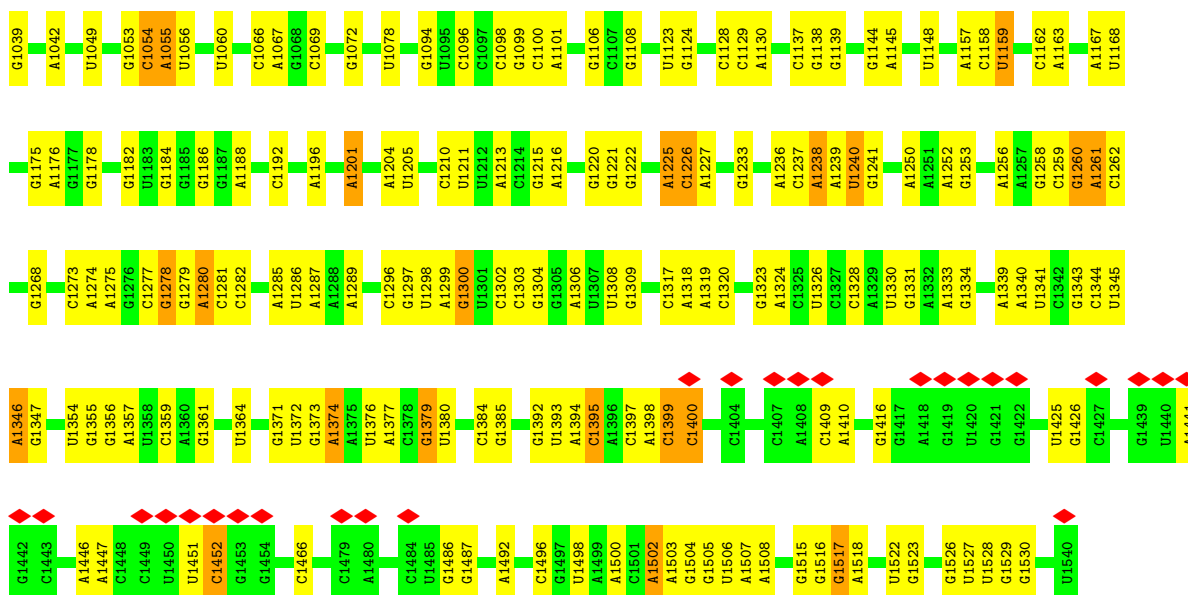
Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

3 Residue-property plots

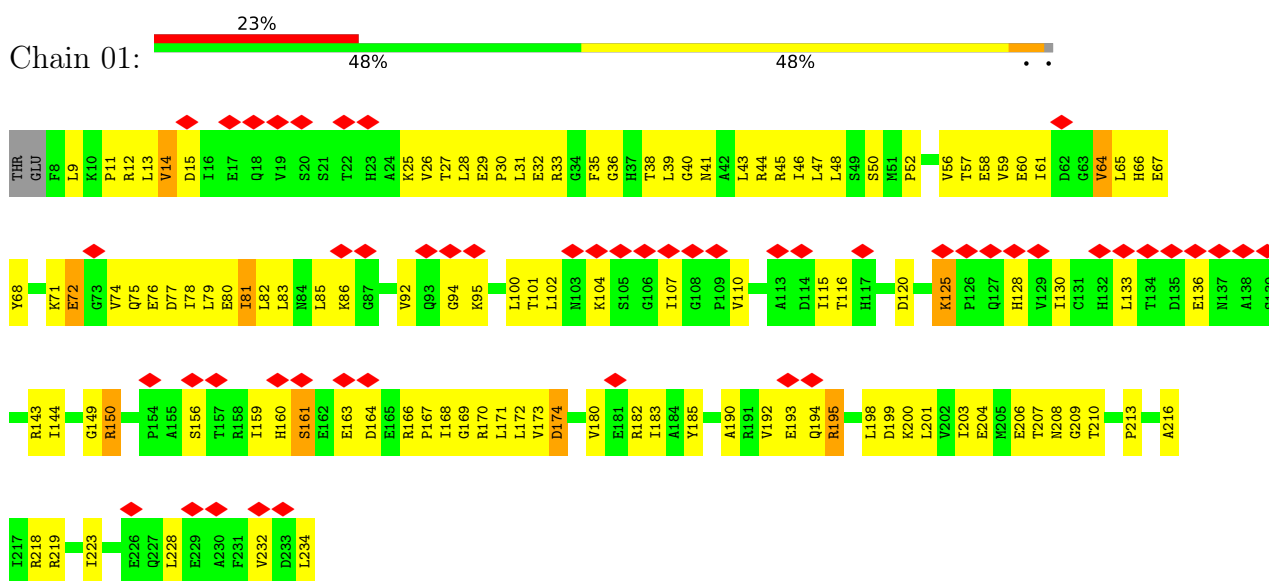
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S rRNA

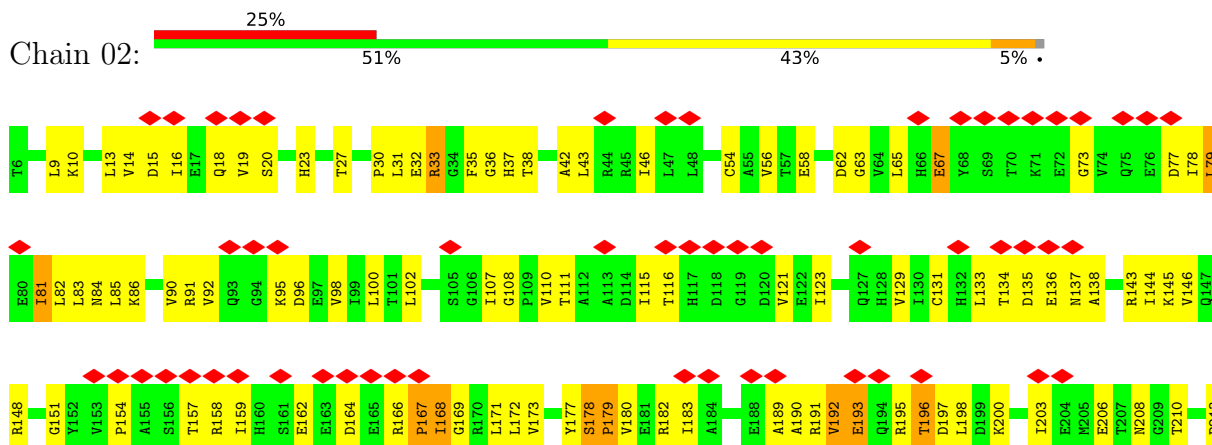




• Molecule 2: DNA-directed RNA polymerase subunit alpha

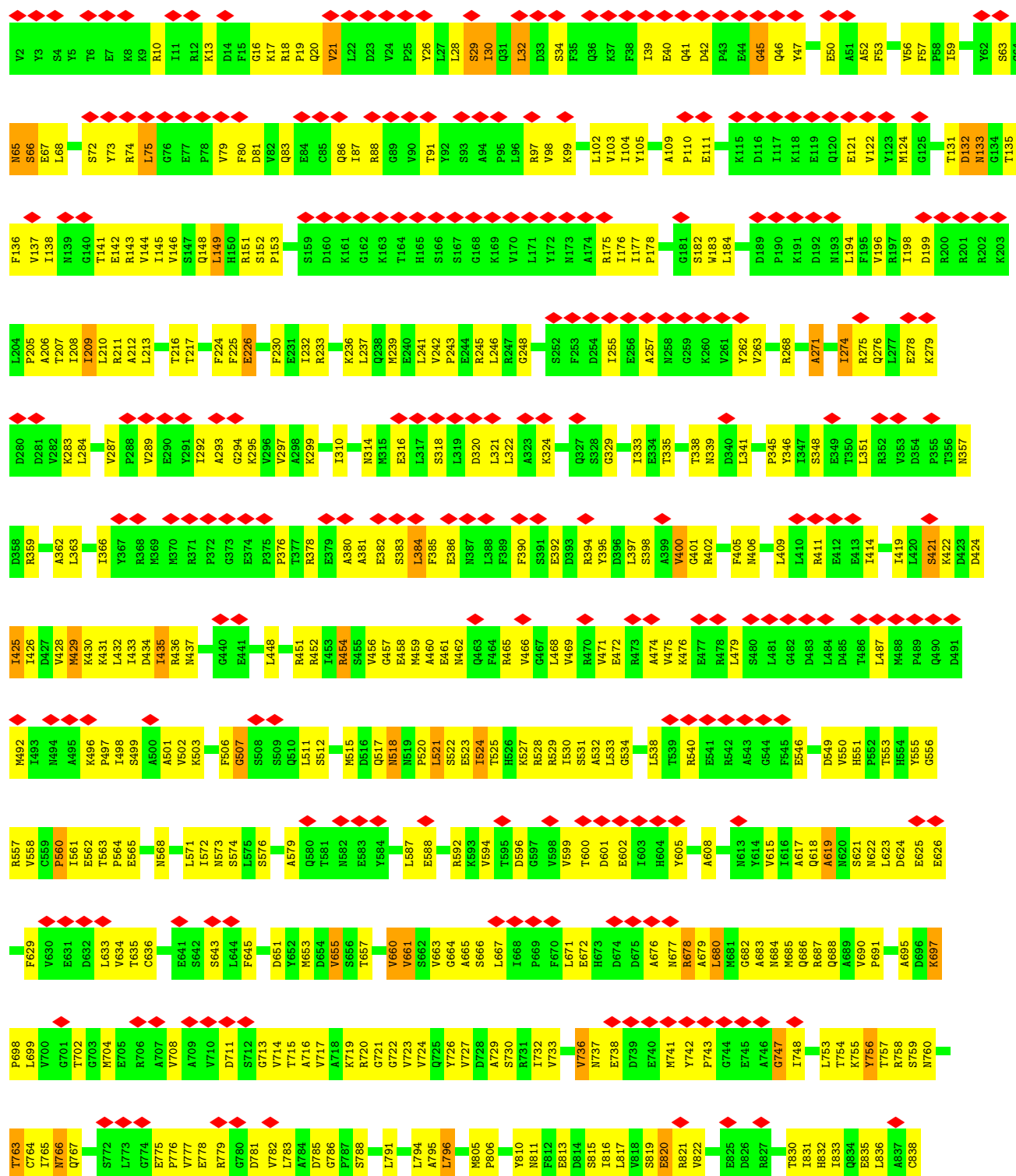


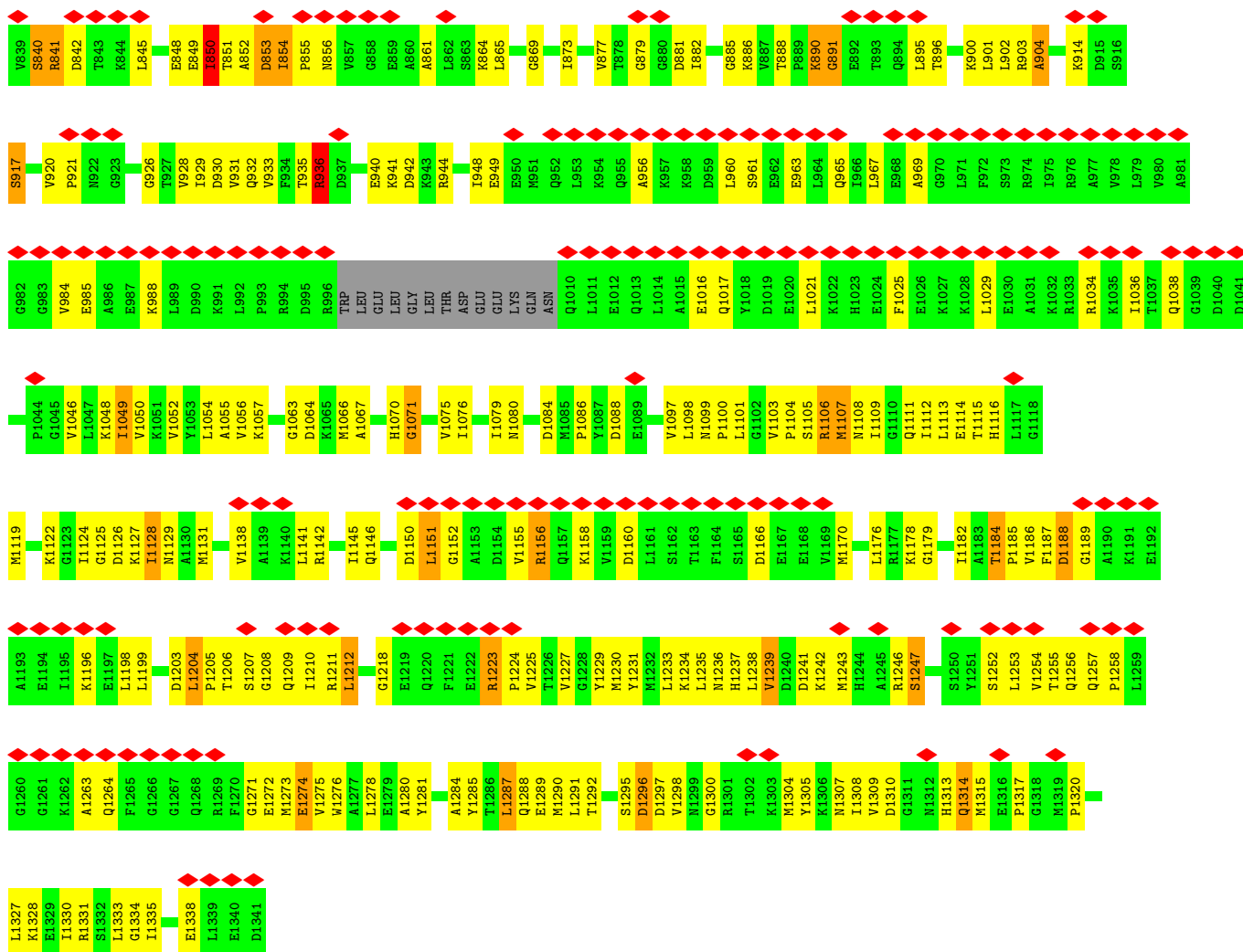
• Molecule 2: DNA-directed RNA polymerase subunit alpha

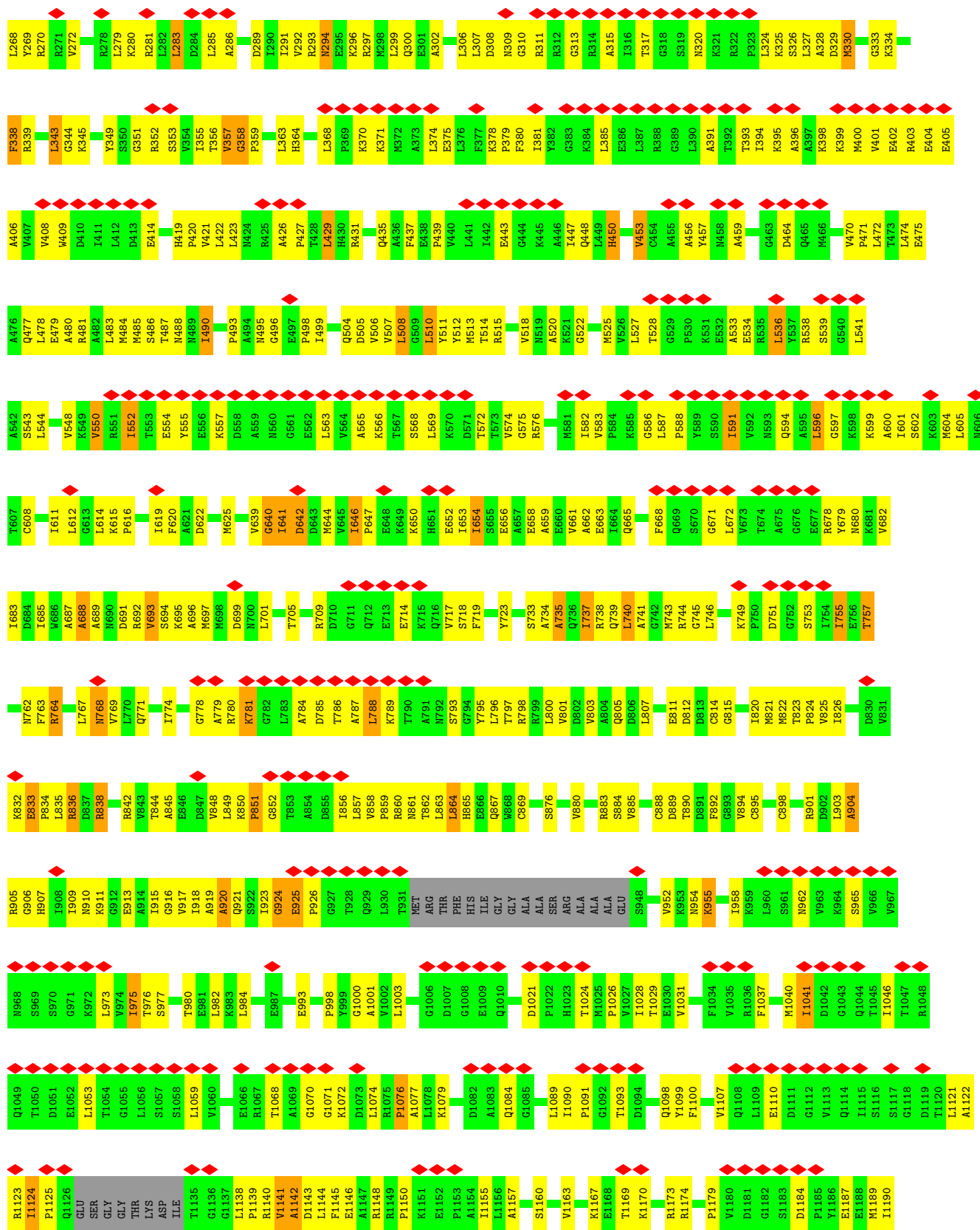


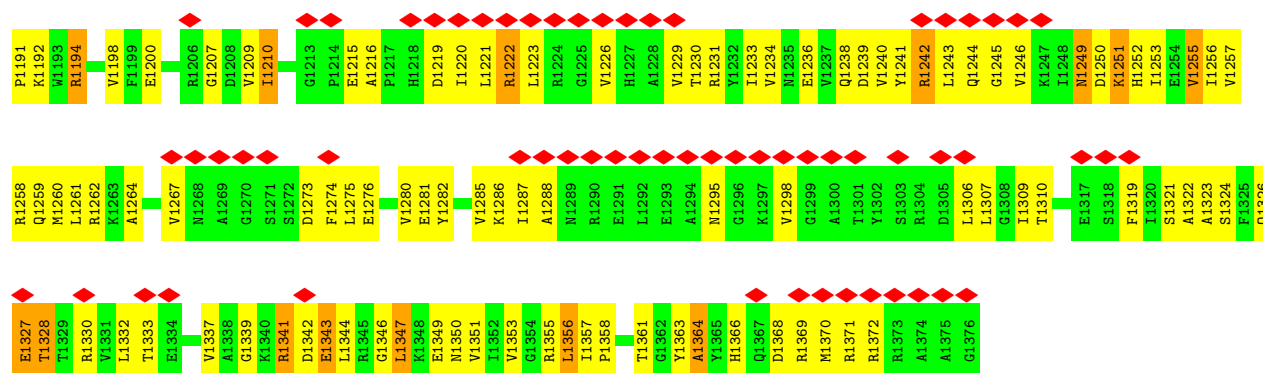


• Molecule 3: DNA-directed RNA polymerase subunit beta

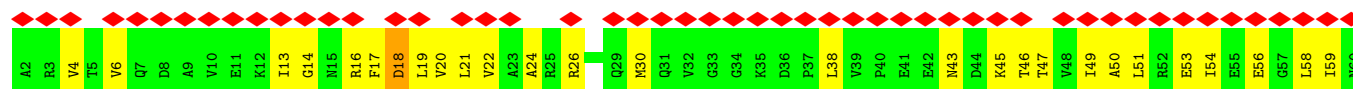
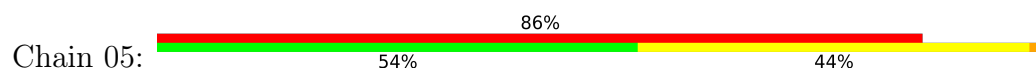




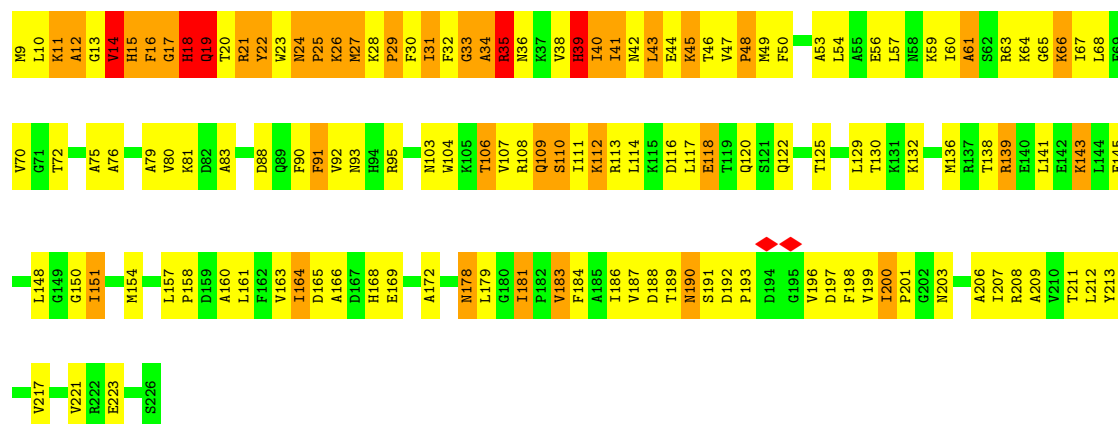




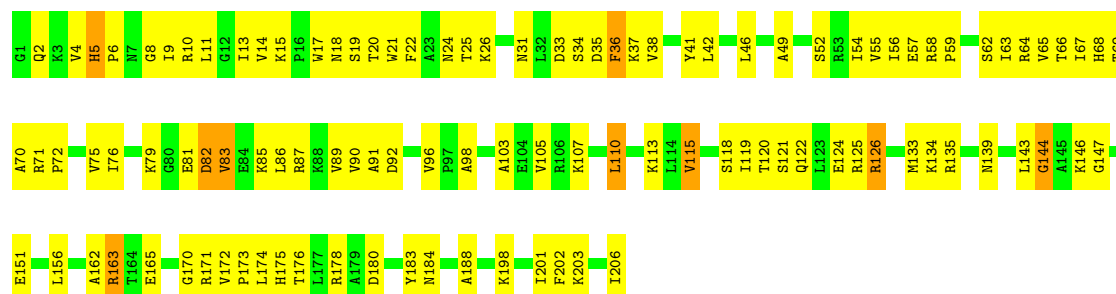
• Molecule 5: DNA-directed RNA polymerase subunit omega



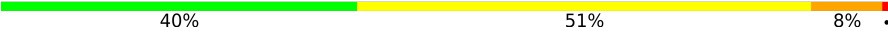
• Molecule 6: 30S ribosomal protein S2

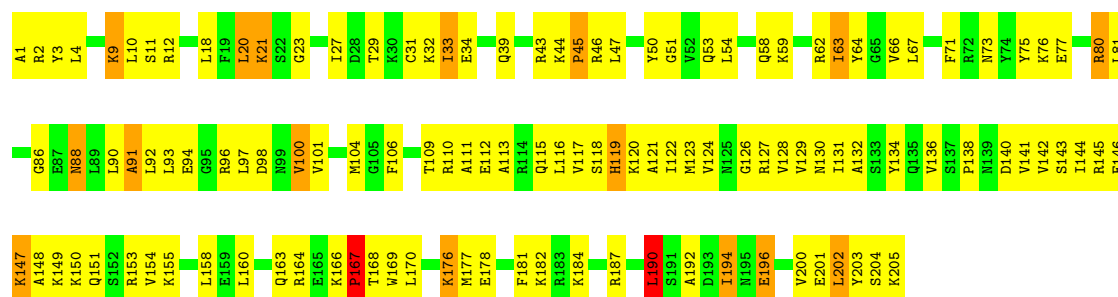


• Molecule 7: 30S ribosomal protein S3



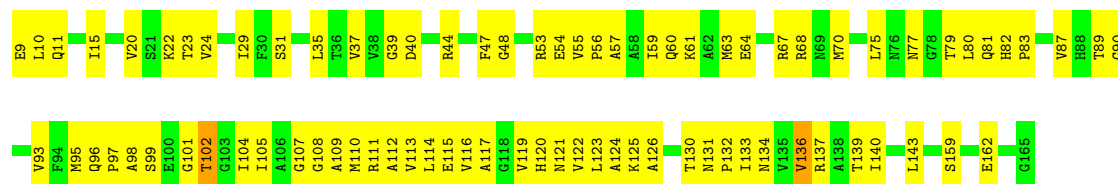
• Molecule 8: 30S ribosomal protein S4

Chain G: 



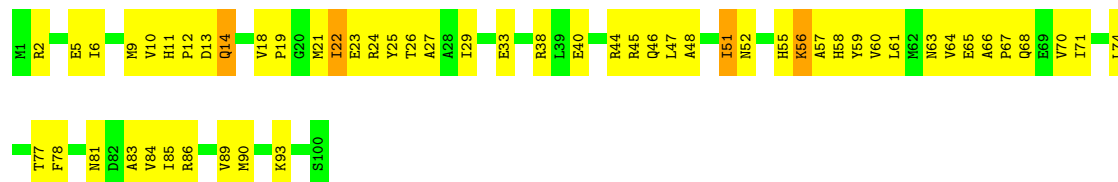
• Molecule 9: 30S ribosomal protein S5

Chain H: 



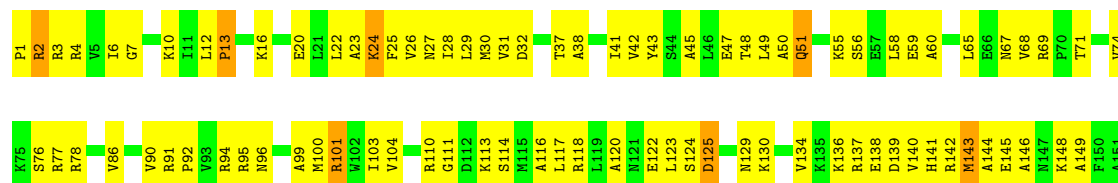
• Molecule 10: 30S ribosomal protein S6

Chain I: 

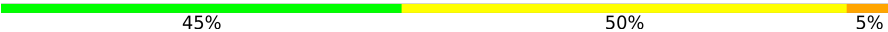


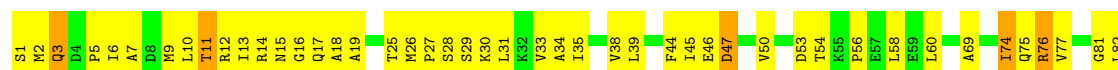
• Molecule 11: 30S ribosomal protein S7

Chain J: 



• Molecule 12: 30S ribosomal protein S8

Chain K: 





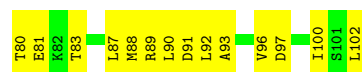
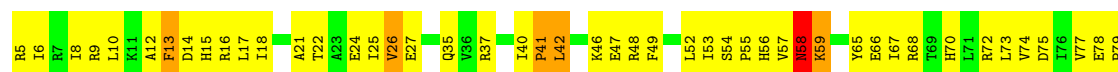
• Molecule 13: 30S ribosomal protein S9

Chain L: 47% 46% 6%



• Molecule 14: 30S ribosomal protein S10

Chain M: 38% 56% 5%



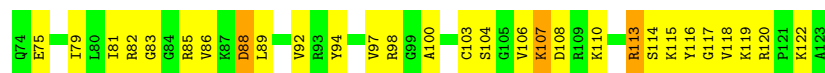
• Molecule 15: 30S ribosomal protein S11

Chain N: 47% 47% 7%



• Molecule 16: 30S ribosomal protein S12

Chain O: 46% 50%



• Molecule 17: 30S ribosomal protein S13

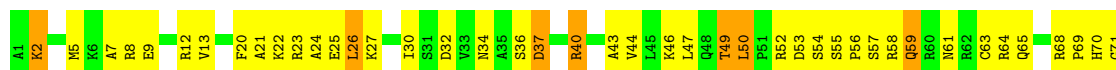
Chain P: 45% 49% 6%





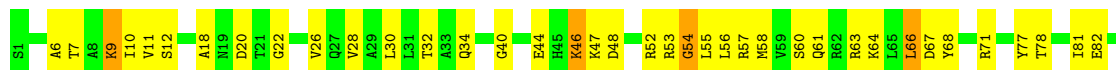
- Molecule 18: 30S ribosomal protein S14

Chain Q: 41% 51% 8%



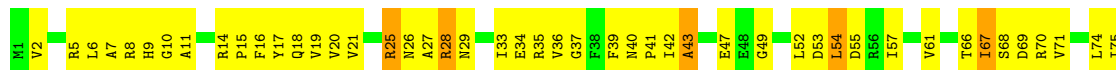
- Molecule 19: 30S ribosomal protein S15

Chain R: 52% 42% 6%



- Molecule 20: 30S ribosomal protein S16

Chain S: 39% 54% 7%



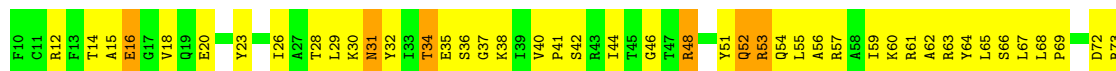
- Molecule 21: 30S ribosomal protein S17

Chain T: 58% 40% 2%

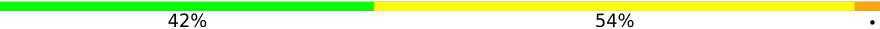


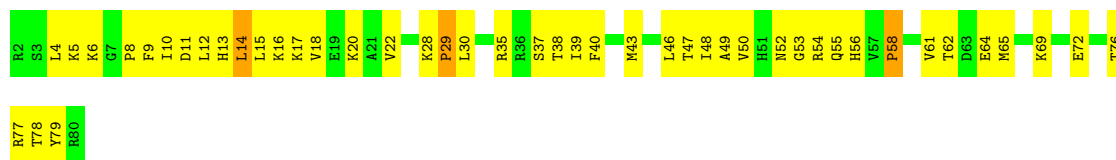
- Molecule 22: 30S ribosomal protein S18

Chain U: 32% 58% 9%

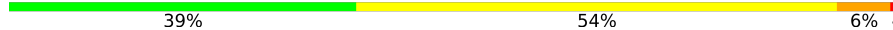


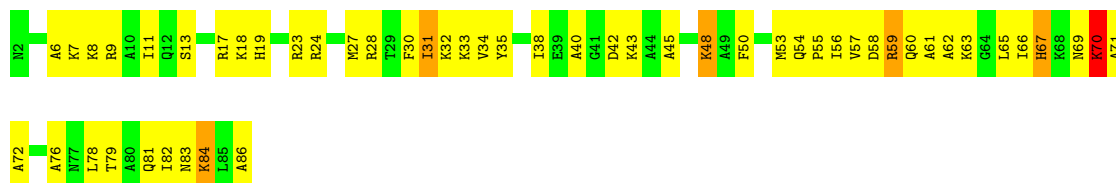
- Molecule 23: 30S ribosomal protein S19

Chain V:  42% 54% .



- Molecule 24: 30S ribosomal protein S20

Chain W:  39% 54% 6% .



- Molecule 25: 30S ribosomal protein S21

Chain X:  5% 57% 32% 8% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21123	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.0	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	22000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	13.228	Depositor
Minimum map value	-3.576	Depositor
Average map value	-0.054	Depositor
Map value standard deviation	0.680	Depositor
Recommended contour level	2	Depositor
Map size (Å)	528.64, 528.64, 528.64	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.888, 1.888, 1.888	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.40	0/36963	0.49	2/57662 (0.0%)
2	01	0.31	0/1774	0.98	7/2405 (0.3%)
2	02	0.31	0/1779	0.95	7/2411 (0.3%)
3	03	0.34	0/10433	1.05	71/14101 (0.5%)
4	04	0.35	0/10528	1.06	96/14224 (0.7%)
5	05	0.31	0/460	0.95	2/620 (0.3%)
6	E	0.43	0/1736	1.36	35/2338 (1.5%)
7	F	0.28	0/1652	1.03	13/2225 (0.6%)
8	G	0.30	0/1665	1.09	18/2227 (0.8%)
9	H	0.31	0/1170	0.94	4/1573 (0.3%)
10	I	0.31	0/836	1.01	5/1128 (0.4%)
11	J	0.31	0/1196	1.04	11/1602 (0.7%)
12	K	0.34	0/989	1.06	6/1326 (0.5%)
13	L	0.30	0/1034	0.96	5/1375 (0.4%)
14	M	0.34	0/797	1.10	5/1077 (0.5%)
15	N	0.35	0/886	1.18	11/1195 (0.9%)
16	O	0.33	0/969	1.12	13/1300 (1.0%)
17	P	0.33	0/893	1.13	9/1193 (0.8%)
18	Q	0.34	0/817	1.10	6/1088 (0.6%)
19	R	0.29	0/722	1.07	8/964 (0.8%)
20	S	0.38	0/659	1.01	5/884 (0.6%)
21	T	0.37	0/658	1.07	3/881 (0.3%)
22	U	0.31	0/545	1.19	11/731 (1.5%)
23	V	0.33	0/653	1.01	2/877 (0.2%)
24	W	0.34	0/671	1.24	11/888 (1.2%)
25	X	0.42	0/551	1.10	3/728 (0.4%)
All	All	0.37	0/81036	0.83	369/117023 (0.3%)

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
1	A	0	3

There are no bond length outliers.

All (369) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	26	LYS	N-CA-C	-21.74	87.66	111.36
2	01	81	ILE	N-CA-C	-10.79	99.24	111.00
6	E	197	ASP	N-CA-C	-10.21	100.35	113.12
4	04	768	ASN	N-CA-C	10.16	124.56	110.24
3	03	209	ILE	N-CA-C	-10.05	103.76	111.90
18	Q	49	THR	N-CA-C	-10.00	99.63	112.23
12	K	16	GLY	N-CA-C	-9.73	102.59	114.66
15	N	115	ILE	N-CA-C	9.62	117.67	108.15
3	03	385	PHE	N-CA-C	9.58	122.61	111.11
3	03	697	LYS	N-CA-C	9.48	121.69	109.93
7	F	110	LEU	N-CA-C	-9.45	101.52	113.43
6	E	166	ALA	N-CA-C	-9.25	102.81	114.56
2	02	36	GLY	N-CA-C	-9.06	103.44	115.32
4	04	764	ARG	N-CA-C	-9.05	101.05	112.90
3	03	896	THR	CA-C-N	9.03	128.63	119.24
3	03	896	THR	C-N-CA	9.03	128.63	119.24
3	03	574	SER	N-CA-C	9.03	121.98	110.24
4	04	245	LEU	CA-C-N	8.94	129.59	120.38
4	04	245	LEU	C-N-CA	8.94	129.59	120.38
6	E	24	ASN	CA-C-N	8.91	130.98	119.84
6	E	24	ASN	C-N-CA	8.91	130.98	119.84
4	04	99	ARG	N-CA-C	-8.80	103.12	114.04
6	E	108	ARG	N-CA-C	-8.80	101.98	112.89
4	04	1222	ARG	N-CA-C	8.79	120.47	111.07
14	M	59	LYS	N-CA-C	8.77	120.45	111.07
6	E	181	ILE	N-CA-C	8.59	118.33	108.96
8	G	50	TYR	N-CA-C	-8.48	103.45	113.88
8	G	21	LYS	N-CA-C	-8.38	100.90	112.30
15	N	75	GLU	N-CA-C	-8.33	102.56	112.89
3	03	274	ILE	N-CA-C	-8.32	102.70	110.53
3	03	840	SER	N-CA-C	8.25	122.65	109.86
3	03	1128	ILE	N-CA-C	-8.17	102.47	110.72
19	R	66	LEU	N-CA-C	-8.17	101.94	112.23
3	03	474	ALA	N-CA-C	-8.07	104.59	114.75
7	F	115	VAL	N-CA-C	-8.03	105.39	111.90
2	01	174	ASP	N-CA-C	8.01	121.90	109.96
4	04	215	LYS	N-CA-C	-8.01	102.63	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	I	22	ILE	N-CA-C	-8.00	102.64	110.72
7	F	36	PHE	N-CA-C	-7.93	104.12	113.88
14	M	58	ASN	N-CA-C	-7.88	94.01	110.80
18	Q	40	ARG	N-CA-C	-7.88	102.30	112.23
7	F	82	ASP	N-CA-C	-7.85	103.49	113.23
24	W	59	ARG	N-CA-C	-7.83	103.86	113.41
19	R	20	ASP	N-CA-C	-7.82	97.70	109.83
6	E	32	PHE	N-CA-C	-7.79	100.64	111.39
8	G	119	HIS	N-CA-C	-7.78	103.85	112.72
4	04	1267	VAL	N-CA-C	7.77	117.72	110.42
4	04	228	VAL	N-CA-C	-7.71	103.28	110.53
3	03	1186	VAL	N-CA-C	7.71	118.25	110.23
4	04	838	ARG	N-CA-C	-7.60	104.91	114.56
2	01	65	LEU	N-CA-C	-7.55	102.40	111.69
19	R	58	MET	N-CA-C	7.49	120.32	111.71
4	04	330	MET	N-CA-C	-7.44	104.20	113.28
24	W	70	LYS	N-CA-C	-7.40	103.15	111.14
4	04	358	GLY	CA-C-N	7.39	127.75	119.32
4	04	358	GLY	C-N-CA	7.39	127.75	119.32
16	O	115	LYS	N-CA-C	-7.33	100.37	110.35
3	03	935	THR	N-CA-C	7.32	120.90	110.14
6	E	79	ALA	N-CA-C	-7.25	103.91	112.89
3	03	511	LEU	N-CA-C	-7.24	104.31	113.43
8	G	176	LYS	N-CA-C	-7.23	104.49	113.38
4	04	642	ASP	N-CA-C	7.22	126.19	110.80
2	02	192	VAL	N-CA-C	-7.21	97.72	108.46
17	P	70	ARG	N-CA-C	-7.16	103.08	111.03
6	E	103	ASN	N-CA-C	-7.16	102.57	112.30
11	J	50	ALA	N-CA-C	-7.15	104.02	112.89
3	03	1184	THR	CA-C-N	7.15	127.41	119.90
3	03	1184	THR	C-N-CA	7.15	127.41	119.90
22	U	52	GLN	N-CA-C	-7.14	104.54	113.18
2	02	84	ASN	N-CA-C	-7.12	103.56	111.82
24	W	18	LYS	N-CA-C	7.10	119.68	111.02
24	W	33	LYS	N-CA-C	-7.05	103.64	111.82
24	W	61	ALA	N-CA-C	-7.01	104.37	114.12
3	03	661	VAL	N-CA-C	6.97	118.86	108.96
8	G	202	LEU	N-CA-C	-6.91	103.36	111.03
13	L	96	GLU	N-CA-C	-6.89	103.55	112.23
2	02	67	GLU	N-CA-C	6.89	121.14	112.87
3	03	32	LEU	N-CA-C	6.88	118.78	111.28
1	A	69	G	C2'-C3'-O3'	6.87	119.81	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	109	GLN	N-CA-C	-6.86	104.38	112.89
22	U	18	VAL	N-CA-C	6.84	118.40	109.58
4	04	140	TYR	N-CA-C	-6.83	103.37	113.61
4	04	1364	ALA	N-CA-C	-6.82	103.78	111.07
18	Q	50	LEU	N-CA-C	-6.81	101.18	109.83
4	04	194	LEU	N-CA-C	6.77	119.24	111.11
3	03	1084	ASP	N-CA-C	-6.75	104.78	113.16
3	03	21	VAL	N-CA-C	-6.74	106.93	113.53
6	E	209	ALA	N-CA-C	-6.71	103.58	111.03
22	U	55	LEU	N-CA-C	-6.71	104.57	112.89
7	F	85	LYS	N-CA-C	-6.70	103.80	112.23
4	04	1243	LEU	N-CA-C	-6.69	105.08	113.18
4	04	668	PHE	N-CA-C	-6.67	104.78	113.12
4	04	294	ASN	N-CA-C	-6.67	103.49	111.69
3	03	1088	ASP	N-CA-C	6.66	117.27	108.07
17	P	104	ASN	N-CA-C	6.64	115.13	108.75
3	03	132	ASP	N-CA-C	-6.63	104.45	112.54
24	W	48	LYS	N-CA-C	-6.62	104.84	113.12
4	04	920	ALA	N-CA-C	-6.62	104.06	111.28
22	U	34	THR	N-CA-C	-6.61	99.82	110.32
3	03	854	ILE	CA-C-N	6.59	126.35	119.76
3	03	854	ILE	C-N-CA	6.59	126.35	119.76
4	04	115	TRP	N-CA-C	6.58	119.01	111.11
22	U	53	ARG	N-CA-C	-6.55	105.44	113.50
19	R	87	ARG	N-CA-C	-6.54	102.62	112.04
6	E	118	GLU	N-CA-C	-6.53	104.16	111.28
3	03	969	ALA	N-CA-C	-6.52	104.26	111.82
17	P	29	SER	N-CA-C	-6.52	104.26	111.36
6	E	15	HIS	N-CA-C	6.51	120.94	113.19
8	G	147	LYS	N-CA-C	-6.49	104.29	111.82
3	03	619	ALA	N-CA-C	-6.49	105.37	113.28
4	04	450	HIS	CA-C-N	6.49	126.71	119.32
4	04	450	HIS	C-N-CA	6.49	126.71	119.32
16	O	75	GLU	N-CA-C	-6.48	105.53	113.50
16	O	113	ARG	N-CA-C	-6.47	105.54	113.50
4	04	833	GLU	CA-C-N	6.47	127.36	120.11
4	04	833	GLU	C-N-CA	6.47	127.36	120.11
6	E	183	VAL	N-CA-C	6.45	116.92	107.37
10	I	85	ILE	N-CA-C	-6.44	106.52	112.96
21	T	14	ASP	N-CA-C	-6.43	104.59	112.88
5	05	18	ASP	N-CA-C	-6.43	104.70	112.54
8	G	88	ASN	N-CA-C	-6.41	104.56	112.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	N	125	LYS	N-CA-C	6.41	117.04	108.38
15	N	93	GLU	N-CA-C	-6.41	97.15	110.80
4	04	50	LYS	CA-C-N	6.41	127.41	119.98
4	04	50	LYS	C-N-CA	6.41	127.41	119.98
24	W	62	ALA	N-CA-C	-6.41	104.16	112.23
4	04	371	LYS	N-CA-C	6.40	118.25	111.28
3	03	226	GLU	N-CA-C	6.39	119.94	110.48
17	P	34	ALA	N-CA-C	-6.33	105.21	113.12
10	I	51	ILE	N-CA-C	6.32	112.98	106.21
4	04	222	LYS	N-CA-C	-6.31	104.40	111.28
24	W	30	PHE	N-CA-C	-6.30	105.08	112.89
24	W	63	LYS	N-CA-C	-6.29	105.57	113.18
7	F	125	ARG	N-CA-C	-6.29	105.55	113.72
3	03	680	LEU	N-CA-C	-6.28	104.36	111.14
17	P	96	VAL	N-CA-C	6.27	119.84	111.44
3	03	940	GLU	N-CA-C	6.25	119.11	110.35
4	04	737	ILE	N-CA-C	-6.25	104.40	110.72
19	R	46	LYS	N-CA-C	6.25	124.12	110.80
12	K	19	ALA	N-CA-C	-6.20	106.32	114.31
3	03	98	VAL	N-CA-C	6.17	117.36	108.48
24	W	31	ILE	N-CA-C	-6.15	103.20	111.44
11	J	74	VAL	N-CA-C	6.14	116.94	108.84
3	03	1225	VAL	N-CA-C	6.13	118.70	109.20
6	E	192	ASP	CA-C-N	6.13	125.75	119.56
6	E	192	ASP	C-N-CA	6.13	125.75	119.56
14	M	13	PHE	N-CA-C	-6.12	106.36	113.88
9	H	61	LYS	N-CA-C	-6.09	105.34	112.89
4	04	757	THR	CA-C-N	6.08	126.05	119.78
4	04	757	THR	C-N-CA	6.08	126.05	119.78
6	E	143	LYS	N-CA-C	6.08	117.99	111.36
16	O	81	ILE	N-CA-C	6.08	116.86	107.99
4	04	539	SER	N-CA-C	-6.08	106.19	113.97
20	S	77	GLU	N-CA-C	-6.08	105.36	112.89
4	04	250	ARG	CA-C-N	6.07	126.03	120.21
4	04	250	ARG	C-N-CA	6.07	126.03	120.21
4	04	270	ARG	N-CA-C	-6.06	104.59	111.07
8	G	9	LYS	N-CA-C	-6.06	105.38	112.89
3	03	1310	ASP	N-CA-C	-6.05	106.43	113.88
3	03	1106	ARG	N-CA-C	6.05	123.44	113.89
4	04	351	GLY	N-CA-C	6.05	122.34	111.03
4	04	640	GLY	N-CA-C	-6.03	103.89	112.81
11	J	149	ALA	N-CA-C	-6.03	105.59	113.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	J	143	MET	N-CA-C	-6.02	105.97	113.38
2	01	125	LYS	CA-C-N	6.01	126.44	119.47
2	01	125	LYS	C-N-CA	6.01	126.44	119.47
4	04	864	LEU	N-CA-C	6.01	117.80	109.15
23	V	76	THR	N-CA-C	-6.00	106.50	113.88
15	N	61	ALA	N-CA-C	-6.00	104.86	111.82
4	04	552	ILE	N-CA-C	5.99	117.99	108.89
16	O	122	LYS	N-CA-C	5.98	118.02	110.24
3	03	1204	LEU	CA-C-N	5.97	127.31	119.84
3	03	1204	LEU	C-N-CA	5.97	127.31	119.84
3	03	678	ARG	N-CA-C	-5.97	105.48	112.89
14	M	26	VAL	N-CA-C	-5.97	104.69	110.72
25	X	44	GLU	N-CA-C	5.97	119.66	112.38
4	04	550	VAL	N-CA-C	5.96	116.52	108.17
4	04	1142	ALA	N-CA-C	-5.95	104.71	111.14
2	02	179	PRO	N-CA-C	-5.94	108.50	114.68
4	04	924	GLY	N-CA-C	-5.93	106.41	115.66
4	04	1327	GLU	N-CA-C	5.93	118.97	108.24
12	K	74	ILE	N-CA-C	5.92	116.17	108.35
3	03	376	PRO	N-CA-C	5.91	120.50	111.34
3	03	524	ILE	N-CA-C	5.89	116.36	110.23
15	N	76	TYR	N-CA-C	-5.88	103.57	112.04
16	O	54	VAL	N-CA-C	5.88	117.80	108.87
4	04	904	ALA	N-CA-C	-5.86	104.97	111.71
7	F	5	HIS	CA-C-N	5.86	127.16	119.84
7	F	5	HIS	C-N-CA	5.86	127.16	119.84
4	04	1346	GLY	N-CA-C	5.83	118.85	111.85
4	04	470	VAL	N-CA-C	5.83	113.65	107.76
12	K	7	ALA	N-CA-C	-5.83	105.00	111.36
15	N	74	LYS	N-CA-C	-5.81	105.96	113.16
3	03	425	ILE	N-CA-C	-5.80	104.70	110.62
25	X	18	ARG	N-CA-C	5.80	117.29	110.97
21	T	80	LYS	N-CA-C	5.78	118.63	110.14
3	03	1212	LEU	N-CA-C	5.76	118.64	109.24
4	04	512	TYR	N-CA-C	-5.76	105.74	112.89
4	04	774	ILE	N-CA-C	-5.75	104.51	112.50
4	04	283	LEU	N-CA-C	-5.74	106.32	113.55
6	E	35	ARG	N-CA-C	5.73	118.91	109.85
16	O	120	ARG	N-CA-C	5.72	121.29	109.11
19	R	18	ALA	N-CA-C	-5.72	104.96	111.14
3	03	421	SER	N-CA-C	5.71	117.89	110.53
22	U	66	SER	N-CA-C	5.71	119.27	111.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	03	133	ASN	N-CA-C	-5.71	104.98	111.14
4	04	646	ILE	CA-C-N	5.69	125.45	119.76
4	04	646	ILE	C-N-CA	5.69	125.45	119.76
4	04	508	LEU	N-CA-C	-5.69	105.22	111.82
4	04	662	ALA	N-CA-C	-5.67	105.86	112.89
3	03	1274	GLU	N-CA-C	-5.66	105.87	112.89
11	J	124	SER	N-CA-C	-5.66	105.10	112.23
11	J	101	ARG	N-CA-C	-5.65	106.93	113.88
18	Q	37	ASP	N-CA-C	5.64	116.01	108.23
3	03	346	TYR	N-CA-C	5.63	117.87	111.11
3	03	268	ARG	N-CA-C	5.61	118.55	109.86
11	J	76	SER	N-CA-C	5.60	117.22	109.15
3	03	318	SER	N-CA-C	5.59	117.74	110.53
2	02	81	ILE	N-CA-C	-5.58	104.92	110.62
8	G	163	GLN	N-CA-C	-5.58	106.51	113.38
6	E	187	VAL	N-CA-C	5.58	120.95	109.34
4	04	233	LYS	CA-C-N	5.58	125.25	119.56
4	04	233	LYS	C-N-CA	5.58	125.25	119.56
4	04	740	LEU	N-CA-C	-5.57	105.78	113.18
15	N	56	LYS	N-CA-C	-5.56	105.76	112.54
4	04	1141	VAL	N-CA-C	-5.55	104.78	112.50
22	U	30	LYS	N-CA-C	-5.55	106.36	113.02
22	U	67	LEU	N-CA-C	-5.55	106.55	113.55
3	03	1156	ARG	N-CA-C	5.55	118.50	110.28
7	F	83	VAL	N-CA-C	-5.55	104.79	112.50
4	04	196	GLN	N-CA-C	-5.53	105.17	111.14
22	U	62	ALA	N-CA-C	-5.52	105.27	112.23
3	03	66	SER	N-CA-C	-5.52	103.40	111.30
4	04	1255	VAL	N-CA-C	-5.52	105.15	110.72
3	03	695	ALA	N-CA-C	5.51	117.72	108.23
4	04	975	ILE	N-CA-C	5.51	115.83	108.11
3	03	1247	SER	N-CA-C	-5.51	108.34	114.62
4	04	856	ILE	N-CA-C	5.51	116.19	109.30
8	G	168	THR	N-CA-C	-5.50	106.64	113.19
22	U	16	GLU	N-CA-C	-5.50	107.21	114.31
4	04	1242	ARG	N-CA-C	-5.49	105.32	112.23
3	03	855	PRO	N-CA-C	5.48	119.80	111.19
3	03	348	SER	N-CA-C	-5.48	105.86	112.54
16	O	9	LYS	CA-C-N	5.48	126.69	119.84
16	O	9	LYS	C-N-CA	5.48	126.69	119.84
3	03	34	SER	N-CA-C	-5.47	105.33	112.23
3	03	1016	GLU	N-CA-C	5.47	117.05	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	106	THR	N-CA-C	-5.47	107.86	114.75
8	G	100	VAL	N-CA-C	-5.46	105.17	110.42
7	F	124	GLU	N-CA-C	-5.46	106.62	113.72
3	03	936	ARG	N-CA-C	5.45	122.41	110.80
8	G	11	SER	N-CA-C	-5.45	105.76	112.90
4	04	687	ALA	N-CA-C	-5.44	105.37	112.23
3	03	462	ASN	N-CA-C	5.44	117.29	111.36
3	03	429	MET	N-CA-C	-5.43	105.44	111.36
15	N	49	SER	N-CA-C	-5.43	106.43	112.57
4	04	536	LEU	N-CA-C	-5.43	105.39	112.23
16	O	7	VAL	N-CA-C	-5.43	105.08	110.62
4	04	1210	ILE	N-CA-C	-5.43	105.41	113.39
6	E	19	GLN	N-CA-C	5.42	122.35	110.80
8	G	94	GLU	N-CA-C	-5.42	106.51	113.23
19	R	54	GLY	N-CA-C	-5.42	105.83	112.77
6	E	61	ALA	N-CA-C	-5.42	106.35	113.12
2	01	64	VAL	N-CA-C	5.41	116.23	106.61
6	E	112	LYS	N-CA-C	-5.40	105.50	111.71
10	I	12	PRO	N-CA-C	-5.40	107.01	113.98
16	O	26	CYS	CA-C-N	5.40	126.59	119.84
16	O	26	CYS	C-N-CA	5.40	126.59	119.84
3	03	904	ALA	N-CA-C	-5.39	107.71	114.56
6	E	198	PHE	N-CA-C	5.38	116.35	107.20
11	J	122	GLU	N-CA-C	5.38	117.90	111.71
6	E	34	ALA	N-CA-C	-5.38	102.52	110.48
4	04	77	ARG	N-CA-C	5.38	118.08	110.50
4	04	851	PRO	N-CA-C	-5.38	107.04	113.98
4	04	1368	ASP	N-CA-C	-5.37	106.23	112.89
21	T	81	ALA	N-CA-C	5.37	122.23	110.80
5	05	14	GLY	N-CA-C	5.37	120.57	114.67
17	P	30	LYS	N-CA-C	-5.37	105.51	111.36
2	01	36	GLY	N-CA-C	-5.36	106.21	113.24
3	03	736	VAL	N-CA-C	5.36	116.50	109.58
6	E	172	ALA	N-CA-C	-5.36	105.60	111.82
8	G	166	LYS	CA-C-N	5.36	126.54	119.84
8	G	166	LYS	C-N-CA	5.36	126.54	119.84
6	E	178	ASN	N-CA-C	-5.36	106.25	112.89
25	X	10	GLU	N-CA-C	5.36	121.65	109.81
7	F	121	SER	N-CA-C	-5.35	106.26	112.89
4	04	1021	ASP	CA-C-N	5.35	125.06	119.82
4	04	1021	ASP	C-N-CA	5.35	125.06	119.82
22	U	31	ASN	N-CA-C	-5.35	107.13	113.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	02	178	SER	N-CA-C	5.32	117.13	109.04
9	H	137	ARG	N-CA-C	-5.32	106.05	112.54
24	W	11	ILE	N-CA-C	-5.30	105.55	110.53
3	03	560	PRO	N-CA-C	-5.29	106.96	113.84
12	K	76	ARG	N-CA-C	5.29	118.69	110.17
3	03	1287	LEU	N-CA-C	-5.28	105.44	111.14
3	03	148	GLN	N-CA-C	5.27	118.29	109.96
15	N	46	ALA	N-CA-C	-5.27	106.36	112.89
3	03	400	VAL	N-CA-C	-5.26	107.28	111.81
4	04	836	ARG	N-CA-C	5.26	117.42	111.11
11	J	71	THR	N-CA-C	-5.26	99.59	110.80
4	04	591	ILE	N-CA-C	5.26	115.98	110.62
4	04	1124	ILE	CA-C-N	5.26	126.41	119.84
4	04	1124	ILE	C-N-CA	5.26	126.41	119.84
3	03	805	MET	CA-C-N	5.25	125.16	119.76
3	03	805	MET	C-N-CA	5.25	125.16	119.76
4	04	1370	MET	N-CA-C	-5.24	105.48	111.14
23	V	58	PRO	N-CA-C	5.23	118.81	111.33
6	E	17	GLY	N-CA-C	5.23	125.57	113.18
18	Q	64	ARG	N-CA-C	5.23	119.29	113.02
13	L	35	GLU	N-CA-C	5.21	119.39	113.19
10	I	25	TYR	N-CA-C	5.20	117.35	111.11
11	J	51	GLN	N-CA-C	-5.20	106.45	112.89
11	J	125	ASP	N-CA-C	-5.19	105.80	111.82
4	04	735	ALA	N-CA-C	-5.19	107.08	113.41
4	04	688	ALA	N-CA-C	-5.18	105.72	111.36
19	R	34	GLN	N-CA-C	-5.18	105.55	111.14
4	04	352	ARG	N-CA-C	5.17	118.14	110.48
6	E	200	ILE	CA-C-N	5.17	126.30	119.84
6	E	200	ILE	C-N-CA	5.17	126.30	119.84
20	S	78	VAL	N-CA-C	-5.17	107.71	112.83
4	04	18	ASP	N-CA-C	5.16	115.19	108.07
3	03	435	ILE	N-CA-C	-5.16	106.87	113.22
3	03	711	ASP	N-CA-C	5.16	115.81	108.54
15	N	32	THR	N-CA-C	5.16	115.83	107.32
3	03	891	GLY	N-CA-C	5.16	118.47	111.72
4	04	788	LEU	N-CA-C	5.16	118.03	111.69
13	L	36	GLN	N-CA-C	-5.16	107.54	113.88
16	O	29	LYS	N-CA-C	5.15	117.37	109.95
9	H	117	ALA	N-CA-C	-5.15	106.97	114.12
3	03	1049	ILE	N-CA-C	5.13	117.08	109.17
4	04	353	SER	N-CA-C	5.13	116.33	108.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	03	20	GLN	N-CA-C	5.13	117.48	110.55
4	04	1356	LEU	N-CA-C	5.13	117.60	109.96
4	04	925	GLU	N-CA-C	-5.12	105.49	112.35
4	04	1194	ARG	N-CA-C	-5.12	102.43	110.36
8	G	63	ILE	CB-CA-C	-5.11	107.37	111.71
6	E	31	ILE	N-CA-C	5.11	119.96	109.34
4	04	755	ILE	N-CA-C	5.11	115.99	109.30
4	04	1240	VAL	N-CA-C	-5.11	105.41	110.62
17	P	12	LYS	N-CA-C	-5.10	100.39	108.14
3	03	856	ASN	N-CA-C	5.10	118.36	111.17
12	K	11	THR	N-CA-C	-5.10	105.80	111.36
7	F	49	ALA	N-CA-C	-5.09	106.67	112.92
4	04	1249	ASN	N-CA-C	-5.08	100.50	108.63
17	P	56	ARG	N-CA-C	-5.08	106.34	112.54
6	E	110	SER	N-CA-C	-5.08	106.59	112.89
18	Q	72	PHE	N-CA-C	5.08	117.46	110.35
20	S	68	SER	N-CA-C	5.07	118.03	110.52
1	A	9	G	N9-C1'-C2'	5.07	119.61	112.00
20	S	53	ASP	N-CA-C	5.07	117.81	108.58
4	04	654	ILE	N-CA-C	-5.07	105.60	110.72
6	E	70	VAL	N-CA-C	5.07	115.14	107.80
4	04	453	VAL	N-CA-C	-5.06	108.57	113.53
4	04	693	VAL	N-CA-C	-5.06	104.76	111.09
4	04	429	LEU	N-CA-C	-5.06	106.85	112.57
7	F	67	ILE	N-CA-C	5.06	114.86	107.37
4	04	665	GLN	N-CA-C	-5.06	105.85	111.36
4	04	699	ASP	N-CA-C	-5.06	105.68	111.14
13	L	98	ARG	N-CA-C	-5.05	107.67	113.88
8	G	91	ALA	N-CA-C	-5.04	105.70	111.14
8	G	29	THR	N-CA-C	-5.04	104.94	111.74
20	S	55	ASP	N-CA-C	5.03	118.88	112.34
4	04	216	LYS	N-CA-C	-5.03	105.98	111.82
6	E	91	PHE	N-CA-C	5.03	116.46	108.96
17	P	20	SER	N-CA-C	-5.02	105.80	111.28
13	L	95	SER	N-CA-C	-5.02	106.66	112.89
9	H	136	VAL	N-CA-C	-5.02	104.71	111.44
14	M	91	ASP	N-CA-C	-5.02	108.18	114.56
3	03	454	ARG	N-CA-C	5.00	118.27	110.32

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	25	C	Sidechain
1	A	872	A	Sidechain
1	A	9	G	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	33012	0	16618	424	0
2	01	1753	0	1780	109	0
2	02	1757	0	1778	101	0
3	03	10272	0	10138	539	0
4	04	10372	0	10512	583	0
5	05	458	0	476	24	0
6	E	1705	0	1732	190	0
7	F	1625	0	1699	80	0
8	G	1643	0	1710	120	0
9	H	1157	0	1199	74	0
10	I	818	0	808	53	0
11	J	1182	0	1240	76	0
12	K	979	0	1034	66	0
13	L	1022	0	1070	65	0
14	M	787	0	828	58	0
15	N	870	0	878	47	0
16	O	955	0	1019	46	0
17	P	884	0	944	61	0
18	Q	805	0	847	63	0
19	R	714	0	737	32	0
20	S	649	0	666	42	0
21	T	649	0	691	27	0
22	U	536	0	552	34	0
23	V	638	0	665	50	0
24	W	665	0	714	53	0
25	X	545	0	579	27	0
All	All	76452	0	60914	2853	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 21.

All (2853) 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)
6:E:26:LYS:O	6:E:29:PRO:HD2	1.44	1.17
6:E:196:VAL:HG21	6:E:199:VAL:HG13	1.32	1.11
4:04:19:ALA:HB1	4:04:1343:GLU:HB3	1.27	1.08
6:E:11:LYS:O	6:E:13:GLY:N	1.88	1.07
4:04:639:VAL:HG12	4:04:640:GLY:H	1.20	1.04
1:A:292:G:H21	1:A:608:A:H61	1.07	1.02
6:E:40:ILE:O	6:E:41:ILE:HG13	1.60	1.01
6:E:34:ALA:O	6:E:40:ILE:HB	1.59	1.01
8:G:167:PRO:HB2	8:G:170:LEU:HB2	1.41	1.00
1:A:1374:A:H4'	11:J:27:ASN:HB3	1.41	0.99
11:J:1:PRO:HG2	11:J:4:ARG:HD3	1.43	0.98
6:E:31:ILE:HG22	6:E:42:ASN:HB2	1.45	0.98
4:04:64:PRO:HG2	4:04:93:THR:H	1.28	0.97
6:E:17:GLY:HA3	6:E:41:ILE:HD12	1.48	0.96
3:03:1127:LYS:HG2	3:03:1204:LEU:HD21	1.49	0.94
6:E:16:PHE:O	6:E:41:ILE:HB	1.67	0.94
3:03:1255:THR:HG22	3:03:1256:GLN:H	1.31	0.93
8:G:10:LEU:HD13	8:G:62:ARG:HG3	1.46	0.93
4:04:1251:LYS:HB2	4:04:1251:LYS:HZ2	1.33	0.93
2:01:29:GLU:HB3	2:01:30:PRO:HD3	1.52	0.92
3:03:151:ARG:HB3	3:03:177:ILE:HD13	1.52	0.92
12:K:28:SER:HB2	12:K:58:LEU:HB2	1.50	0.92
6:E:21:ARG:C	6:E:23:TRP:H	1.71	0.91
9:H:75:LEU:HD13	9:H:119:VAL:HG22	1.52	0.91
6:E:47:VAL:HB	6:E:48:PRO:HD3	1.52	0.91
3:03:732:ILE:HG13	3:03:753:LEU:HD11	1.51	0.91
4:04:1252:HIS:O	4:04:1255:VAL:HG22	1.70	0.91
3:03:30:ILE:H	3:03:30:ILE:HD12	1.34	0.91
3:03:796:LEU:H	3:03:796:LEU:HD12	1.35	0.91
2:01:102:LEU:HD23	2:01:115:ILE:HG12	1.51	0.91
6:E:44:GLU:O	6:E:48:PRO:HD2	1.70	0.91
6:E:38:VAL:O	6:E:39:HIS:HB2	1.68	0.90
1:A:376:G:H2'	1:A:377:G:H5''	1.53	0.90
13:L:118:ARG:HB3	13:L:122:ARG:HB3	1.52	0.90
4:04:19:ALA:HB1	4:04:1343:GLU:CB	2.01	0.90
1:A:961:U:H3	1:A:1201:A:H61	1.15	0.89
3:03:933:VAL:HG21	3:03:944:ARG:HE	1.37	0.89
22:U:57:ARG:HB3	22:U:61:ARG:HH12	1.38	0.89
1:A:410:G:H21	1:A:432:A:H62	1.21	0.88
14:M:70:HIS:HB3	14:M:72:ARG:HH12	1.39	0.88
1:A:974:A:H5'	18:Q:70:HIS:HB3	1.54	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:759:SER:HB3	3:03:763:THR:HB	1.55	0.88
4:04:19:ALA:CB	4:04:1343:GLU:HB3	2.03	0.87
10:I:29:ILE:HD13	10:I:64:VAL:HG21	1.55	0.87
3:03:502:VAL:HG13	3:03:503:LYS:HD2	1.55	0.87
1:A:1259:C:H3'	1:A:1260:G:H5''	1.56	0.87
4:04:557:LYS:HB3	4:04:563:LEU:HG	1.56	0.87
1:A:831:A:H3'	1:A:832:G:H5''	1.56	0.87
3:03:145:ILE:HG12	3:03:512:SER:HB2	1.57	0.86
2:02:35:PHE:HA	2:02:38:THR:HG22	1.55	0.86
2:02:208:ASN:HD21	2:02:210:THR:HG23	1.40	0.86
1:A:1304:G:H21	1:A:1333:A:H62	1.20	0.86
4:04:850:LYS:HB3	4:04:851:PRO:HD2	1.56	0.86
3:03:1199:LEU:HD13	3:03:1206:THR:HA	1.57	0.86
8:G:64:TYR:HA	8:G:110:ARG:HD2	1.56	0.86
14:M:40:ILE:HB	14:M:73:LEU:HB2	1.58	0.86
2:01:31:LEU:HB2	2:01:199:ASP:O	1.76	0.86
1:A:1158:C:H2'	1:A:1159:U:H4'	1.58	0.86
2:01:190:ALA:HB2	2:01:200:LYS:HB2	1.57	0.86
3:03:708:VAL:HG11	3:03:794:LEU:HD22	1.58	0.86
4:04:925:GLU:HB3	4:04:926:PRO:HD3	1.58	0.86
4:04:120:LEU:HB3	4:04:121:PRO:HD3	1.58	0.85
13:L:98:ARG:HG2	13:L:103:VAL:HB	1.58	0.85
12:K:102:VAL:HG12	12:K:125:ILE:HD12	1.58	0.85
3:03:1212:LEU:HD11	3:03:1227:VAL:HG11	1.60	0.84
2:01:25:LYS:HG2	2:01:204:GLU:HA	1.59	0.84
6:E:33:GLY:HA2	6:E:41:ILE:O	1.77	0.84
3:03:929:ILE:HG13	3:03:930:ASP:H	1.41	0.84
1:A:403:C:H4'	8:G:118:SER:OG	1.77	0.84
3:03:42:ASP:HB2	3:03:50:GLU:HG3	1.60	0.84
3:03:685:MET:HG2	3:03:1235:LEU:HD21	1.58	0.84
8:G:43:ARG:NH1	8:G:43:ARG:HB3	1.92	0.84
1:A:981:U:H3'	1:A:982:U:H5''	1.60	0.83
3:03:845:LEU:HD11	3:03:891:GLY:HA2	1.60	0.83
4:04:143:SER:HB3	4:04:159:ILE:HB	1.60	0.83
3:03:297:VAL:HG22	3:03:299:LYS:H	1.41	0.83
3:03:532:ALA:HB1	3:03:538:LEU:HB2	1.60	0.82
4:04:1146:GLU:HB2	4:04:1148:ARG:HG3	1.60	0.82
4:04:515:ARG:HH22	4:04:719:PHE:HA	1.44	0.82
2:01:14:VAL:HG22	2:01:15:ASP:H	1.45	0.82
2:02:100:LEU:HD21	2:02:121:VAL:HG21	1.60	0.82
4:04:272:VAL:HG22	4:04:302:ALA:HB1	1.62	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:768:ASN:HD21	4:04:771:GLN:HG2	1.44	0.82
1:A:323:U:H4'	24:W:13:SER:HA	1.61	0.82
2:02:159:ILE:HA	2:02:172:LEU:HD11	1.61	0.82
13:L:91:GLU:HA	13:L:94:ARG:HB2	1.61	0.82
3:03:690:VAL:HG11	3:03:1234:LYS:HD3	1.62	0.81
4:04:1173:ARG:HB2	4:04:1192:LYS:HB3	1.63	0.81
4:04:1174:ARG:HG2	4:04:1189:MET:HE1	1.62	0.81
1:A:179:A:H61	1:A:196:A:H62	1.28	0.81
4:04:849:LEU:HD23	4:04:849:LEU:H	1.44	0.81
18:Q:53:ASP:HA	18:Q:58:ARG:HD3	1.59	0.81
22:U:48:ARG:H	22:U:48:ARG:HD2	1.44	0.81
24:W:42:ASP:HB3	24:W:45:ALA:HB3	1.60	0.81
4:04:102:MET:SD	4:04:246:PRO:HD3	2.21	0.81
4:04:504:GLN:O	4:04:507:VAL:HG12	1.81	0.81
9:H:35:LEU:HD22	9:H:133:ILE:HG12	1.60	0.81
21:T:24:ILE:HB	21:T:41:THR:HB	1.63	0.81
6:E:21:ARG:O	6:E:23:TRP:HD1	1.64	0.81
2:01:180:VAL:HB	2:01:183:ILE:HD11	1.63	0.81
3:03:1330:ILE:HB	3:03:1335:ILE:HD12	1.62	0.81
17:P:16:ILE:HD12	17:P:16:ILE:H	1.46	0.81
6:E:31:ILE:CG2	6:E:42:ASN:HB2	2.10	0.80
4:04:399:LYS:HB3	4:04:403:ARG:HH12	1.46	0.80
11:J:49:LEU:HB3	11:J:120:ALA:HA	1.60	0.80
1:A:1502:A:H8	1:A:1505:G:H22	1.27	0.80
2:02:166:ARG:HB2	2:02:167:PRO:HD3	1.63	0.80
8:G:18:LEU:HB3	8:G:63:ILE:HG12	1.63	0.80
3:03:873:ILE:HA	3:03:928:VAL:HG23	1.62	0.80
3:03:56:VAL:HG11	3:03:468:LEU:HD13	1.64	0.80
11:J:78:ARG:H	11:J:78:ARG:HD2	1.47	0.79
1:A:92:U:H2'	1:A:93:U:H4'	1.64	0.79
4:04:56:LEU:HD21	4:04:269:TYR:HB2	1.62	0.79
8:G:117:VAL:HG22	8:G:122:ILE:HD12	1.61	0.79
4:04:209:ASN:HA	4:04:214:ARG:HD3	1.65	0.79
3:03:532:ALA:HB3	3:03:571:LEU:HB3	1.63	0.79
18:Q:26:LEU:HD22	18:Q:43:ALA:HA	1.65	0.79
3:03:561:ILE:HG23	3:03:676:ALA:HB1	1.64	0.79
4:04:1024:THR:HG22	4:04:1026:PRO:HD3	1.64	0.79
19:R:28:VAL:HG11	19:R:66:LEU:HD21	1.63	0.79
8:G:1:ALA:HB1	8:G:67:LEU:HD11	1.65	0.78
1:A:1157:A:H61	1:A:1178:G:H1'	1.47	0.78
6:E:41:ILE:HG22	6:E:42:ASN:N	1.97	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:24:LEU:HD13	4:04:25:ALA:N	1.98	0.78
9:H:44:ARG:HG2	9:H:70:MET:HE3	1.66	0.78
20:S:21:VAL:HG12	20:S:33:ILE:HD12	1.66	0.78
1:A:1250:A:H4'	13:L:68:GLY:HA2	1.64	0.78
3:03:525:THR:HG23	3:03:687:ARG:HB3	1.65	0.78
1:A:372:C:H42	1:A:389:A:H62	1.29	0.78
18:Q:73:LEU:HD12	18:Q:83:VAL:HG21	1.66	0.78
4:04:557:LYS:HA	4:04:563:LEU:HA	1.64	0.78
9:H:96:GLN:HB3	9:H:123:LEU:HB2	1.65	0.78
11:J:6:ILE:HG13	11:J:7:GLY:H	1.49	0.78
16:O:86:VAL:HG21	16:O:89:LEU:HD13	1.66	0.78
6:E:11:LYS:HE2	6:E:11:LYS:HA	1.65	0.77
3:03:1151:LEU:HD23	3:03:1151:LEU:H	1.47	0.77
23:V:40:PHE:H	23:V:43:MET:HE2	1.49	0.77
3:03:151:ARG:HH12	3:03:175:ARG:HD2	1.49	0.77
3:03:1086:PRO:HB2	3:03:1212:LEU:HD23	1.66	0.77
1:A:934:C:H42	1:A:938:A:H61	1.32	0.77
4:04:863:LEU:HD11	4:04:901:ARG:HB3	1.66	0.77
3:03:617:ALA:HB3	3:03:653:MET:HA	1.66	0.77
3:03:211:ARG:HH21	3:03:351:LEU:HB3	1.50	0.77
4:04:11:GLN:HG3	4:04:13:LYS:H	1.50	0.77
11:J:24:LYS:HA	11:J:27:ASN:HD22	1.49	0.77
1:A:39:G:H2'	1:A:40:C:H5''	1.67	0.77
4:04:1264:ALA:HB2	4:04:1280:VAL:HG22	1.65	0.77
1:A:414:A:H62	1:A:430:A:H61	1.30	0.76
3:03:758:ARG:HG2	3:03:759:SER:H	1.49	0.76
4:04:201:LEU:HD11	4:04:220:ARG:HH11	1.50	0.76
23:V:14:LEU:O	23:V:18:VAL:HG23	1.85	0.76
1:A:1496:C:H1'	1:A:1517:G:H1	1.50	0.76
6:E:23:TRP:HB2	6:E:189:THR:CG2	2.16	0.76
3:03:466:VAL:O	3:03:469:VAL:HG22	1.86	0.76
17:P:22:TYR:HB3	17:P:65:GLU:HG2	1.67	0.76
3:03:697:LYS:H	3:03:697:LYS:HD3	1.50	0.76
4:04:976:THR:HG22	4:04:1028:ILE:HG13	1.68	0.76
4:04:1221:LEU:HD23	4:04:1229:VAL:HG11	1.66	0.76
1:A:149:A:H61	1:A:172:A:H62	1.31	0.75
4:04:1040:MET:HE3	4:04:1076:PRO:HB2	1.69	0.75
17:P:3:ILE:HG21	17:P:55:LEU:HD11	1.67	0.75
2:01:86:LYS:HE2	2:01:174:ASP:HB2	1.68	0.75
2:02:136:GLU:HG2	2:02:137:ASN:H	1.51	0.75
2:02:151:GLY:O	2:02:177:TYR:HB2	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:38:ILE:HD13	24:W:81:GLN:HE21	1.50	0.75
1:A:244:U:H4'	1:A:245:U:H5'	1.67	0.75
4:04:755:ILE:HG22	4:04:757:THR:H	1.51	0.75
6:E:23:TRP:O	6:E:189:THR:O	2.04	0.75
3:03:522:SER:HA	3:03:687:ARG:HA	1.68	0.75
3:03:1046:VAL:HG13	3:03:1049:ILE:HG21	1.69	0.75
17:P:3:ILE:HD13	17:P:21:ILE:HD11	1.69	0.75
9:H:79:THR:HA	9:H:121:ASN:HB2	1.69	0.75
3:03:206:ALA:HB1	3:03:429:MET:HE2	1.69	0.74
4:04:157:GLN:HE22	4:04:188:LEU:HD13	1.52	0.74
6:E:23:TRP:HB2	6:E:189:THR:HG23	1.69	0.74
9:H:93:VAL:HG22	9:H:126:ALA:HA	1.68	0.74
6:E:36:ASN:HB2	6:E:40:ILE:HD11	1.67	0.74
4:04:641:ILE:HG13	4:04:642:ASP:H	1.53	0.74
7:F:68:HIS:HA	7:F:103:ALA:HB3	1.67	0.74
9:H:10:LEU:HD12	9:H:11:GLN:N	2.01	0.74
23:V:62:THR:H	23:V:65:MET:HE3	1.52	0.74
3:03:434:ASP:HA	3:03:437:ASN:HD22	1.53	0.74
4:04:309:ASN:ND2	4:04:315:ALA:H	1.85	0.74
6:E:40:ILE:HG22	6:E:41:ILE:N	2.01	0.74
20:S:54:LEU:H	20:S:54:LEU:HD12	1.50	0.74
9:H:80:LEU:HG	9:H:81:GLN:H	1.51	0.74
3:03:21:VAL:HG21	3:03:601:ASP:HB3	1.68	0.74
3:03:633:LEU:HD12	3:03:633:LEU:O	1.87	0.74
3:03:1199:LEU:CD1	3:03:1206:THR:HA	2.18	0.74
4:04:156:ARG:HD3	4:04:157:GLN:HE21	1.52	0.74
4:04:892:PHE:H	4:04:1281:GLU:HG2	1.52	0.74
23:V:49:ALA:HA	23:V:58:PRO:HA	1.70	0.74
2:01:71:LYS:HB2	2:01:78:ILE:HD11	1.69	0.74
5:05:26:ARG:HG3	5:05:30:MET:HE2	1.69	0.74
1:A:392:C:H2'	1:A:393:A:H8	1.52	0.73
4:04:973:LEU:HB3	4:04:1003:LEU:HB2	1.68	0.73
4:04:1249:ASN:HD21	4:04:1251:LYS:HE3	1.52	0.73
25:X:45:ARG:NH1	25:X:45:ARG:HB2	2.02	0.73
7:F:56:ILE:HG23	7:F:65:VAL:HG22	1.68	0.73
12:K:94:VAL:HG12	12:K:95:MET:HG3	1.71	0.73
3:03:763:THR:HG22	3:03:764:CYS:H	1.53	0.73
15:N:83:VAL:HG21	15:N:106:ILE:HD13	1.69	0.73
1:A:1308:U:H5''	17:P:96:VAL:HG22	1.69	0.73
1:A:1373:G:H4'	11:J:30:MET:HE1	1.70	0.73
2:02:18:GLN:HG3	2:02:20:SER:H	1.50	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:16:ILE:HD12	17:P:16:ILE:N	2.04	0.73
17:P:82:LEU:HD11	23:V:65:MET:HG3	1.71	0.73
1:A:216:U:H4'	1:A:464:U:H4'	1.70	0.73
2:01:104:LYS:HG2	2:01:110:VAL:HG22	1.69	0.73
8:G:118:SER:HA	8:G:130:ASN:HB2	1.70	0.73
1:A:1285:A:H4'	1:A:1286:U:H5''	1.71	0.73
4:04:689:ALA:O	4:04:693:VAL:HG23	1.89	0.73
4:04:749:LYS:HE2	4:04:751:ASP:HB2	1.68	0.73
6:E:81:LYS:HE3	6:E:93:ASN:ND2	2.04	0.72
9:H:10:LEU:HD22	9:H:67:ARG:HH21	1.54	0.72
1:A:552:U:H4'	16:O:82:ARG:HD2	1.71	0.72
1:A:624:C:H4'	20:S:11:ALA:HB2	1.69	0.72
4:04:289:ASP:HA	4:04:292:VAL:HG22	1.71	0.72
6:E:23:TRP:CE3	6:E:189:THR:HG21	2.24	0.72
2:01:82:LEU:HD23	2:01:85:LEU:HD12	1.70	0.72
3:03:661:VAL:HB	3:03:665:ALA:HB3	1.72	0.72
7:F:113:LYS:HG2	7:F:184:ASN:HD22	1.54	0.72
11:J:113:LYS:HD2	11:J:117:LEU:HD22	1.68	0.72
6:E:67:ILE:HG12	6:E:160:ALA:HB3	1.72	0.72
8:G:43:ARG:HB3	8:G:43:ARG:HH11	1.52	0.72
4:04:93:THR:HG22	4:04:94:GLN:H	1.54	0.72
11:J:49:LEU:HD22	11:J:123:LEU:HB3	1.71	0.72
11:J:29:LEU:HD23	11:J:42:VAL:HG22	1.72	0.72
4:04:485:MET:HE3	4:04:486:SER:H	1.54	0.71
8:G:86:GLY:O	8:G:196:GLU:HG3	1.88	0.71
16:O:65:TYR:HB2	16:O:92:VAL:HG11	1.72	0.71
4:04:358:GLY:HA3	4:04:448:GLN:HB3	1.72	0.71
3:03:1271:GLY:O	3:03:1275:VAL:HG23	1.91	0.71
14:M:52:LEU:HD21	14:M:59:LYS:HE2	1.73	0.71
16:O:24:GLU:O	16:O:26:CYS:N	2.24	0.71
4:04:64:PRO:HG2	4:04:93:THR:N	2.04	0.71
17:P:82:LEU:HD13	23:V:64:GLU:HB2	1.73	0.71
1:A:50:A:H4'	1:A:51:A:H5'	1.73	0.71
1:A:770:C:H1'	1:A:900:A:H2	1.55	0.71
3:03:131:THR:HG22	3:03:132:ASP:H	1.54	0.71
10:I:48:ALA:HB1	22:U:69:PRO:HD3	1.72	0.71
20:S:6:LEU:HG	20:S:71:VAL:HG22	1.71	0.71
1:A:831:A:C3'	1:A:832:G:H5''	2.21	0.71
6:E:20:THR:HA	6:E:38:VAL:O	1.91	0.71
6:E:42:ASN:HD21	6:E:45:LYS:HB2	1.55	0.71
3:03:556:GLY:N	3:03:660:VAL:HG23	2.06	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:861:ALA:HA	3:03:864:LYS:HE2	1.73	0.71
6:E:34:ALA:HB3	6:E:43:LEU:HD11	1.72	0.71
6:E:40:ILE:O	6:E:41:ILE:CG1	2.38	0.71
24:W:43:LYS:HB3	24:W:86:ALA:HB2	1.73	0.71
3:03:52:ALA:HA	3:03:461:GLU:HG3	1.73	0.71
4:04:114:ILE:HD13	4:04:310:GLY:HA3	1.72	0.71
18:Q:56:PRO:HA	18:Q:59:GLN:HB2	1.73	0.71
7:F:24:ASN:ND2	7:F:25:THR:H	1.89	0.70
24:W:67:HIS:HB2	24:W:70:LYS:HZ3	1.56	0.70
3:03:13:LYS:HD3	3:03:1182:ILE:HG12	1.71	0.70
3:03:138:ILE:HD12	3:03:143:ARG:HD2	1.73	0.70
13:L:35:GLU:HA	13:L:39:GLY:HA3	1.72	0.70
1:A:1399:C:H1'	1:A:1400:C:OP2	1.92	0.70
4:04:101:ARG:O	4:04:246:PRO:HG3	1.91	0.70
4:04:483:LEU:HD12	4:04:484:MET:HG3	1.73	0.70
4:04:639:VAL:HG12	4:04:640:GLY:N	1.99	0.70
4:04:975:ILE:HG22	4:04:977:SER:H	1.55	0.70
4:04:858:VAL:HG21	4:04:864:LEU:HD21	1.73	0.70
15:N:74:LYS:HD3	15:N:74:LYS:H	1.56	0.70
1:A:150:U:H3	1:A:171:A:H62	1.38	0.70
3:03:28:LEU:HD21	3:03:524:ILE:HG23	1.74	0.70
4:04:110:PRO:O	4:04:182:ALA:HB3	1.92	0.70
1:A:81:A:H2'	1:A:82:G:H4'	1.73	0.70
4:04:527:LEU:HD21	4:04:533:ALA:HB2	1.73	0.70
5:05:58:LEU:HG	5:05:59:ILE:HG12	1.74	0.70
8:G:97:LEU:HD22	8:G:134:TYR:HB3	1.72	0.70
1:A:9:G:H5'	9:H:107:GLY:HA3	1.74	0.70
3:03:563:THR:HG23	3:03:680:LEU:HG	1.73	0.70
24:W:32:LYS:HA	24:W:35:TYR:HB2	1.72	0.70
1:A:550:G:H21	16:O:114:SER:HB3	1.57	0.70
2:01:150:ARG:HD2	2:01:150:ARG:O	1.92	0.70
3:03:363:LEU:HD23	3:03:366:ILE:HD12	1.74	0.69
3:03:592:ARG:HG3	3:03:655:VAL:HG22	1.74	0.69
4:04:263:SER:H	4:04:266:ASN:HD22	1.40	0.69
17:P:76:ILE:O	17:P:80:MET:HG3	1.92	0.69
23:V:10:ILE:HG22	23:V:40:PHE:HE1	1.56	0.69
9:H:54:GLU:HB2	9:H:57:ALA:HB3	1.74	0.69
14:M:80:THR:H	14:M:83:THR:HB	1.58	0.69
21:T:12:VAL:HG12	21:T:21:VAL:O	1.92	0.69
1:A:958:A:C2	23:V:53:GLY:HA3	2.28	0.69
2:02:90:VAL:HG22	2:02:123:ILE:HD13	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:12:ARG:HG2	8:G:33:ILE:HA	1.73	0.69
2:01:192:VAL:HG22	2:01:193:GLU:H	1.57	0.69
6:E:190:ASN:HD22	6:E:190:ASN:N	1.88	0.69
24:W:79:THR:HA	24:W:82:ILE:HG12	1.75	0.69
24:W:79:THR:HG23	24:W:82:ILE:HD11	1.73	0.69
11:J:1:PRO:HD2	11:J:4:ARG:HB2	1.73	0.69
12:K:106:SER:HB2	12:K:120:LEU:HD22	1.74	0.69
1:A:614:C:H2'	1:A:615:G:H5''	1.74	0.69
2:02:172:LEU:HD23	2:02:172:LEU:H	1.57	0.68
4:04:1155:ILE:HD13	4:04:1190:ILE:HG23	1.75	0.68
4:04:1256:ILE:HG22	4:04:1260:MET:HE2	1.74	0.68
6:E:27:MET:HG3	6:E:189:THR:HA	1.75	0.68
10:I:47:LEU:HD21	10:I:57:ALA:HB3	1.74	0.68
4:04:475:GLU:HA	5:05:20:VAL:HG11	1.74	0.68
4:04:1041:ILE:HD12	4:04:1041:ILE:N	2.08	0.68
6:E:157:LEU:HD23	6:E:157:LEU:H	1.59	0.68
2:02:43:LEU:HD22	2:02:203:ILE:HD13	1.73	0.68
3:03:97:ARG:HB3	3:03:121:GLU:HA	1.74	0.68
1:A:9:G:H4'	9:H:108:GLY:H	1.59	0.68
3:03:565:GLU:H	3:03:684:ASN:HB2	1.59	0.68
3:03:672:GLU:HB2	4:04:769:VAL:HG22	1.74	0.68
5:05:58:LEU:HD23	5:05:58:LEU:H	1.58	0.68
6:E:34:ALA:HB3	6:E:43:LEU:CD1	2.24	0.68
9:H:132:PRO:O	9:H:136:VAL:HG23	1.94	0.68
2:02:15:ASP:HB3	2:02:27:THR:HB	1.74	0.68
11:J:6:ILE:HG13	11:J:7:GLY:N	2.08	0.68
20:S:9:HIS:O	20:S:16:PHE:HB3	1.93	0.68
1:A:1372:U:H5''	13:L:72:SER:HB3	1.76	0.68
4:04:857:LEU:HD12	4:04:858:VAL:HG12	1.74	0.68
23:V:52:ASN:HD21	23:V:54:ARG:HG2	1.58	0.68
1:A:501:C:H2'	1:A:502:A:H8	1.59	0.68
3:03:533:LEU:HD11	3:03:568:ASN:HB3	1.76	0.68
3:03:721:GLY:HA2	3:03:777:VAL:HG23	1.75	0.68
17:P:16:ILE:H	17:P:16:ILE:CD1	2.07	0.68
2:01:195:ARG:HA	2:01:195:ARG:HE	1.58	0.68
3:03:836:LEU:HD21	3:03:921:PRO:HD3	1.76	0.68
4:04:111:THR:HB	4:04:239:LEU:HB2	1.75	0.68
4:04:472:LEU:HD23	4:04:472:LEU:H	1.57	0.68
9:H:55:VAL:N	9:H:56:PRO:HD2	2.08	0.68
3:03:618:GLN:HG2	3:03:619:ALA:H	1.57	0.67
10:I:67:PRO:HB2	10:I:70:VAL:HG23	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:33:ILE:HD12	15:N:33:ILE:O	1.93	0.67
3:03:145:ILE:HA	3:03:512:SER:HA	1.76	0.67
6:E:21:ARG:C	6:E:23:TRP:N	2.42	0.67
10:I:6:ILE:HG12	10:I:89:VAL:HG12	1.75	0.67
15:N:52:ARG:HD3	15:N:56:LYS:HD2	1.76	0.67
8:G:117:VAL:CG2	8:G:122:ILE:HD12	2.23	0.67
4:04:38:VAL:HA	4:04:61:ILE:HD13	1.76	0.67
7:F:107:LYS:HB2	7:F:110:LEU:HB2	1.77	0.67
4:04:201:LEU:HD11	4:04:220:ARG:NH1	2.09	0.67
8:G:190:LEU:HD12	8:G:192:ALA:H	1.57	0.67
23:V:49:ALA:HB1	23:V:56:HIS:O	1.94	0.67
2:02:54:CYS:HB2	2:02:91:ARG:HA	1.77	0.67
3:03:88:ARG:HG3	3:03:932:GLN:HG3	1.75	0.67
3:03:143:ARG:HD3	3:03:507:GLY:HA3	1.77	0.67
3:03:1104:PRO:HA	4:04:740:LEU:HD22	1.76	0.67
6:E:213:TYR:O	6:E:217:VAL:HG23	1.94	0.67
3:03:738:GLU:HA	3:03:741:MET:HB3	1.76	0.67
4:04:378:LYS:HB2	4:04:379:PRO:HD3	1.76	0.67
7:F:113:LYS:HG2	7:F:184:ASN:ND2	2.10	0.67
8:G:150:LYS:HB2	8:G:155:LYS:HE3	1.77	0.67
15:N:53:GLY:H	15:N:56:LYS:HG3	1.60	0.67
22:U:15:ALA:HB2	22:U:48:ARG:NH1	2.10	0.67
3:03:242:VAL:HG11	3:03:245:ARG:HH11	1.58	0.67
1:A:1399:C:H4'	1:A:1400:C:H2'	1.77	0.66
2:01:13:LEU:HD23	2:01:13:LEU:H	1.61	0.66
3:03:1333:LEU:HD21	4:04:307:LEU:HD11	1.77	0.66
9:H:104:ILE:HG13	9:H:122:VAL:HG22	1.74	0.66
1:A:675:A:O2'	15:N:116:PRO:HB3	1.95	0.66
4:04:79:LYS:HA	4:04:81:ARG:HH11	1.60	0.66
4:04:485:MET:HB3	4:04:488:ASN:HD22	1.59	0.66
4:04:1229:VAL:O	4:04:1233:ILE:HG13	1.96	0.66
6:E:136:MET:HA	6:E:136:MET:HE2	1.77	0.66
4:04:919:ALA:HB3	4:04:1255:VAL:HG21	1.76	0.66
6:E:118:GLU:HG3	6:E:122:GLN:HE21	1.60	0.66
8:G:116:LEU:O	8:G:121:ALA:HB3	1.94	0.66
16:O:28:GLN:OE1	16:O:82:ARG:HA	1.95	0.66
3:03:1291:LEU:HD22	4:04:1351:VAL:HG13	1.76	0.66
14:M:10:LEU:HD13	14:M:22:THR:HG22	1.77	0.66
14:M:54:SER:HB2	14:M:58:ASN:HB2	1.78	0.66
19:R:28:VAL:HG12	19:R:86:LEU:HD22	1.78	0.66
1:A:1252:A:H61	1:A:1285:A:H61	1.44	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:22:LYS:HB3	9:H:29:ILE:HG23	1.78	0.66
3:03:149:LEU:HD23	3:03:149:LEU:C	2.20	0.66
1:A:151:A:H62	1:A:170:U:H3	1.42	0.66
2:01:50:SER:HG	2:02:35:PHE:HE1	1.44	0.66
3:03:196:VAL:HG12	3:03:206:ALA:HA	1.78	0.66
3:03:380:ALA:O	3:03:384:LEU:HD13	1.95	0.66
1:A:440:C:H2'	1:A:441:A:H5''	1.77	0.66
1:A:716:A:C2	15:N:119:GLY:HA2	2.30	0.66
9:H:39:GLY:HA3	9:H:116:VAL:HB	1.77	0.66
9:H:107:GLY:H	9:H:110:MET:HE2	1.59	0.66
1:A:599:C:H5''	12:K:87:ARG:HB3	1.78	0.65
4:04:697:MET:HE1	4:04:738:ARG:HA	1.78	0.65
4:04:848:VAL:HB	4:04:858:VAL:HG12	1.78	0.65
13:L:18:VAL:HG22	13:L:64:ILE:HG23	1.78	0.65
2:02:30:PRO:C	2:02:31:LEU:HD22	2.22	0.65
3:03:176:ILE:HD12	3:03:184:LEU:HD23	1.78	0.65
3:03:816:ILE:HG12	3:03:1098:LEU:HD21	1.78	0.65
4:04:293:ARG:HG2	4:04:296:LYS:HD2	1.79	0.65
4:04:359:PRO:O	4:04:625:MET:HE1	1.97	0.65
4:04:1327:GLU:OE1	4:04:1330:ARG:HD3	1.96	0.65
6:E:23:TRP:HE3	6:E:189:THR:HG21	1.61	0.65
23:V:17:LYS:HG2	23:V:30:LEU:HD23	1.78	0.65
1:A:105:G:H22	1:A:379:C:H4'	1.62	0.65
17:P:74:MET:HA	17:P:74:MET:HE3	1.77	0.65
20:S:5:ARG:HA	20:S:71:VAL:HG21	1.78	0.65
3:03:1255:THR:HG22	3:03:1256:GLN:N	2.10	0.65
6:E:161:LEU:HD23	6:E:183:VAL:HG22	1.78	0.65
1:A:1279:G:H4'	1:A:1281:C:H41	1.61	0.65
4:04:245:LEU:HD22	4:04:327:LEU:HD22	1.78	0.65
8:G:100:VAL:O	8:G:104:MET:HG2	1.95	0.65
22:U:38:LYS:NZ	22:U:38:LYS:HB3	2.12	0.65
1:A:751:U:H2'	1:A:752:G:H5'	1.79	0.65
4:04:130:MET:HG3	4:04:131:PRO:HD2	1.77	0.65
6:E:130:THR:HG21	6:E:132:LYS:HD2	1.78	0.65
4:04:107:LEU:HB2	4:04:240:THR:O	1.96	0.65
4:04:398:LYS:O	4:04:401:VAL:HG22	1.96	0.65
8:G:121:ALA:HB1	8:G:148:ALA:HB2	1.79	0.65
15:N:109:ILE:HD12	15:N:109:ILE:N	2.12	0.65
1:A:252:U:O2	1:A:252:U:H2'	1.95	0.65
1:A:1100:C:OP2	6:E:95:ARG:HD3	1.97	0.65
6:E:67:ILE:HG12	6:E:160:ALA:CB	2.27	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:139:THR:O	9:H:143:LEU:HG	1.97	0.65
20:S:52:LEU:HD13	20:S:75:ILE:HD13	1.79	0.65
22:U:32:TYR:O	22:U:40:VAL:HG23	1.98	0.65
4:04:68:TYR:HA	4:04:92:VAL:HB	1.79	0.64
4:04:832:LYS:O	4:04:834:PRO:HD3	1.96	0.64
8:G:116:LEU:HD13	8:G:154:VAL:HG22	1.79	0.64
13:L:60:LEU:O	13:L:60:LEU:HD12	1.96	0.64
4:04:459:ALA:HB1	4:04:464:ASP:OD2	1.97	0.64
4:04:1361:THR:OG1	5:05:17:PHE:HB3	1.97	0.64
8:G:124:VAL:HG12	8:G:129:VAL:HB	1.77	0.64
16:O:53:ARG:HA	16:O:63:THR:HA	1.80	0.64
3:03:667:LEU:HD23	3:03:686:GLN:NE2	2.12	0.64
4:04:375:GLU:HA	4:04:378:LYS:HE2	1.78	0.64
4:04:851:PRO:HB3	4:04:876:SER:HB2	1.78	0.64
6:E:15:HIS:CE1	6:E:46:THR:HG22	2.33	0.64
3:03:59:ILE:HD12	3:03:68:LEU:HD23	1.78	0.64
4:04:641:ILE:HG13	4:04:642:ASP:N	2.10	0.64
6:E:42:ASN:ND2	6:E:45:LYS:HB2	2.12	0.64
23:V:43:MET:HA	23:V:46:LEU:HD12	1.79	0.64
3:03:890:LYS:HB2	3:03:890:LYS:NZ	2.13	0.64
14:M:70:HIS:HB3	14:M:72:ARG:NH1	2.10	0.64
17:P:15:VAL:O	17:P:19:THR:HG23	1.97	0.64
17:P:55:LEU:HD12	17:P:56:ARG:N	2.13	0.64
1:A:980:C:H4'	18:Q:58:ARG:HH21	1.61	0.64
1:A:1240:U:H4'	11:J:37:THR:HG22	1.78	0.64
1:A:1280:A:O2'	1:A:1281:C:H5'	1.97	0.64
3:03:864:LYS:HG3	3:03:865:LEU:HD12	1.79	0.64
4:04:768:ASN:HD21	4:04:771:GLN:CG	2.11	0.64
4:04:822:MET:HE2	4:04:822:MET:HA	1.78	0.64
6:E:10:LEU:O	6:E:11:LYS:O	2.16	0.64
13:L:47:VAL:HA	13:L:79:ARG:HB3	1.79	0.64
1:A:309:A:H5''	20:S:29:ASN:OD1	1.98	0.64
3:03:436:ARG:HA	3:03:436:ARG:HE	1.62	0.64
3:03:687:ARG:HD2	3:03:688:GLN:HG3	1.79	0.64
12:K:77:VAL:HG23	12:K:126:CYS:HA	1.80	0.64
1:A:752:G:H5''	19:R:68:TYR:OH	1.96	0.64
6:E:15:HIS:C	6:E:17:GLY:H	2.05	0.64
18:Q:20:PHE:HE2	18:Q:54:SER:HB3	1.60	0.64
1:A:245:U:H3	1:A:283:U:H3	1.45	0.64
3:03:1281:TYR:HE2	4:04:484:MET:HG2	1.63	0.64
4:04:105:ILE:HB	4:04:242:LEU:HB3	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:32:LYS:H	8:G:32:LYS:HD2	1.62	0.64
22:U:12:ARG:NH2	22:U:16:GLU:HG3	2.13	0.64
22:U:57:ARG:O	22:U:61:ARG:HG3	1.98	0.64
3:03:754:THR:O	3:03:767:GLN:HB2	1.98	0.64
6:E:11:LYS:HG3	6:E:15:HIS:ND1	2.13	0.64
1:A:396:C:O2'	1:A:397:A:H5'	1.97	0.63
4:04:587:LEU:HD13	4:04:608:CYS:HB2	1.80	0.63
18:Q:22:LYS:C	18:Q:24:ALA:H	2.07	0.63
18:Q:46:LYS:HA	18:Q:49:THR:OG1	1.99	0.63
3:03:248:GLY:O	3:03:341:LEU:HD13	1.99	0.63
8:G:59:LYS:O	8:G:63:ILE:HG13	1.98	0.63
17:P:48:SER:HB2	17:P:51:GLN:HG3	1.79	0.63
20:S:34:GLU:HG2	20:S:35:ARG:H	1.63	0.63
6:E:81:LYS:HE3	6:E:93:ASN:HD21	1.61	0.63
9:H:131:ASN:HB3	9:H:134:ASN:HB2	1.80	0.63
10:I:6:ILE:HD11	10:I:71:ILE:HD12	1.79	0.63
1:A:437:U:O2'	1:A:438:U:H5'	1.98	0.63
3:03:634:VAL:HG13	3:03:636:CYS:SG	2.39	0.63
6:E:186:ILE:HA	6:E:200:ILE:O	1.97	0.63
7:F:107:LYS:NZ	7:F:144:GLY:HA3	2.12	0.63
9:H:15:ILE:HG21	9:H:109:ALA:HB2	1.79	0.63
10:I:44:ARG:HH22	10:I:56:LYS:HE3	1.64	0.63
12:K:9:MET:O	12:K:13:ILE:HG13	1.99	0.63
1:A:1302:C:C5	17:P:16:ILE:HG12	2.33	0.63
2:02:190:ALA:HB2	2:02:200:LYS:HB2	1.79	0.63
3:03:454:ARG:HG2	3:03:458:GLU:OE2	1.97	0.63
8:G:23:GLY:HA2	8:G:160:LEU:HD11	1.80	0.63
1:A:818:G:H3'	1:A:819:A:H5'	1.80	0.63
1:A:1060:U:H4'	14:M:53:ILE:HG12	1.79	0.63
9:H:40:ASP:OD1	9:H:44:ARG:HB3	1.99	0.63
24:W:67:HIS:HB2	24:W:70:LYS:NZ	2.12	0.63
1:A:1297:G:H21	11:J:113:LYS:HB3	1.64	0.63
2:02:167:PRO:O	2:02:168:ILE:HG23	1.99	0.63
4:04:845:ALA:HB2	4:04:883:ARG:N	2.14	0.63
8:G:91:ALA:HB1	8:G:184:LYS:HD2	1.79	0.63
18:Q:40:ARG:HH11	23:V:6:LYS:HD2	1.63	0.63
6:E:23:TRP:HH2	6:E:33:GLY:HA3	1.64	0.63
8:G:77:GLU:HG2	8:G:80:ARG:NH2	2.14	0.63
9:H:15:ILE:N	9:H:15:ILE:HD12	2.14	0.63
17:P:49:GLU:HA	17:P:52:ILE:HD12	1.79	0.63
21:T:61:ARG:NH1	21:T:61:ARG:HB3	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:614:C:C3'	1:A:615:G:H5''	2.29	0.63
2:01:156:SER:O	2:01:159:ILE:HG22	1.99	0.63
3:03:1207:SER:C	3:03:1209:GLN:H	2.06	0.63
4:04:800:LEU:HB3	4:04:920:ALA:HB1	1.81	0.63
16:O:71:HIS:HB2	16:O:73:LEU:HD13	1.81	0.63
1:A:715:A:H2'	1:A:716:A:H8	1.64	0.62
3:03:392:GLU:HG3	3:03:392:GLU:O	1.98	0.62
3:03:853:ASP:CG	3:03:854:ILE:H	2.07	0.62
4:04:640:GLY:O	4:04:641:ILE:C	2.42	0.62
6:E:165:ASP:HB2	6:E:169:GLU:OE1	1.98	0.62
20:S:6:LEU:HD22	20:S:17:TYR:HB3	1.80	0.62
7:F:110:LEU:HG	7:F:203:LYS:NZ	2.14	0.62
18:Q:97:LYS:NZ	18:Q:97:LYS:HB2	2.13	0.62
23:V:5:LYS:HG3	23:V:6:LYS:HE2	1.80	0.62
1:A:1123:U:H2'	1:A:1124:G:C8	2.34	0.62
1:A:392:C:H2'	1:A:393:A:C8	2.34	0.62
2:01:48:LEU:HD23	2:01:183:ILE:HD13	1.80	0.62
6:E:23:TRP:CH2	6:E:33:GLY:HA3	2.33	0.62
8:G:64:TYR:HA	8:G:110:ARG:CD	2.30	0.62
1:A:1253:G:OP1	14:M:46:LYS:HB2	1.98	0.62
6:E:21:ARG:O	6:E:23:TRP:CD1	2.51	0.62
15:N:107:THR:HG23	15:N:108:ASN:OD1	2.00	0.62
2:02:65:LEU:HB3	2:02:171:LEU:HG	1.81	0.62
4:04:20:ILE:O	4:04:1343:GLU:HA	2.00	0.62
12:K:120:LEU:HD12	12:K:120:LEU:O	2.00	0.62
1:A:219:U:H2'	1:A:220:G:H5''	1.81	0.62
9:H:110:MET:HE1	9:H:125:LYS:HA	1.81	0.62
3:03:152:SER:HA	3:03:452:ARG:HB2	1.82	0.62
3:03:758:ARG:HG2	3:03:759:SER:N	2.14	0.62
4:04:147:ILE:HG22	4:04:188:LEU:HG	1.82	0.62
4:04:1142:ALA:O	4:04:1146:GLU:HG2	1.99	0.62
6:E:47:VAL:CB	6:E:48:PRO:HD3	2.29	0.62
7:F:171:ARG:HG2	7:F:173:PRO:HD3	1.80	0.62
2:01:57:THR:HG22	2:01:58:GLU:HG3	1.81	0.62
3:03:1070:HIS:NE2	3:03:1114:GLU:HG2	2.15	0.62
13:L:114:LYS:HB2	13:L:117:LEU:HD12	1.81	0.62
1:A:1098:C:OP1	6:E:143:LYS:HD3	2.00	0.62
2:01:47:LEU:O	2:01:180:VAL:HG21	1.99	0.62
2:02:83:LEU:HG	2:02:86:LYS:HE2	1.81	0.62
3:03:594:VAL:HG22	3:03:599:VAL:HG13	1.82	0.62
3:03:1290:MET:O	3:03:1295:SER:HB3	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:393:THR:HG23	4:04:396:ALA:H	1.64	0.62
17:P:72:ILE:O	17:P:76:ILE:HG13	1.99	0.62
3:03:274:ILE:O	3:03:278:GLU:HG3	2.00	0.61
3:03:1138:VAL:HG12	3:03:1170:MET:HB2	1.82	0.61
4:04:814:CYS:HB2	4:04:889:ASP:HB3	1.82	0.61
6:E:117:LEU:HD22	6:E:141:LEU:HD13	1.81	0.61
18:Q:27:LYS:HD2	18:Q:27:LYS:O	2.00	0.61
3:03:429:MET:O	3:03:433:ILE:HG13	2.00	0.61
3:03:476:LYS:HA	3:03:479:LEU:HD12	1.82	0.61
4:04:1251:LYS:HZ2	4:04:1251:LYS:CB	2.09	0.61
18:Q:7:ALA:C	18:Q:9:GLU:H	2.07	0.61
3:03:136:PHE:HB2	3:03:143:ARG:O	1.98	0.61
6:E:125:THR:HG22	6:E:129:LEU:HD22	1.82	0.61
18:Q:12:ARG:HH21	18:Q:58:ARG:NH2	1.98	0.61
2:01:45:ARG:HH11	2:02:37:HIS:HB3	1.63	0.61
2:02:107:ILE:HG12	2:02:135:ASP:HA	1.82	0.61
3:03:657:THR:HG21	3:03:1185:PRO:HB3	1.83	0.61
4:04:1223:LEU:O	4:04:1223:LEU:HD13	2.00	0.61
24:W:38:ILE:HG21	24:W:81:GLN:HE21	1.65	0.61
3:03:283:LYS:HB2	3:03:283:LYS:NZ	2.16	0.61
3:03:1230:MET:HG2	3:03:1231:TYR:H	1.66	0.61
4:04:214:ARG:O	4:04:217:LEU:HB3	2.00	0.61
8:G:167:PRO:CB	8:G:170:LEU:HB2	2.24	0.61
14:M:55:PRO:HA	18:Q:81:ILE:HD11	1.83	0.61
21:T:35:LYS:NZ	21:T:35:LYS:HB3	2.16	0.61
4:04:858:VAL:HG13	4:04:858:VAL:O	2.00	0.61
7:F:133:MET:HE1	7:F:165:GLU:HG3	1.82	0.61
1:A:719:C:H42	22:U:63:ARG:HH12	1.48	0.61
3:03:135:THR:HG21	3:03:515:MET:HE1	1.82	0.61
3:03:209:ILE:O	3:03:213:LEU:HG	2.00	0.61
3:03:232:ILE:HG12	3:03:237:LEU:HD23	1.82	0.61
3:03:1103:VAL:HB	3:03:1104:PRO:HD3	1.82	0.61
3:03:1141:LEU:O	3:03:1145:ILE:HG12	2.01	0.61
8:G:86:GLY:HA3	9:H:102:THR:HG21	1.80	0.61
15:N:12:ARG:N	15:N:76:TYR:HA	2.15	0.61
17:P:77:LYS:NZ	17:P:77:LYS:HB3	2.16	0.61
3:03:217:THR:HG23	3:03:351:LEU:HD13	1.83	0.61
3:03:588:GLU:HB3	3:03:605:TYR:HB3	1.83	0.61
3:03:1119:MET:O	3:03:1119:MET:HE3	2.01	0.61
3:03:1185:PRO:HB2	3:03:1189:GLY:HA2	1.81	0.61
3:03:1280:ALA:O	4:04:918:ILE:HG22	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:397:LEU:HD13	3:03:405:PHE:HE2	1.66	0.61
4:04:317:THR:HB	4:04:324:LEU:HD21	1.83	0.61
4:04:423:LEU:HD22	4:04:437:PHE:HD2	1.64	0.61
4:04:554:GLU:OE2	4:04:566:LYS:HE3	1.99	0.61
4:04:738:ARG:HD2	4:04:738:ARG:O	2.00	0.61
4:04:1282:TYR:O	4:04:1286:LYS:HG2	2.01	0.61
6:E:25:PRO:C	6:E:28:LYS:H	2.08	0.61
6:E:196:VAL:CG2	6:E:199:VAL:HG13	2.21	0.61
8:G:123:MET:HE2	8:G:145:ARG:HA	1.83	0.61
12:K:10:LEU:HD23	12:K:13:ILE:HD12	1.83	0.61
4:04:78:LEU:H	4:04:78:LEU:HD12	1.65	0.61
4:04:1241:TYR:HA	4:04:1244:GLN:HB2	1.82	0.61
7:F:120:THR:HG23	7:F:188:ALA:HA	1.83	0.61
8:G:200:VAL:O	8:G:204:SER:HB2	2.00	0.61
14:M:52:LEU:HB2	18:Q:80:ARG:HD2	1.82	0.61
15:N:86:LYS:NZ	15:N:86:LYS:HB3	2.15	0.61
3:03:704:MET:O	3:03:708:VAL:HG23	2.02	0.60
6:E:118:GLU:O	6:E:122:GLN:HG3	2.01	0.60
13:L:16:ALA:HB2	13:L:66:VAL:HG23	1.82	0.60
18:Q:43:ALA:O	18:Q:47:LEU:HB2	2.01	0.60
1:A:180:U:H3	1:A:195:A:H62	1.47	0.60
1:A:588:G:H5''	12:K:5:PRO:HD3	1.82	0.60
1:A:1256:A:H2'	7:F:26:LYS:HD2	1.83	0.60
3:03:850:ILE:HD12	3:03:850:ILE:N	2.16	0.60
12:K:74:ILE:HD12	12:K:128:VAL:HG13	1.82	0.60
1:A:518:C:H4'	1:A:519:C:H5''	1.84	0.60
4:04:954:ASN:HB2	4:04:984:LEU:HD21	1.83	0.60
10:I:18:VAL:HG12	10:I:19:PRO:HD3	1.82	0.60
14:M:48:ARG:HA	14:M:66:GLU:HA	1.83	0.60
3:03:985:GLU:HG2	3:03:988:LYS:HD3	1.83	0.60
4:04:1046:ILE:HD12	4:04:1059:LEU:HD13	1.84	0.60
6:E:40:ILE:HG22	6:E:41:ILE:H	1.67	0.60
14:M:8:ILE:HG12	14:M:100:ILE:HG22	1.84	0.60
14:M:56:HIS:CD2	14:M:57:VAL:HG12	2.36	0.60
1:A:78:A:H2'	1:A:79:G:H4'	1.84	0.60
4:04:81:ARG:HD3	4:04:81:ARG:H	1.67	0.60
6:E:19:GLN:O	6:E:39:HIS:HB3	2.00	0.60
8:G:144:ILE:HD12	8:G:177:MET:HB2	1.83	0.60
20:S:67:ILE:HD12	20:S:67:ILE:N	2.16	0.60
2:02:168:ILE:O	2:02:168:ILE:HG13	2.02	0.60
3:03:230:PHE:CE1	3:03:239:MET:HG3	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:358:GLY:N	4:04:359:PRO:HD3	2.16	0.60
18:Q:2:LYS:HE3	18:Q:5:MET:HB2	1.84	0.60
1:A:1238:A:C2'	1:A:1239:A:H5'	2.31	0.60
3:03:104:ILE:H	3:03:104:ILE:HD12	1.66	0.60
3:03:1338:GLU:HB2	4:04:21:LYS:HE3	1.83	0.60
4:04:652:GLU:O	4:04:656:GLU:HG3	2.02	0.60
6:E:27:MET:SD	6:E:193:PRO:HG2	2.41	0.60
6:E:45:LYS:O	6:E:49:MET:HB2	2.02	0.60
10:I:93:LYS:HB3	10:I:93:LYS:NZ	2.17	0.60
12:K:6:ILE:HG21	12:K:76:ARG:NH1	2.16	0.60
2:01:29:GLU:OE2	2:01:190:ALA:HB1	2.01	0.60
1:A:944:G:H21	1:A:1339:A:H62	1.50	0.60
2:02:102:LEU:HD23	2:02:115:ILE:HG12	1.82	0.60
3:03:145:ILE:HD11	3:03:506:PHE:HA	1.83	0.60
3:03:230:PHE:HE1	3:03:239:MET:HG3	1.67	0.60
3:03:832:HIS:HE2	3:03:1238:LEU:HD22	1.66	0.60
4:04:478:LEU:HD12	5:05:20:VAL:HG13	1.84	0.60
12:K:95:MET:HB3	12:K:98:LEU:HB2	1.84	0.60
22:U:57:ARG:HB3	22:U:61:ARG:NH1	2.12	0.60
24:W:65:LEU:O	24:W:65:LEU:HD23	2.02	0.60
4:04:109:SER:HB3	4:04:299:LEU:HD23	1.82	0.60
4:04:784:ALA:O	4:04:787:ALA:HB3	2.02	0.60
8:G:100:VAL:HG21	8:G:136:VAL:HG21	1.84	0.60
3:03:496:LYS:HB3	3:03:497:PRO:HD3	1.84	0.59
3:03:882:ILE:HD12	3:03:882:ILE:N	2.16	0.59
6:E:27:MET:O	6:E:28:LYS:C	2.45	0.59
8:G:90:LEU:HD23	8:G:93:LEU:HD12	1.84	0.59
10:I:10:VAL:HB	10:I:83:ALA:HB1	1.84	0.59
1:A:663:A:H61	1:A:742:G:H1	1.48	0.59
1:A:1210:C:H2'	1:A:1211:U:H5'	1.84	0.59
3:03:17:LYS:HD2	3:03:1155:VAL:HG11	1.85	0.59
3:03:1104:PRO:CA	4:04:740:LEU:HD22	2.33	0.59
4:04:71:LEU:O	4:04:71:LEU:HD13	2.02	0.59
4:04:518:VAL:HG22	4:04:709:ARG:HB3	1.85	0.59
14:M:9:ARG:HA	14:M:73:LEU:HD23	1.85	0.59
2:02:182:ARG:HD3	2:02:183:ILE:N	2.17	0.59
3:03:557:ARG:HG3	3:03:558:VAL:HG23	1.84	0.59
4:04:93:THR:HG22	4:04:94:GLN:N	2.18	0.59
11:J:22:LEU:O	11:J:26:VAL:HG23	2.03	0.59
14:M:80:THR:HG22	14:M:81:GLU:H	1.67	0.59
3:03:755:LYS:HD2	3:03:767:GLN:HB3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:247:PRO:C	4:04:249:LEU:H	2.10	0.59
1:A:1372:U:H2'	1:A:1373:G:O4'	2.03	0.59
6:E:191:SER:C	6:E:193:PRO:HD3	2.27	0.59
23:V:10:ILE:HG22	23:V:40:PHE:CE1	2.37	0.59
3:03:487:LEU:HD23	3:03:487:LEU:H	1.66	0.59
3:03:838:CYS:HB3	3:03:1050:VAL:HG22	1.83	0.59
3:03:1063:GLY:H	3:03:1076:ILE:HG23	1.68	0.59
4:04:910:ASN:HB2	4:04:913:GLU:HB2	1.85	0.59
4:04:919:ALA:CB	4:04:1255:VAL:HG21	2.32	0.59
10:I:52:ASN:HD22	10:I:52:ASN:N	1.99	0.59
12:K:44:PHE:HE2	12:K:100:ILE:HD11	1.68	0.59
1:A:1157:A:N6	1:A:1178:G:H1'	2.17	0.59
2:01:9:LEU:HD11	2:01:198:LEU:HD11	1.85	0.59
2:01:45:ARG:NH1	2:02:37:HIS:HB3	2.18	0.59
3:03:1313:HIS:O	4:04:474:LEU:HD22	2.02	0.59
4:04:903:LEU:HG	4:04:904:ALA:H	1.68	0.59
4:04:1257:VAL:HA	4:04:1260:MET:HE3	1.84	0.59
6:E:90:PHE:HB3	6:E:150:GLY:O	2.02	0.59
1:A:323:U:C4'	24:W:13:SER:HA	2.32	0.59
1:A:614:C:C2'	1:A:615:G:H5''	2.32	0.59
2:02:224:LEU:HD23	2:02:224:LEU:O	2.01	0.59
3:03:690:VAL:CG1	3:03:1234:LYS:HB3	2.33	0.59
3:03:944:ARG:O	3:03:948:ILE:HG13	2.03	0.59
4:04:144:TYR:HB2	4:04:160:LEU:HB2	1.85	0.59
4:04:594:GLN:HG3	4:04:596:LEU:H	1.67	0.59
4:04:1031:VAL:HG12	4:04:1091:PRO:HD3	1.83	0.59
17:P:85:TYR:O	17:P:89:ARG:HG2	2.02	0.59
19:R:60:SER:O	19:R:64:LYS:HG3	2.03	0.59
21:T:18:LYS:O	21:T:19:SER:HB2	2.03	0.59
1:A:722:G:H4'	25:X:49:LYS:NZ	2.18	0.59
3:03:726:TYR:HB3	3:03:733:VAL:HB	1.84	0.59
3:03:1285:TYR:HB2	4:04:479:GLU:OE1	2.03	0.59
20:S:52:LEU:HD13	20:S:75:ILE:CD1	2.33	0.59
1:A:439:U:H5''	8:G:120:LYS:NZ	2.18	0.58
1:A:751:U:C2'	1:A:752:G:H5'	2.33	0.58
2:01:29:GLU:CB	2:01:30:PRO:HD3	2.31	0.58
3:03:39:ILE:HG12	3:03:39:ILE:O	2.02	0.58
4:04:220:ARG:NH1	4:04:224:LEU:HD11	2.18	0.58
4:04:1160:SER:O	4:04:1179:PRO:HG3	2.03	0.58
1:A:229:U:H2'	1:A:230:G:C8	2.38	0.58
2:01:208:ASN:OD1	2:01:210:THR:HG23	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:02:56:VAL:HA	2:02:146:VAL:HA	1.85	0.58
2:02:190:ALA:O	2:02:198:LEU:HB2	2.03	0.58
4:04:1347:LEU:O	4:04:1351:VAL:HG23	2.03	0.58
6:E:18:HIS:O	6:E:40:ILE:HA	2.03	0.58
6:E:190:ASN:HD22	6:E:190:ASN:H	1.47	0.58
9:H:55:VAL:H	9:H:56:PRO:HD2	1.67	0.58
21:T:35:LYS:HB3	21:T:35:LYS:HZ3	1.66	0.58
2:01:79:LEU:O	2:01:79:LEU:HD13	2.03	0.58
2:02:43:LEU:HD22	2:02:203:ILE:CD1	2.33	0.58
4:04:572:THR:OG1	4:04:576:ARG:HD2	2.04	0.58
4:04:801:VAL:O	4:04:805:GLN:HG3	2.02	0.58
8:G:169:TRP:CD1	8:G:170:LEU:HG	2.38	0.58
1:A:39:G:C2'	1:A:40:C:H5''	2.32	0.58
1:A:626:G:H2'	1:A:627:G:H8	1.69	0.58
3:03:518:ASN:O	3:03:691:PRO:HG3	2.04	0.58
11:J:138:GLU:HB3	11:J:142:ARG:HH12	1.68	0.58
15:N:113:THR:O	15:N:115:ILE:HG13	2.02	0.58
23:V:55:GLN:HG3	23:V:56:HIS:H	1.68	0.58
24:W:54:GLN:C	24:W:56:ILE:H	2.09	0.58
1:A:542:G:H5'	8:G:9:LYS:HE2	1.85	0.58
2:01:59:VAL:HG22	2:01:144:ILE:HA	1.84	0.58
3:03:841:ARG:HA	3:03:848:GLU:OE1	2.03	0.58
4:04:272:VAL:HG21	4:04:306:LEU:HD11	1.84	0.58
4:04:587:LEU:HD11	4:04:591:ILE:HG21	1.85	0.58
8:G:146:GLU:HA	8:G:149:LYS:HB2	1.85	0.58
17:P:15:VAL:HB	17:P:16:ILE:HD12	1.85	0.58
2:01:12:ARG:O	2:01:30:PRO:HD2	2.03	0.58
2:02:54:CYS:SG	2:02:92:VAL:HG22	2.43	0.58
2:02:208:ASN:ND2	2:02:210:THR:HG23	2.16	0.58
3:03:520:PRO:HG3	3:03:714:VAL:HG11	1.85	0.58
3:03:1334:GLY:C	4:04:25:ALA:HB3	2.28	0.58
4:04:374:LEU:O	4:04:378:LYS:HG3	2.04	0.58
8:G:53:GLN:HE22	9:H:111:ARG:HH12	1.52	0.58
9:H:37:VAL:HG11	9:H:113:VAL:HG22	1.85	0.58
14:M:17:LEU:HD21	14:M:93:ALA:HB1	1.86	0.58
1:A:578:C:H2'	1:A:579:A:C8	2.39	0.58
1:A:1240:U:H4'	11:J:37:THR:CG2	2.34	0.58
3:03:1046:VAL:HG12	3:03:1049:ILE:HD13	1.86	0.58
4:04:1342:ASP:O	4:04:1344:LEU:N	2.37	0.58
9:H:96:GLN:NE2	9:H:97:PRO:HD2	2.18	0.58
1:A:501:C:H2'	1:A:502:A:C8	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:523:A:C2'	1:A:524:G:H5''	2.33	0.58
2:02:154:PRO:HG3	4:04:541:LEU:HD22	1.86	0.58
3:03:1112:ILE:HG23	4:04:641:ILE:N	2.19	0.58
4:04:224:LEU:O	4:04:228:VAL:HG23	2.04	0.58
12:K:15:ASN:HA	12:K:18:ALA:HB3	1.86	0.58
23:V:29:PRO:HA	23:V:47:THR:O	2.02	0.58
4:04:427:PRO:O	4:04:429:LEU:HD22	2.03	0.58
8:G:113:ALA:O	8:G:117:VAL:HG23	2.03	0.58
17:P:14:ALA:HB3	17:P:40:GLU:O	2.04	0.58
4:04:650:LYS:O	4:04:654:ILE:HG13	2.03	0.58
6:E:19:GLN:HG2	6:E:41:ILE:HD11	1.86	0.58
16:O:100:ALA:HB3	16:O:103:CYS:HB3	1.86	0.58
1:A:932:C:H5''	11:J:3:ARG:NH2	2.19	0.57
1:A:1144:G:H2'	1:A:1145:A:C8	2.39	0.57
1:A:1527:U:O2'	1:A:1528:U:H5'	2.03	0.57
3:03:764:CYS:HB3	3:03:831:ILE:O	2.04	0.57
4:04:865:HIS:CE1	4:04:867:GLN:HB2	2.39	0.57
20:S:54:LEU:H	20:S:54:LEU:CD1	2.16	0.57
24:W:34:VAL:O	24:W:38:ILE:HG13	2.03	0.57
1:A:1297:G:H21	11:J:114:SER:H	1.52	0.57
2:02:81:ILE:HG23	2:02:131:CYS:HB3	1.84	0.57
3:03:131:THR:HG22	3:03:132:ASP:N	2.19	0.57
3:03:211:ARG:NH2	3:03:351:LEU:HB3	2.19	0.57
6:E:107:VAL:O	6:E:111:ILE:HG13	2.04	0.57
7:F:107:LYS:HZ3	7:F:144:GLY:HA3	1.68	0.57
24:W:38:ILE:HD13	24:W:81:GLN:NE2	2.17	0.57
1:A:321:A:H61	1:A:332:G:H1	1.52	0.57
3:03:521:LEU:O	3:03:521:LEU:HD13	2.04	0.57
3:03:715:THR:HB	3:03:785:ASP:HA	1.85	0.57
4:04:955:LYS:C	4:04:955:LYS:HD3	2.30	0.57
6:E:63:ARG:HA	6:E:63:ARG:HE	1.69	0.57
8:G:145:ARG:HH21	8:G:147:LYS:HG3	1.70	0.57
23:V:39:ILE:HG23	23:V:43:MET:HE3	1.85	0.57
1:A:1238:A:H2'	1:A:1239:A:H5'	1.85	0.57
2:02:228:LEU:HA	2:02:231:PHE:HD2	1.69	0.57
3:03:40:GLU:HG2	3:03:41:GLN:H	1.69	0.57
4:04:513:MET:HA	4:04:544:LEU:HD21	1.86	0.57
4:04:534:GLU:O	4:04:538:ARG:HG2	2.05	0.57
4:04:797:THR:HG22	4:04:924:GLY:HA3	1.84	0.57
11:J:55:LYS:HE3	11:J:60:ALA:HA	1.85	0.57
1:A:1072:G:N2	6:E:106:THR:HG21	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:426:ALA:HB3	4:04:427:PRO:HD3	1.87	0.57
5:05:38:LEU:H	5:05:38:LEU:HD12	1.69	0.57
6:E:129:LEU:HD23	6:E:129:LEU:H	1.68	0.57
7:F:107:LYS:HB3	7:F:143:LEU:HD21	1.86	0.57
18:Q:36:SER:HB3	23:V:6:LYS:HZ3	1.69	0.57
20:S:28:ARG:HD2	20:S:28:ARG:C	2.29	0.57
20:S:28:ARG:HE	20:S:29:ASN:ND2	2.03	0.57
1:A:618:C:H5''	1:A:620:C:OP2	2.03	0.57
3:03:448:LEU:HA	3:03:451:ARG:HB2	1.86	0.57
15:N:43:TRP:HZ3	15:N:45:THR:HG23	1.70	0.57
21:T:21:VAL:O	21:T:21:VAL:HG13	2.05	0.57
1:A:29:U:O2'	1:A:30:U:H5'	2.05	0.57
3:03:864:LYS:HZ2	3:03:881:ASP:HB3	1.70	0.57
4:04:405:GLU:O	4:04:408:VAL:HG22	2.03	0.57
6:E:21:ARG:O	6:E:23:TRP:N	2.36	0.57
6:E:31:ILE:CB	6:E:42:ASN:HB2	2.34	0.57
6:E:139:ARG:NH1	6:E:139:ARG:HB2	2.20	0.57
10:I:44:ARG:HA	10:I:58:HIS:HA	1.87	0.57
12:K:10:LEU:HD22	12:K:74:ILE:HD11	1.87	0.57
16:O:17:LYS:HB2	16:O:17:LYS:NZ	2.20	0.57
16:O:19:ASN:O	16:O:21:PRO:HD3	2.03	0.57
18:Q:36:SER:HB3	23:V:6:LYS:NZ	2.20	0.57
2:02:154:PRO:HB2	2:02:157:THR:HG22	1.87	0.57
3:03:1122:LYS:HG2	3:03:1229:TYR:CD2	2.39	0.57
4:04:406:ALA:HA	4:04:409:TRP:HD1	1.70	0.57
11:J:20:GLU:HA	11:J:23:ALA:HB3	1.87	0.57
1:A:1233:G:OP1	13:L:124:PRO:HB2	2.05	0.57
3:03:405:PHE:O	3:03:409:LEU:HG	2.05	0.57
3:03:835:GLU:C	3:03:836:LEU:HD12	2.30	0.57
4:04:65:VAL:HG21	4:04:71:LEU:HD23	1.87	0.57
4:04:456:ALA:HB2	4:04:499:ILE:HG23	1.87	0.57
4:04:865:HIS:HE1	4:04:867:GLN:HB2	1.70	0.57
6:E:11:LYS:HG3	6:E:15:HIS:CE1	2.40	0.57
9:H:105:ILE:HD12	9:H:105:ILE:N	2.20	0.57
14:M:65:TYR:HB3	18:Q:95:LEU:HD11	1.86	0.57
1:A:1108:G:H5'	7:F:175:HIS:ND1	2.19	0.56
2:01:228:LEU:O	2:01:232:VAL:HG23	2.04	0.56
3:03:66:SER:OG	3:03:487:LEU:HD11	2.05	0.56
3:03:402:ARG:HA	3:03:405:PHE:HD2	1.70	0.56
3:03:1046:VAL:CG1	3:03:1049:ILE:HG21	2.35	0.56
4:04:796:LEU:O	4:04:800:LEU:HD13	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:821:MET:HG3	4:04:823:THR:HG23	1.87	0.56
4:04:850:LYS:C	4:04:852:GLY:N	2.63	0.56
4:04:1333:THR:O	4:04:1337:VAL:HG13	2.05	0.56
7:F:156:LEU:HD12	7:F:156:LEU:O	2.04	0.56
10:I:66:ALA:HB3	10:I:71:ILE:HD11	1.87	0.56
19:R:81:ILE:HG22	19:R:86:LEU:CD1	2.35	0.56
1:A:1239:A:H5''	1:A:1240:U:H5	1.69	0.56
2:01:192:VAL:HG22	2:01:193:GLU:N	2.18	0.56
3:03:564:PRO:HD2	3:03:572:ILE:HG13	1.86	0.56
3:03:1025:PHE:O	3:03:1029:LEU:HD13	2.05	0.56
4:04:1226:VAL:O	4:04:1229:VAL:HG12	2.05	0.56
6:E:42:ASN:ND2	6:E:42:ASN:C	2.62	0.56
1:A:656:G:H4'	19:R:61:GLN:HE21	1.70	0.56
1:A:730:G:H2'	1:A:731:G:O4'	2.05	0.56
2:01:28:LEU:HD12	2:01:28:LEU:N	2.19	0.56
3:03:431:LYS:O	3:03:435:ILE:HG13	2.05	0.56
4:04:179:LYS:HD2	4:04:293:ARG:HH22	1.70	0.56
4:04:481:ARG:HH11	4:04:481:ARG:HG3	1.70	0.56
4:04:863:LEU:HG	4:04:901:ARG:HD3	1.88	0.56
13:L:48:ARG:O	13:L:52:GLU:HG3	2.05	0.56
17:P:3:ILE:HD11	17:P:7:ASN:HD22	1.70	0.56
19:R:68:TYR:HD1	19:R:71:ARG:HH21	1.53	0.56
20:S:7:ALA:HB3	20:S:18:GLN:HB2	1.87	0.56
1:A:1128:C:O2'	1:A:1129:C:H5'	2.04	0.56
3:03:206:ALA:O	3:03:209:ILE:HG22	2.05	0.56
3:03:562:GLU:OE2	3:03:664:GLY:HA3	2.06	0.56
4:04:66:LYS:HB3	4:04:69:GLU:HB3	1.87	0.56
4:04:952:VAL:HG22	4:04:954:ASN:H	1.70	0.56
6:E:10:LEU:C	6:E:11:LYS:O	2.48	0.56
10:I:61:LEU:HD12	10:I:61:LEU:N	2.20	0.56
11:J:92:PRO:HA	11:J:95:ARG:HB2	1.87	0.56
18:Q:71:GLY:O	18:Q:79:SER:HA	2.05	0.56
3:03:257:ALA:HB3	3:03:262:TYR:HE2	1.69	0.56
4:04:749:LYS:HD3	4:04:753:SER:HB2	1.87	0.56
4:04:1107:VAL:HA	4:04:1122:ALA:HA	1.87	0.56
7:F:4:VAL:HG11	7:F:9:ILE:HD12	1.87	0.56
9:H:64:GLU:O	9:H:68:ARG:HB2	2.06	0.56
10:I:38:ARG:HG3	10:I:40:GLU:HG3	1.86	0.56
10:I:55:HIS:CE1	10:I:56:LYS:HE2	2.40	0.56
12:K:9:MET:HG3	12:K:26:MET:SD	2.45	0.56
7:F:118:SER:O	7:F:122:GLN:HG2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:113:LYS:HE2	13:L:118:ARG:O	2.05	0.56
3:03:1151:LEU:HD23	3:03:1151:LEU:N	2.19	0.56
4:04:334:LYS:H	4:04:338:PHE:HD1	1.54	0.56
9:H:59:ILE:O	9:H:63:MET:HG2	2.06	0.56
13:L:18:VAL:HG13	13:L:64:ILE:HG12	1.87	0.56
22:U:42:SER:HB3	22:U:52:GLN:HG2	1.88	0.56
1:A:229:U:H5''	20:S:33:ILE:HD13	1.88	0.56
1:A:952:U:O4	17:P:102:LYS:HD3	2.04	0.56
5:05:6:VAL:HG11	5:05:51:LEU:HD11	1.88	0.56
8:G:33:ILE:HG23	8:G:33:ILE:O	2.06	0.56
17:P:48:SER:O	17:P:52:ILE:HG13	2.06	0.56
19:R:64:LYS:O	19:R:67:ASP:HB3	2.05	0.56
3:03:241:LEU:O	3:03:243:PRO:HD3	2.05	0.56
3:03:518:ASN:HB3	3:03:763:THR:HG21	1.87	0.56
4:04:395:LYS:HA	4:04:398:LYS:HE2	1.88	0.56
10:I:38:ARG:HA	10:I:38:ARG:HE	1.71	0.56
20:S:8:ARG:HB3	20:S:28:ARG:NH2	2.21	0.56
1:A:877:G:H21	12:K:3:GLN:HE21	1.53	0.56
3:03:838:CYS:HB3	3:03:1050:VAL:CG2	2.35	0.56
3:03:1292:THR:O	3:03:1296:ASP:HB3	2.06	0.56
4:04:59:ALA:HB1	4:04:90:VAL:HG11	1.88	0.56
4:04:505:ASP:HA	4:04:508:LEU:HD13	1.87	0.56
5:05:45:LYS:O	5:05:49:ILE:HG13	2.06	0.56
9:H:136:VAL:O	9:H:140:ILE:HG12	2.06	0.56
11:J:96:ASN:HB3	11:J:100:MET:CE	2.36	0.56
1:A:367:U:O2'	1:A:368:U:H4'	2.06	0.55
1:A:427:U:H1'	1:A:541:G:H5''	1.87	0.55
2:02:100:LEU:HB2	2:02:144:ILE:HG23	1.88	0.55
4:04:738:ARG:HD2	4:04:738:ARG:C	2.31	0.55
4:04:1259:GLN:HA	4:04:1262:ARG:HG3	1.87	0.55
5:05:46:THR:HA	5:05:49:ILE:HD12	1.88	0.55
8:G:190:LEU:CD1	8:G:192:ALA:H	2.17	0.55
1:A:722:G:H4'	25:X:49:LYS:HZ3	1.70	0.55
1:A:1072:G:H21	6:E:106:THR:HG21	1.70	0.55
3:03:81:ASP:OD2	3:03:83:GLN:HB2	2.06	0.55
3:03:255:ILE:HB	3:03:263:VAL:HB	1.87	0.55
4:04:264:ASP:HB3	4:04:324:LEU:HD22	1.88	0.55
1:A:404:G:H5'	8:G:115:GLN:HE22	1.71	0.55
1:A:1225:A:H5'	1:A:1226:C:OP2	2.07	0.55
3:03:406:ASN:HB3	3:03:411:ARG:HB2	1.87	0.55
4:04:857:LEU:CD1	4:04:858:VAL:HG12	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:104:ILE:HD11	9:H:114:LEU:HB2	1.89	0.55
18:Q:55:SER:HA	18:Q:57:SER:H	1.70	0.55
1:A:292:G:H21	1:A:608:A:N6	1.91	0.55
2:01:14:VAL:HG22	2:01:15:ASP:N	2.19	0.55
3:03:182:SER:H	3:03:395:TYR:HE1	1.53	0.55
3:03:239:MET:HE3	3:03:241:LEU:HD13	1.88	0.55
3:03:756:TYR:HA	3:03:765:ILE:O	2.07	0.55
8:G:97:LEU:O	8:G:101:VAL:HG23	2.06	0.55
11:J:96:ASN:HB3	11:J:100:MET:HE2	1.88	0.55
13:L:7:GLY:HA3	13:L:85:ALA:HB2	1.89	0.55
14:M:21:ALA:O	14:M:25:ILE:HG12	2.06	0.55
15:N:73:VAL:HB	15:N:78:ILE:HD11	1.89	0.55
1:A:941:G:H21	13:L:122:ARG:HH22	1.54	0.55
2:02:158:ARG:HA	2:02:158:ARG:HE	1.70	0.55
3:03:216:THR:HG22	3:03:217:THR:H	1.71	0.55
3:03:902:LEU:HD13	22:U:12:ARG:H	1.72	0.55
4:04:21:LYS:HB2	4:04:1341:ARG:NE	2.22	0.55
4:04:1241:TYR:HB3	4:04:1246:VAL:HB	1.87	0.55
6:E:114:LEU:HD11	6:E:145:GLU:OE1	2.07	0.55
14:M:13:PHE:HB3	18:Q:94:GLY:HA3	1.88	0.55
16:O:98:ARG:HB2	16:O:116:TYR:HD1	1.70	0.55
1:A:912:C:H5''	16:O:42:LYS:NZ	2.21	0.55
2:01:76:GLU:HB3	2:01:80:GLU:OE1	2.07	0.55
2:01:194:GLN:O	2:01:195:ARG:HB2	2.05	0.55
3:03:239:MET:HE2	3:03:287:VAL:HG11	1.88	0.55
4:04:658:GLU:O	4:04:661:VAL:HG22	2.06	0.55
4:04:833:GLU:HB2	4:04:1242:ARG:HH12	1.72	0.55
6:E:9:MET:HA	6:E:9:MET:HE2	1.89	0.55
8:G:12:ARG:HA	8:G:34:GLU:H	1.72	0.55
8:G:143:SER:HA	8:G:178:GLU:HA	1.89	0.55
22:U:23:TYR:OH	22:U:65:LEU:HD22	2.06	0.55
25:X:17:ARG:O	25:X:21:ARG:HG2	2.05	0.55
1:A:974:A:OP1	18:Q:70:HIS:HB2	2.07	0.55
4:04:807:LEU:HD11	4:04:894:VAL:HG23	1.89	0.55
6:E:139:ARG:HB2	6:E:139:ARG:HH11	1.72	0.55
9:H:31:SER:HA	9:H:53:ARG:HA	1.89	0.55
22:U:51:TYR:HA	22:U:54:GLN:HB2	1.89	0.55
1:A:17:U:H5'	9:H:20:VAL:HG12	1.88	0.55
1:A:612:C:H5'	8:G:80:ARG:NH1	2.22	0.55
1:A:614:C:H3'	1:A:615:G:H5''	1.88	0.55
2:01:234:LEU:HD11	2:02:217:ILE:HD12	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:555:TYR:CD1	4:04:565:ALA:HB2	2.42	0.55
7:F:86:LEU:O	7:F:90:VAL:HG23	2.06	0.55
8:G:176:LYS:NZ	8:G:178:GLU:HB3	2.22	0.55
10:I:9:MET:HE2	10:I:59:TYR:HE1	1.70	0.55
19:R:9:LYS:NZ	19:R:9:LYS:HB3	2.21	0.55
3:03:900:LYS:O	3:03:901:LEU:HB2	2.06	0.55
3:03:1036:ILE:O	3:03:1036:ILE:HG22	2.06	0.55
7:F:9:ILE:HG13	18:Q:97:LYS:HD3	1.89	0.55
10:I:81:ASN:ND2	10:I:83:ALA:HB3	2.22	0.55
24:W:53:MET:HA	24:W:56:ILE:HD13	1.89	0.55
1:A:577:G:H1'	1:A:816:A:H2'	1.88	0.55
1:A:826:C:H4'	12:K:12:ARG:HG2	1.89	0.55
4:04:155:GLU:HG3	4:04:156:ARG:H	1.72	0.55
4:04:859:PRO:HG2	4:04:862:THR:OG1	2.07	0.55
1:A:570:G:H2'	1:A:571:U:C6	2.42	0.54
2:02:65:LEU:HB2	2:02:169:GLY:HA2	1.88	0.54
3:03:1304:MET:O	3:03:1308:ILE:HG12	2.07	0.54
6:E:35:ARG:HH11	6:E:35:ARG:HB2	1.70	0.54
1:A:1379:G:O2'	1:A:1380:U:H5'	2.08	0.54
3:03:91:THR:HG23	3:03:138:ILE:HA	1.89	0.54
3:03:104:ILE:HD12	3:03:104:ILE:N	2.21	0.54
3:03:615:VAL:HG13	3:03:651:ASP:H	1.72	0.54
3:03:723:VAL:HG22	3:03:776:PRO:HG3	1.89	0.54
8:G:98:ASP:HB3	8:G:132:ALA:HB1	1.90	0.54
24:W:84:LYS:HB2	24:W:84:LYS:NZ	2.22	0.54
1:A:440:C:C3'	1:A:441:A:H5''	2.36	0.54
1:A:1240:U:O4'	11:J:41:ILE:HD11	2.08	0.54
3:03:472:GLU:HG2	3:03:476:LYS:HE3	1.89	0.54
4:04:217:LEU:HD13	4:04:217:LEU:C	2.33	0.54
7:F:57:GLU:HB2	7:F:64:ARG:HB3	1.90	0.54
16:O:113:ARG:HA	16:O:118:VAL:HB	1.88	0.54
1:A:741:G:H4'	19:R:54:GLY:HA3	1.88	0.54
3:03:196:VAL:CG1	3:03:206:ALA:HA	2.37	0.54
3:03:1106:ARG:O	3:03:1107:MET:HB2	2.08	0.54
4:04:8:LEU:HB2	4:04:1371:ARG:HH12	1.73	0.54
4:04:317:THR:HG23	4:04:320:ASN:HB3	1.90	0.54
4:04:522:GLY:O	4:04:525:MET:HG2	2.07	0.54
6:E:31:ILE:HG13	6:E:33:GLY:H	1.72	0.54
7:F:115:VAL:HG21	7:F:201:ILE:HD11	1.89	0.54
12:K:34:ALA:O	12:K:38:VAL:HG23	2.08	0.54
15:N:85:VAL:HG11	15:N:92:ARG:HD2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:993:G:H2'	1:A:993:G:N3	2.22	0.54
1:A:1277:C:O2'	1:A:1278:G:H4'	2.08	0.54
3:03:338:THR:HG22	3:03:339:ASN:N	2.23	0.54
3:03:736:VAL:HG12	3:03:737:ASN:O	2.07	0.54
3:03:1151:LEU:H	3:03:1151:LEU:CD2	2.18	0.54
4:04:326:SER:O	4:04:330:MET:HG3	2.07	0.54
20:S:40:ASN:HD21	20:S:42:ILE:HG13	1.72	0.54
1:A:104:G:OP2	24:W:8:LYS:HD3	2.07	0.54
1:A:376:G:C2'	1:A:377:G:H5''	2.32	0.54
1:A:774:G:H2'	1:A:775:G:H5'	1.89	0.54
1:A:1030:U:H3'	1:A:1031:C:H5'	1.90	0.54
3:03:275:ARG:O	3:03:279:LYS:HG3	2.08	0.54
3:03:697:LYS:HZ3	3:03:1178:LYS:HD2	1.71	0.54
3:03:810:TYR:HB3	3:03:817:LEU:HD13	1.90	0.54
4:04:280:LYS:HA	4:04:283:LEU:HD12	1.88	0.54
4:04:833:GLU:HG3	4:04:838:ARG:HD2	1.89	0.54
9:H:104:ILE:HG13	9:H:122:VAL:CG2	2.38	0.54
11:J:137:ARG:HH11	11:J:141:HIS:CE1	2.26	0.54
14:M:56:HIS:HD2	14:M:57:VAL:HG12	1.73	0.54
16:O:98:ARG:NH1	16:O:106:VAL:HG12	2.23	0.54
25:X:45:ARG:HB2	25:X:45:ARG:CZ	2.38	0.54
2:01:9:LEU:HD23	2:01:9:LEU:H	1.72	0.54
2:01:166:ARG:N	2:01:167:PRO:HD2	2.22	0.54
4:04:155:GLU:HG3	4:04:156:ARG:N	2.23	0.54
4:04:1068:THR:O	4:04:1072:LYS:HG3	2.07	0.54
12:K:17:GLN:NE2	12:K:69:ALA:HB1	2.23	0.54
21:T:26:ARG:O	21:T:26:ARG:HD3	2.08	0.54
2:01:32:GLU:HB2	2:01:35:PHE:CE2	2.43	0.54
8:G:18:LEU:HD22	8:G:63:ILE:HD11	1.89	0.54
17:P:63:VAL:HG21	17:P:68:LEU:HD13	1.90	0.54
20:S:70:ARG:O	20:S:74:LEU:HG	2.08	0.54
3:03:226:GLU:N	3:03:226:GLU:CD	2.66	0.54
4:04:114:ILE:HG23	4:04:115:TRP:CD1	2.43	0.54
4:04:490:ILE:O	4:04:498:PRO:HA	2.07	0.54
4:04:496:GLY:O	4:04:498:PRO:HD3	2.08	0.54
4:04:842:ARG:HG2	4:04:1251:LYS:HE3	1.89	0.54
8:G:97:LEU:HD23	8:G:132:ALA:HA	1.90	0.54
11:J:91:ARG:O	11:J:95:ARG:HG3	2.07	0.54
24:W:56:ILE:O	24:W:59:ARG:HB3	2.07	0.54
4:04:693:VAL:HG21	4:04:743:MET:HE3	1.90	0.54
9:H:89:THR:O	9:H:89:THR:HG22	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:144:ALA:O	11:J:148:LYS:HG3	2.08	0.54
1:A:440:C:C2'	1:A:441:A:H5''	2.37	0.53
1:A:486:U:HO2'	1:A:487:A:H8	1.56	0.53
1:A:837:U:H2'	1:A:838:G:H8	1.72	0.53
2:01:95:LYS:HE3	2:01:120:ASP:OD2	2.08	0.53
3:03:538:LEU:O	3:03:571:LEU:HD13	2.07	0.53
3:03:623:LEU:HD12	3:03:623:LEU:O	2.08	0.53
3:03:682:GLY:HA2	3:03:685:MET:HE3	1.90	0.53
4:04:22:ILE:HG23	4:04:22:ILE:O	2.08	0.53
4:04:653:ILE:HD13	4:04:692:ARG:HB3	1.89	0.53
4:04:1221:LEU:HD13	4:04:1221:LEU:C	2.32	0.53
4:04:1366:HIS:HA	4:04:1369:ARG:HB2	1.90	0.53
6:E:54:LEU:HD23	6:E:57:LEU:HD23	1.90	0.53
8:G:9:LYS:HA	8:G:12:ARG:HD3	1.88	0.53
10:I:22:ILE:O	10:I:26:THR:HG22	2.08	0.53
13:L:66:VAL:HG13	13:L:74:GLN:NE2	2.23	0.53
17:P:14:ALA:HB1	17:P:33:LEU:HD11	1.90	0.53
20:S:52:LEU:O	20:S:54:LEU:HD12	2.08	0.53
21:T:13:SER:HB2	21:T:21:VAL:CG1	2.38	0.53
1:A:1500:A:H5''	1:A:1508:A:H5''	1.89	0.53
3:03:74:ARG:HB2	3:03:99:LYS:HE3	1.90	0.53
3:03:338:THR:HG22	3:03:339:ASN:H	1.74	0.53
3:03:576:SER:HB2	3:03:579:ALA:HB2	1.90	0.53
3:03:1304:MET:HE3	3:03:1315:MET:HB2	1.89	0.53
4:04:268:LEU:HD21	4:04:324:LEU:HD12	1.91	0.53
4:04:431:ARG:HD3	4:04:493:PRO:HG3	1.89	0.53
17:P:39:ALA:HB3	17:P:42:VAL:HG11	1.90	0.53
23:V:12:LEU:HD23	23:V:12:LEU:H	1.73	0.53
1:A:71:A:H3'	1:A:72:A:H5''	1.91	0.53
1:A:563:A:N3	1:A:563:A:H2'	2.21	0.53
1:A:880:C:H2'	1:A:881:G:H8	1.73	0.53
4:04:21:LYS:HB2	4:04:1341:ARG:HE	1.73	0.53
4:04:569:LEU:HD12	4:04:569:LEU:N	2.22	0.53
8:G:115:GLN:O	8:G:119:HIS:HB2	2.09	0.53
15:N:124:LYS:HD2	15:N:124:LYS:C	2.32	0.53
20:S:11:ALA:HB3	20:S:14:ARG:HB2	1.90	0.53
3:03:563:THR:HG23	3:03:563:THR:O	2.09	0.53
3:03:830:THR:HG21	3:03:1238:LEU:HD21	1.90	0.53
14:M:57:VAL:O	14:M:58:ASN:ND2	2.41	0.53
14:M:80:THR:HG22	14:M:81:GLU:N	2.22	0.53
25:X:41:PRO:O	25:X:42:THR:C	2.52	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:02:213:PRO:O	2:02:217:ILE:HG13	2.08	0.53
3:03:1327:LEU:O	3:03:1330:ILE:HG12	2.08	0.53
4:04:1369:ARG:HA	4:04:1372:ARG:HB3	1.90	0.53
6:E:40:ILE:C	6:E:41:ILE:HG13	2.33	0.53
6:E:63:ARG:HA	6:E:63:ARG:NE	2.24	0.53
12:K:91:LEU:HD21	12:K:112:ASP:HB2	1.90	0.53
16:O:85:ARG:HG3	16:O:85:ARG:HH11	1.73	0.53
17:P:28:ARG:O	17:P:31:ALA:HB3	2.08	0.53
18:Q:71:GLY:HA3	18:Q:79:SER:HB3	1.89	0.53
3:03:697:LYS:NZ	3:03:1178:LYS:HD2	2.23	0.53
3:03:727:VAL:HG22	3:03:732:ILE:HG23	1.90	0.53
3:03:1256:GLN:NE2	3:03:1298:VAL:HB	2.23	0.53
3:03:1334:GLY:O	4:04:25:ALA:HB3	2.08	0.53
4:04:850:LYS:HB3	4:04:851:PRO:CD	2.35	0.53
6:E:23:TRP:HB2	6:E:189:THR:HG21	1.90	0.53
6:E:29:PRO:O	6:E:31:ILE:N	2.41	0.53
6:E:35:ARG:HA	6:E:40:ILE:HG13	1.90	0.53
18:Q:87:ALA:HA	18:Q:92:ILE:HD13	1.89	0.53
19:R:87:ARG:HG3	19:R:88:ARG:NH1	2.23	0.53
1:A:59:A:H3'	1:A:60:A:H5'	1.89	0.53
1:A:552:U:H2'	1:A:553:A:H8	1.74	0.53
1:A:917:G:H2'	1:A:918:A:C8	2.44	0.53
1:A:1222:G:H5''	23:V:77:ARG:HH21	1.71	0.53
3:03:292:ILE:HG23	3:03:295:LYS:HD2	1.91	0.53
3:03:864:LYS:HG3	3:03:865:LEU:CD1	2.38	0.53
6:E:117:LEU:HD23	6:E:117:LEU:O	2.09	0.53
7:F:59:PRO:HG2	7:F:62:SER:OG	2.09	0.53
11:J:6:ILE:CG1	11:J:7:GLY:H	2.21	0.53
19:R:6:ALA:O	19:R:10:ILE:HG13	2.08	0.53
1:A:615:G:H2'	1:A:616:G:C8	2.44	0.53
3:03:502:VAL:HG13	3:03:503:LYS:N	2.24	0.53
4:04:705:THR:OG1	4:04:718:SER:HA	2.08	0.53
4:04:764:ARG:HD3	4:04:764:ARG:C	2.34	0.53
4:04:911:LYS:HE2	4:04:1363:TYR:HE2	1.74	0.53
4:04:1350:ASN:HB2	4:04:1357:ILE:HG22	1.91	0.53
7:F:42:LEU:HD23	7:F:54:ILE:HD13	1.91	0.53
7:F:147:GLY:HA2	7:F:170:GLY:HA3	1.90	0.53
8:G:202:LEU:C	8:G:204:SER:H	2.17	0.53
14:M:6:ILE:HD11	14:M:79:PRO:HB3	1.90	0.53
18:Q:9:GLU:O	18:Q:13:VAL:HG23	2.08	0.53
1:A:1148:U:HI'	13:L:17:ARG:HD3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1306:A:H61	1:A:1331:G:H1'	1.73	0.53
2:01:185:TYR:HB2	2:01:201:LEU:HD11	1.90	0.53
3:03:882:ILE:HD12	3:03:882:ILE:H	1.74	0.53
4:04:306:LEU:O	4:04:327:LEU:HG	2.08	0.53
12:K:29:SER:O	12:K:33:VAL:HG23	2.09	0.53
13:L:62:LEU:HD12	13:L:62:LEU:O	2.08	0.53
14:M:15:HIS:O	14:M:18:ILE:HG22	2.08	0.53
1:A:578:C:H2'	1:A:579:A:H8	1.73	0.53
1:A:1124:G:C5'	14:M:37:ARG:HG3	2.39	0.53
3:03:817:LEU:HD12	3:03:1080:ASN:HD21	1.74	0.53
4:04:179:LYS:HB2	4:04:184:ALA:HB2	1.91	0.53
7:F:11:LEU:HA	7:F:15:LYS:HB2	1.91	0.53
7:F:69:THR:HG21	7:F:75:VAL:HG21	1.91	0.53
11:J:43:TYR:O	11:J:47:GLU:HG2	2.09	0.53
17:P:14:ALA:HB1	17:P:33:LEU:CD1	2.39	0.53
17:P:18:LEU:HD22	17:P:21:ILE:HD11	1.91	0.53
24:W:6:ALA:C	24:W:8:LYS:H	2.15	0.53
1:A:12:U:H2'	1:A:13:U:H5''	1.91	0.52
1:A:328:C:H4'	1:A:329:A:H5'	1.91	0.52
1:A:414:A:H2'	1:A:414:A:N3	2.24	0.52
1:A:577:G:C1'	1:A:816:A:H2'	2.39	0.52
3:03:436:ARG:HA	3:03:436:ARG:NE	2.23	0.52
3:03:521:LEU:HG	3:03:667:LEU:HD22	1.90	0.52
4:04:1231:ARG:HG2	4:04:1231:ARG:HH11	1.74	0.52
4:04:1363:TYR:HA	4:04:1366:HIS:HB2	1.89	0.52
6:E:26:LYS:C	6:E:28:LYS:N	2.67	0.52
6:E:164:ILE:HG23	6:E:186:ILE:HD11	1.91	0.52
12:K:13:ILE:O	12:K:17:GLN:HG2	2.09	0.52
19:R:26:VAL:O	19:R:30:LEU:HD13	2.07	0.52
19:R:53:ARG:HG3	19:R:56:LEU:HD23	1.91	0.52
24:W:56:ILE:HD12	24:W:56:ILE:N	2.24	0.52
3:03:708:VAL:CG1	3:03:794:LEU:HD22	2.35	0.52
4:04:98:ARG:O	4:04:248:ASP:HB2	2.08	0.52
4:04:355:ILE:CD1	4:04:464:ASP:HB2	2.39	0.52
5:05:38:LEU:HD12	5:05:38:LEU:N	2.24	0.52
2:01:166:ARG:H	2:01:167:PRO:HD2	1.74	0.52
2:01:195:ARG:HA	2:01:195:ARG:NE	2.24	0.52
4:04:111:THR:HG23	4:04:300:GLN:NE2	2.24	0.52
4:04:1350:ASN:HA	4:04:1353:VAL:HG12	1.91	0.52
6:E:18:HIS:O	6:E:40:ILE:CA	2.56	0.52
7:F:113:LYS:O	7:F:113:LYS:HD3	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:125:ASP:OD1	11:J:130:LYS:HE2	2.10	0.52
22:U:34:THR:O	22:U:36:SER:N	2.42	0.52
24:W:28:ARG:HA	24:W:31:ILE:HD12	1.90	0.52
1:A:273:U:C2'	1:A:274:A:H5'	2.40	0.52
1:A:722:G:H1	1:A:733:G:H1	1.56	0.52
1:A:1328:C:O3'	17:P:28:ARG:HB2	2.10	0.52
1:A:1359:C:H2'	1:A:1361:G:OP2	2.09	0.52
3:03:1103:VAL:C	3:03:1105:SER:H	2.17	0.52
4:04:597:GLY:H	4:04:600:ALA:HB3	1.74	0.52
13:L:128:LYS:HB2	13:L:128:LYS:NZ	2.24	0.52
20:S:57:ILE:O	20:S:61:VAL:HG23	2.10	0.52
24:W:24:ARG:O	24:W:27:MET:HB3	2.10	0.52
25:X:17:ARG:HB3	25:X:20:LYS:HD2	1.92	0.52
1:A:326:G:H2'	1:A:327:A:H5'	1.92	0.52
1:A:550:G:N2	16:O:114:SER:HB3	2.24	0.52
2:02:172:LEU:H	2:02:172:LEU:CD2	2.23	0.52
3:03:533:LEU:HD11	3:03:568:ASN:CB	2.40	0.52
3:03:854:ILE:O	3:03:854:ILE:HG23	2.09	0.52
4:04:81:ARG:HH22	6:E:206:ALA:HB1	1.73	0.52
6:E:23:TRP:CD1	6:E:25:PRO:HD3	2.44	0.52
6:E:151:ILE:HG13	6:E:154:MET:SD	2.49	0.52
9:H:22:LYS:HB3	9:H:29:ILE:CG2	2.38	0.52
3:03:109:ALA:O	3:03:111:GLU:N	2.43	0.52
3:03:498:ILE:N	3:03:498:ILE:HD12	2.24	0.52
3:03:929:ILE:HG13	3:03:930:ASP:N	2.19	0.52
3:03:1204:LEU:HB3	3:03:1205:PRO:HD2	1.91	0.52
4:04:293:ARG:HA	4:04:296:LYS:HB2	1.90	0.52
4:04:824:PRO:O	4:04:826:ILE:HG13	2.10	0.52
4:04:1138:LEU:HB3	4:04:1139:PRO:HD3	1.92	0.52
4:04:1323:ALA:HB1	4:04:1328:THR:HG23	1.92	0.52
23:V:40:PHE:H	23:V:43:MET:CE	2.21	0.52
3:03:523:GLU:O	3:03:527:LYS:HG3	2.08	0.52
3:03:714:VAL:HB	3:03:786:GLY:HA3	1.92	0.52
3:03:1109:ILE:O	3:03:1109:ILE:HG12	2.08	0.52
4:04:842:ARG:NH2	4:04:884:SER:HB2	2.24	0.52
6:E:31:ILE:HB	6:E:41:ILE:O	2.09	0.52
1:A:539:A:H2'	1:A:540:G:C8	2.45	0.52
1:A:974:A:OP2	18:Q:70:HIS:O	2.28	0.52
1:A:1096:C:H4'	6:E:136:MET:SD	2.50	0.52
2:01:75:GLN:HG3	2:01:76:GLU:HG3	1.92	0.52
2:02:158:ARG:HA	2:02:158:ARG:NE	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:550:VAL:HG23	3:03:560:PRO:HG2	1.91	0.52
3:03:1297:ASP:HB3	3:03:1300:GLY:H	1.74	0.52
4:04:77:ARG:NH2	6:E:18:HIS:NE2	2.55	0.52
4:04:145:VAL:HG21	4:04:188:LEU:HD11	1.91	0.52
4:04:220:ARG:HH12	4:04:224:LEU:HD11	1.75	0.52
4:04:850:LYS:C	4:04:852:GLY:H	2.18	0.52
6:E:15:HIS:C	6:E:17:GLY:N	2.68	0.52
8:G:109:THR:HG22	8:G:111:ALA:H	1.75	0.52
9:H:95:MET:HG2	9:H:124:ALA:CB	2.40	0.52
9:H:159:SER:HB3	9:H:162:GLU:HB2	1.91	0.52
15:N:81:LEU:HD23	15:N:81:LEU:H	1.75	0.52
17:P:19:THR:HG22	17:P:25:GLY:HA2	1.92	0.52
21:T:7:LEU:CD2	21:T:24:ILE:HD13	2.40	0.52
23:V:78:THR:HG22	23:V:79:TYR:H	1.73	0.52
1:A:39:G:C3'	1:A:40:C:H5''	2.40	0.52
2:01:26:VAL:HG22	2:01:203:ILE:HB	1.92	0.52
2:01:79:LEU:HD13	2:01:79:LEU:C	2.34	0.52
2:02:14:VAL:O	2:02:14:VAL:HG13	2.09	0.52
3:03:1207:SER:O	3:03:1209:GLN:N	2.43	0.52
3:03:1278:LEU:HB3	3:03:1287:LEU:HD13	1.91	0.52
4:04:1140:ARG:HA	4:04:1143:ASP:OD2	2.10	0.52
6:E:47:VAL:HB	6:E:48:PRO:CD	2.31	0.52
6:E:67:ILE:HA	6:E:160:ALA:HB3	1.90	0.52
14:M:14:ASP:HB2	14:M:17:LEU:HB3	1.92	0.52
24:W:23:ARG:HD2	24:W:60:GLN:HE22	1.74	0.52
2:02:108:GLY:O	2:02:133:LEU:HB3	2.09	0.52
3:03:623:LEU:HD12	3:03:623:LEU:C	2.34	0.52
4:04:325:LYS:HD3	4:04:329:ASP:HB3	1.91	0.52
4:04:678:ARG:O	4:04:682:VAL:HG23	2.10	0.52
4:04:901:ARG:HD2	4:04:906:GLY:O	2.10	0.52
1:A:893:C:H2'	1:A:894:G:H8	1.74	0.51
1:A:893:C:H4'	1:A:1416:G:H5'	1.91	0.51
4:04:678:ARG:HH11	4:04:682:VAL:HG21	1.75	0.51
4:04:848:VAL:HB	4:04:858:VAL:CG1	2.39	0.51
4:04:1306:LEU:C	4:04:1307:LEU:HD12	2.36	0.51
7:F:20:THR:HB	7:F:57:GLU:OE1	2.09	0.51
17:P:106:ARG:HD3	17:P:109:LYS:HD2	1.91	0.51
23:V:35:ARG:NH1	23:V:50:VAL:HG23	2.25	0.51
1:A:972:C:H4'	14:M:59:LYS:HG3	1.92	0.51
3:03:30:ILE:H	3:03:30:ILE:CD1	2.11	0.51
4:04:1037:PHE:HE2	4:04:1110:GLU:HA	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:42:ASN:O	6:E:43:LEU:C	2.49	0.51
7:F:18:ASN:HA	7:F:55:VAL:HG12	1.92	0.51
8:G:27:ILE:HB	8:G:33:ILE:HG12	1.93	0.51
11:J:58:LEU:C	11:J:58:LEU:HD23	2.35	0.51
15:N:27:ASN:O	15:N:56:LYS:HB3	2.09	0.51
22:U:38:LYS:HB3	22:U:38:LYS:HZ3	1.74	0.51
1:A:758:C:H4'	1:A:880:C:H4'	1.93	0.51
2:02:33:ARG:H	2:02:33:ARG:HD3	1.76	0.51
3:03:255:ILE:HD12	3:03:263:VAL:HB	1.93	0.51
4:04:292:VAL:O	4:04:296:LYS:HG3	2.10	0.51
4:04:679:TYR:O	4:04:683:ILE:HG13	2.10	0.51
4:04:1275:LEU:C	4:04:1275:LEU:HD12	2.36	0.51
7:F:180:ASP:OD2	7:F:203:LYS:HD2	2.10	0.51
12:K:111:THR:OG1	12:K:113:ARG:HG3	2.11	0.51
14:M:57:VAL:O	14:M:57:VAL:HG13	2.09	0.51
17:P:72:ILE:HG13	17:P:73:SER:N	2.25	0.51
2:01:77:ASP:HB2	2:01:80:GLU:HG3	1.92	0.51
2:02:16:ILE:O	2:02:16:ILE:HG13	2.09	0.51
2:02:115:ILE:HG22	2:02:116:THR:N	2.26	0.51
3:03:633:LEU:HD12	3:03:633:LEU:C	2.35	0.51
4:04:146:VAL:HG21	4:04:154:LEU:HB2	1.93	0.51
4:04:242:LEU:CD2	4:04:272:VAL:HG11	2.40	0.51
4:04:909:ILE:HD11	4:04:913:GLU:HG2	1.92	0.51
4:04:1239:ASP:O	4:04:1242:ARG:HB2	2.11	0.51
4:04:1342:ASP:C	4:04:1344:LEU:H	2.17	0.51
10:I:18:VAL:CG1	10:I:19:PRO:HD3	2.40	0.51
11:J:139:ASP:O	11:J:143:MET:HG2	2.09	0.51
1:A:557:G:H2'	1:A:558:G:O4'	2.11	0.51
1:A:1220:G:H2'	1:A:1221:G:C8	2.46	0.51
3:03:556:GLY:HA2	3:03:660:VAL:HA	1.93	0.51
7:F:72:PRO:O	7:F:76:ILE:HG12	2.11	0.51
11:J:69:ARG:HG3	11:J:95:ARG:HB3	1.92	0.51
13:L:51:LEU:HD21	13:L:82:ILE:HG21	1.91	0.51
20:S:78:VAL:HG13	20:S:80:LYS:H	1.75	0.51
1:A:1371:G:H4'	13:L:70:GLY:H	1.76	0.51
3:03:421:SER:O	3:03:425:ILE:HG13	2.10	0.51
3:03:434:ASP:HA	3:03:437:ASN:ND2	2.23	0.51
4:04:919:ALA:O	4:04:923:ILE:HG13	2.10	0.51
7:F:83:VAL:HA	7:F:86:LEU:HD12	1.91	0.51
10:I:89:VAL:C	10:I:90:MET:HE2	2.35	0.51
12:K:10:LEU:HD22	12:K:74:ILE:CD1	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1318:A:H2'	1:A:1319:A:H5'	1.93	0.51
2:01:182:ARG:C	2:01:183:ILE:HD12	2.35	0.51
3:03:242:VAL:O	3:03:246:LEU:HG	2.10	0.51
4:04:48:THR:O	4:04:50:LYS:N	2.42	0.51
4:04:205:LEU:HD13	4:04:205:LEU:C	2.36	0.51
4:04:472:LEU:H	4:04:472:LEU:CD2	2.22	0.51
4:04:803:VAL:HG22	4:04:1259:GLN:HB3	1.93	0.51
11:J:129:ASN:C	11:J:134:VAL:HG11	2.36	0.51
2:01:207:THR:HG22	2:01:209:GLY:H	1.75	0.51
2:02:111:THR:HA	2:02:129:VAL:HA	1.92	0.51
3:03:320:ASP:O	3:03:324:LYS:HG3	2.11	0.51
3:03:524:ILE:HD12	3:03:708:VAL:HG13	1.92	0.51
4:04:380:PHE:HZ	4:04:472:LEU:HA	1.76	0.51
6:E:72:THR:HG22	6:E:95:ARG:NH2	2.25	0.51
10:I:18:VAL:N	10:I:19:PRO:CD	2.74	0.51
14:M:77:VAL:HG12	14:M:78:GLU:N	2.26	0.51
14:M:102:LEU:N	14:M:102:LEU:HD23	2.26	0.51
16:O:56:LEU:HD13	16:O:58:ASN:HD21	1.76	0.51
20:S:28:ARG:HH11	20:S:29:ASN:ND2	2.08	0.51
1:A:1124:G:H5'	14:M:37:ARG:HG3	1.93	0.51
3:03:83:GLN:O	3:03:87:ILE:HG13	2.11	0.51
3:03:1104:PRO:HB3	4:04:737:ILE:HG12	1.92	0.51
4:04:1222:ARG:HG2	4:04:1222:ARG:HH11	1.75	0.51
4:04:1236:GLU:O	4:04:1239:ASP:HB3	2.11	0.51
8:G:121:ALA:HB1	8:G:148:ALA:CB	2.40	0.51
8:G:202:LEU:O	8:G:205:LYS:HG2	2.11	0.51
11:J:24:LYS:HB2	11:J:24:LYS:NZ	2.25	0.51
17:P:55:LEU:HD12	17:P:55:LEU:C	2.36	0.51
22:U:41:PRO:HB2	22:U:44:ILE:HG12	1.92	0.51
1:A:244:U:C4'	1:A:245:U:H5'	2.37	0.51
1:A:681:A:H2'	1:A:682:G:H8	1.76	0.51
1:A:1049:U:H5'	1:A:1201:A:OP2	2.11	0.51
1:A:1066:C:H2'	1:A:1067:A:O4'	2.11	0.51
1:A:1526:G:H2'	1:A:1527:U:C6	2.46	0.51
2:02:31:LEU:HD12	2:02:35:PHE:HB3	1.93	0.51
3:03:621:SER:HB3	3:03:629:PHE:HE1	1.76	0.51
6:E:20:THR:O	6:E:22:TYR:N	2.44	0.51
6:E:158:PRO:HG2	6:E:181:ILE:HD13	1.93	0.51
8:G:167:PRO:C	8:G:169:TRP:H	2.18	0.51
9:H:68:ARG:O	9:H:68:ARG:HD3	2.11	0.51
10:I:38:ARG:HA	10:I:38:ARG:NE	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:16:ILE:N	17:P:16:ILE:CD1	2.71	0.51
3:03:690:VAL:HG11	3:03:1234:LYS:HB3	1.93	0.50
4:04:57:PHE:CZ	4:04:252:LEU:HB2	2.46	0.50
4:04:865:HIS:HA	4:04:901:ARG:HH21	1.76	0.50
4:04:1330:ARG:HB3	4:04:1330:ARG:NH1	2.26	0.50
5:05:18:ASP:O	5:05:22:VAL:HG23	2.11	0.50
21:T:13:SER:HB2	21:T:21:VAL:HG12	1.93	0.50
1:A:219:U:C3'	1:A:220:G:H5''	2.41	0.50
3:03:551:HIS:CE1	3:03:553:THR:HG23	2.45	0.50
4:04:510:LEU:O	4:04:514:THR:HG22	2.11	0.50
4:04:525:MET:O	4:04:548:VAL:HG13	2.12	0.50
8:G:66:VAL:HG12	8:G:67:LEU:N	2.26	0.50
10:I:19:PRO:HA	10:I:22:ILE:HG13	1.93	0.50
15:N:30:ILE:HG23	15:N:30:ILE:O	2.11	0.50
17:P:101:THR:HG22	17:P:105:ALA:HB2	1.93	0.50
23:V:11:ASP:OD2	23:V:37:SER:HB2	2.12	0.50
1:A:1236:A:H2'	1:A:1237:C:O4'	2.10	0.50
2:02:191:ARG:HH11	4:04:370:LYS:HZ1	1.59	0.50
3:03:1104:PRO:CB	4:04:737:ILE:HG12	2.40	0.50
4:04:60:ARG:HA	4:04:90:VAL:HG22	1.94	0.50
4:04:394:ILE:O	4:04:398:LYS:HG3	2.12	0.50
4:04:1350:ASN:HB3	4:04:1355:ARG:O	2.10	0.50
6:E:148:LEU:O	6:E:151:ILE:HG22	2.11	0.50
7:F:33:ASP:O	7:F:37:LYS:HG2	2.10	0.50
7:F:63:ILE:HG21	7:F:90:VAL:HG12	1.93	0.50
10:I:6:ILE:HG12	10:I:89:VAL:CG1	2.42	0.50
12:K:35:ILE:O	12:K:39:LEU:HG	2.11	0.50
25:X:17:ARG:HH21	25:X:21:ARG:NH2	2.09	0.50
2:01:102:LEU:HD13	2:01:102:LEU:C	2.35	0.50
3:03:931:VAL:HG13	3:03:1052:VAL:HG22	1.93	0.50
4:04:123:ARG:HG3	4:04:1337:VAL:HB	1.93	0.50
4:04:220:ARG:O	4:04:223:LEU:HB3	2.12	0.50
6:E:19:GLN:HE21	6:E:188:ASP:HB3	1.76	0.50
8:G:58:GLN:HE21	8:G:58:GLN:HA	1.76	0.50
18:Q:40:ARG:NH1	23:V:6:LYS:HD2	2.26	0.50
1:A:18:C:H4'	1:A:1078:U:O2	2.11	0.50
3:03:716:ALA:O	3:03:783:LEU:HD23	2.11	0.50
4:04:485:MET:HE3	4:04:486:SER:N	2.24	0.50
4:04:659:ALA:O	4:04:663:GLU:HG2	2.10	0.50
4:04:885:VAL:O	4:04:1258:ARG:HD2	2.12	0.50
7:F:110:LEU:HG	7:F:203:LYS:HZ3	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:523:A:H2'	1:A:524:G:H5''	1.92	0.50
2:01:68:TYR:OH	3:03:1057:LYS:HG2	2.11	0.50
3:03:316:GLU:H	3:03:316:GLU:CD	2.20	0.50
3:03:1257:GLN:OE1	3:03:1257:GLN:HA	2.12	0.50
4:04:1179:PRO:HD2	4:04:1184:ASP:HA	1.93	0.50
13:L:74:GLN:O	13:L:78:ILE:HG13	2.11	0.50
19:R:81:ILE:HG22	19:R:86:LEU:HD12	1.92	0.50
1:A:1056:U:H5'	7:F:162:ALA:HB2	1.93	0.50
2:01:219:ARG:O	2:01:223:ILE:HG13	2.11	0.50
3:03:42:ASP:HB2	3:03:50:GLU:CG	2.39	0.50
4:04:245:LEU:HB3	4:04:249:LEU:HD12	1.93	0.50
4:04:506:VAL:O	4:04:510:LEU:HD12	2.11	0.50
4:04:680:ASN:HA	4:04:683:ILE:HD12	1.94	0.50
4:04:975:ILE:HD13	4:04:980:THR:HG21	1.94	0.50
5:05:50:ALA:O	5:05:54:ILE:HG12	2.12	0.50
7:F:172:VAL:HG12	7:F:174:LEU:HD12	1.94	0.50
15:N:43:TRP:CZ3	15:N:45:THR:HG23	2.47	0.50
22:U:59:ILE:O	22:U:63:ARG:HG3	2.12	0.50
1:A:161:A:H61	1:A:347:G:H21	1.58	0.50
1:A:426:U:H5'	8:G:32:LYS:HE2	1.94	0.50
2:01:130:ILE:N	2:01:130:ILE:HD12	2.27	0.50
2:02:56:VAL:HG21	2:02:144:ILE:HD11	1.94	0.50
3:03:224:PHE:HA	3:03:430:LYS:HE2	1.94	0.50
3:03:697:LYS:H	3:03:697:LYS:CD	2.22	0.50
3:03:1246:ARG:HD3	3:03:1247:SER:N	2.27	0.50
4:04:419:HIS:O	4:04:421:VAL:HG13	2.11	0.50
4:04:423:LEU:HD22	4:04:437:PHE:CD2	2.45	0.50
4:04:844:THR:HB	4:04:860:ARG:O	2.12	0.50
4:04:1229:VAL:HG13	4:04:1230:THR:N	2.25	0.50
6:E:27:MET:CG	6:E:189:THR:HA	2.41	0.50
6:E:208:ARG:HA	6:E:211:THR:OG1	2.12	0.50
11:J:138:GLU:HB3	11:J:142:ARG:NH1	2.26	0.50
16:O:107:LYS:HB2	16:O:107:LYS:NZ	2.27	0.50
18:Q:27:LYS:HD2	18:Q:27:LYS:C	2.37	0.50
24:W:54:GLN:N	24:W:55:PRO:CD	2.75	0.50
1:A:376:G:H2'	1:A:377:G:C5'	2.32	0.50
2:01:11:PRO:HG3	2:02:227:GLN:HA	1.94	0.50
4:04:60:ARG:C	4:04:60:ARG:HD3	2.37	0.50
4:04:364:HIS:HB3	5:05:4:VAL:HG23	1.94	0.50
4:04:420:PRO:O	4:04:471:PRO:HG2	2.11	0.50
4:04:768:ASN:ND2	4:04:771:GLN:HG2	2.21	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:17:GLY:HA2	6:E:203:ASN:HB2	1.94	0.50
6:E:27:MET:CB	6:E:189:THR:HA	2.42	0.50
7:F:206:ILE:OXT	7:F:206:ILE:HG12	2.11	0.50
8:G:106:PHE:CG	8:G:144:ILE:HD11	2.47	0.50
9:H:55:VAL:N	9:H:56:PRO:CD	2.75	0.50
23:V:30:LEU:H	23:V:30:LEU:HD12	1.76	0.50
1:A:613:C:OP1	8:G:81:LEU:HD23	2.12	0.49
1:A:1343:G:H4'	13:L:123:ARG:HB2	1.94	0.49
3:03:241:LEU:HG	3:03:246:LEU:HD11	1.94	0.49
4:04:57:PHE:CE2	4:04:252:LEU:HD22	2.46	0.49
4:04:156:ARG:HD3	4:04:156:ARG:O	2.12	0.49
4:04:355:ILE:HD11	4:04:464:ASP:HB2	1.92	0.49
4:04:984:LEU:HB3	4:04:993:GLU:H	1.77	0.49
12:K:106:SER:H	12:K:120:LEU:HD13	1.76	0.49
18:Q:46:LYS:O	18:Q:50:LEU:HD13	2.12	0.49
1:A:102:G:O2'	1:A:151:A:H1'	2.11	0.49
1:A:1299:A:H2'	1:A:1300:G:H4'	1.94	0.49
3:03:1331:ARG:HG2	3:03:1331:ARG:HH11	1.76	0.49
4:04:582:ILE:O	4:04:582:ILE:HG22	2.12	0.49
4:04:863:LEU:CD1	4:04:901:ARG:HB3	2.41	0.49
4:04:1191:PRO:HB2	4:04:1194:ARG:HG2	1.94	0.49
4:04:1253:ILE:O	4:04:1257:VAL:HG23	2.12	0.49
6:E:23:TRP:CE2	6:E:25:PRO:HG3	2.47	0.49
6:E:42:ASN:C	6:E:42:ASN:HD22	2.19	0.49
8:G:201:GLU:O	8:G:204:SER:HB3	2.12	0.49
2:02:115:ILE:HG22	2:02:116:THR:H	1.77	0.49
2:02:182:ARG:HH11	2:02:182:ARG:HG3	1.77	0.49
3:03:456:VAL:HA	3:03:459:MET:HE3	1.93	0.49
3:03:886:LYS:HB3	3:03:917:SER:HA	1.94	0.49
4:04:1343:GLU:H	4:04:1343:GLU:CD	2.20	0.49
5:05:16:ARG:HG2	5:05:16:ARG:O	2.13	0.49
13:L:10:ARG:HA	13:L:14:SER:O	2.13	0.49
13:L:94:ARG:O	13:L:98:ARG:HG3	2.12	0.49
14:M:68:ARG:CZ	18:Q:96:LYS:HD2	2.42	0.49
25:X:49:LYS:O	25:X:53:VAL:HG23	2.13	0.49
2:01:35:PHE:HA	2:01:38:THR:HB	1.95	0.49
3:03:232:ILE:HD11	3:03:333:ILE:HD11	1.94	0.49
4:04:422:LEU:HD13	4:04:471:PRO:HG3	1.94	0.49
4:04:1071:GLY:HA2	4:04:1074:LEU:HD12	1.94	0.49
5:05:53:GLU:O	5:05:58:LEU:HD23	2.12	0.49
9:H:75:LEU:HD13	9:H:119:VAL:CG2	2.35	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:92:PRO:HA	11:J:95:ARG:HD2	1.94	0.49
12:K:28:SER:CB	12:K:58:LEU:HB2	2.35	0.49
18:Q:46:LYS:HA	18:Q:49:THR:HG1	1.76	0.49
6:E:13:GLY:O	6:E:14:VAL:HG13	2.12	0.49
6:E:68:LEU:HD11	6:E:92:VAL:HG23	1.93	0.49
11:J:2:ARG:O	11:J:2:ARG:HG2	2.13	0.49
17:P:27:THR:HG22	17:P:30:LYS:HD2	1.94	0.49
18:Q:65:GLN:OE1	18:Q:78:LEU:HD21	2.11	0.49
1:A:576:C:H2'	1:A:578:C:OP2	2.11	0.49
2:02:83:LEU:HA	2:02:86:LYS:HG3	1.94	0.49
3:03:431:LYS:HE2	3:03:435:ILE:HD11	1.94	0.49
3:03:546:GLU:HA	3:03:549:ASP:OD2	2.12	0.49
3:03:1196:LYS:N	3:03:1196:LYS:HD2	2.28	0.49
3:03:1253:LEU:C	3:03:1253:LEU:HD13	2.37	0.49
3:03:1272:GLU:O	3:03:1275:VAL:HB	2.13	0.49
4:04:1076:PRO:O	4:04:1100:PHE:HA	2.13	0.49
5:05:56:GLU:HB2	5:05:58:LEU:HD22	1.95	0.49
11:J:134:VAL:O	11:J:138:GLU:HG2	2.13	0.49
16:O:41:PRO:HB3	16:O:89:LEU:HG	1.94	0.49
19:R:48:ASP:O	19:R:52:ARG:HG2	2.13	0.49
23:V:55:GLN:HG3	23:V:56:HIS:N	2.27	0.49
23:V:78:THR:HG22	23:V:79:TYR:N	2.27	0.49
1:A:219:U:C2'	1:A:220:G:H5''	2.42	0.49
1:A:454:G:H22	1:A:478:A:H2	1.59	0.49
2:01:183:ILE:HD12	2:01:183:ILE:N	2.27	0.49
2:02:35:PHE:HA	2:02:38:THR:CG2	2.37	0.49
2:02:86:LYS:HD3	2:02:173:VAL:HB	1.95	0.49
3:03:518:ASN:HB2	3:03:691:PRO:HD3	1.94	0.49
4:04:217:LEU:O	4:04:221:ILE:HG22	2.13	0.49
4:04:740:LEU:HD12	4:04:763:PHE:HB2	1.94	0.49
6:E:23:TRP:CE2	6:E:25:PRO:CG	2.96	0.49
8:G:59:LYS:NZ	8:G:194:ILE:HA	2.27	0.49
8:G:90:LEU:HD12	8:G:187:ARG:HG2	1.95	0.49
16:O:69:GLU:OE1	16:O:108:ASP:HB3	2.12	0.49
17:P:2:ARG:H	17:P:8:ILE:HA	1.78	0.49
19:R:40:GLY:O	19:R:44:GLU:HG2	2.12	0.49
25:X:10:GLU:HA	25:X:12:PHE:CE1	2.47	0.49
1:A:521:G:OP1	16:O:69:GLU:HG3	2.12	0.49
1:A:1384:C:H2'	1:A:1385:G:C8	2.48	0.49
2:01:167:PRO:C	2:01:169:GLY:H	2.20	0.49
3:03:75:LEU:HD22	3:03:75:LEU:N	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:448:LEU:HD23	3:03:451:ARG:HG3	1.95	0.49
4:04:619:ILE:HG23	4:04:620:PHE:N	2.28	0.49
4:04:746:LEU:N	4:04:746:LEU:HD12	2.28	0.49
6:E:26:LYS:O	6:E:28:LYS:N	2.45	0.49
8:G:76:LYS:O	8:G:80:ARG:HG3	2.12	0.49
8:G:77:GLU:O	8:G:81:LEU:HG	2.12	0.49
13:L:72:SER:HA	13:L:75:ALA:HB3	1.94	0.49
1:A:546:A:OP1	8:G:67:LEU:HD22	2.12	0.49
1:A:741:G:H2'	1:A:742:G:C8	2.48	0.49
1:A:1130:A:N6	1:A:1144:G:H1'	2.27	0.49
3:03:362:ALA:O	3:03:366:ILE:HG13	2.12	0.49
3:03:397:LEU:HD13	3:03:405:PHE:CE2	2.48	0.49
3:03:471:VAL:O	3:03:475:VAL:HG23	2.13	0.49
3:03:961:SER:O	3:03:965:GLN:HG2	2.13	0.49
3:03:963:GLU:O	3:03:967:LEU:HD13	2.13	0.49
3:03:1257:GLN:HA	3:03:1258:PRO:HD3	1.68	0.49
3:03:1297:ASP:OD1	3:03:1320:PRO:HA	2.13	0.49
6:E:19:GLN:O	6:E:39:HIS:CB	2.61	0.49
6:E:42:ASN:HD21	6:E:45:LYS:N	2.11	0.49
6:E:217:VAL:O	6:E:221:VAL:HG23	2.13	0.49
11:J:90:VAL:HG13	11:J:95:ARG:HE	1.77	0.49
15:N:92:ARG:HA	15:N:96:ILE:HG13	1.95	0.49
23:V:52:ASN:ND2	23:V:54:ARG:HG2	2.25	0.49
25:X:19:PHE:HA	25:X:22:SER:HB2	1.95	0.49
2:02:189:ALA:HB2	4:04:443:GLU:HB2	1.94	0.49
3:03:724:VAL:HG22	3:03:775:GLU:H	1.77	0.49
4:04:518:VAL:HG11	4:04:714:GLU:HB3	1.94	0.49
4:04:599:LYS:O	4:04:602:SER:HB3	2.13	0.49
4:04:733:SER:O	4:04:737:ILE:HG13	2.13	0.49
4:04:865:HIS:HB3	4:04:901:ARG:HE	1.78	0.49
6:E:110:SER:O	6:E:113:ARG:HB3	2.13	0.49
17:P:42:VAL:HG22	17:P:43:LYS:N	2.27	0.49
18:Q:68:ARG:HH12	18:Q:81:ILE:HG13	1.78	0.49
19:R:32:THR:HG21	19:R:86:LEU:HB3	1.95	0.49
23:V:12:LEU:C	23:V:14:LEU:H	2.21	0.49
1:A:545:C:O2'	1:A:546:A:H5'	2.12	0.48
2:01:27:THR:C	2:01:28:LEU:HD12	2.38	0.48
2:01:77:ASP:O	2:01:81:ILE:HG13	2.13	0.48
2:01:125:LYS:HE2	2:01:128:HIS:HB2	1.94	0.48
2:01:161:SER:C	2:01:163:GLU:H	2.21	0.48
3:03:18:ARG:HH12	3:03:622:ASN:HA	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:241:LEU:CG	3:03:246:LEU:HD11	2.43	0.48
3:03:748:ILE:HD12	3:03:748:ILE:N	2.28	0.48
3:03:817:LEU:HB3	3:03:1097:VAL:HB	1.95	0.48
3:03:819:SER:O	3:03:820:GLU:C	2.55	0.48
4:04:19:ALA:HB1	4:04:1343:GLU:CG	2.43	0.48
4:04:108:ALA:HB3	4:04:279:LEU:HD13	1.94	0.48
4:04:520:ALA:HB1	4:04:543:SER:HB3	1.93	0.48
6:E:11:LYS:O	6:E:12:ALA:C	2.52	0.48
8:G:58:GLN:HA	8:G:58:GLN:NE2	2.28	0.48
10:I:18:VAL:HA	10:I:21:MET:HE3	1.94	0.48
10:I:60:VAL:C	10:I:61:LEU:HD12	2.38	0.48
21:T:7:LEU:HD21	21:T:24:ILE:HG21	1.94	0.48
1:A:66:A:H1'	1:A:173:U:H2'	1.94	0.48
1:A:1486:G:H2'	1:A:1487:G:C8	2.48	0.48
3:03:698:PRO:HG3	3:03:1231:TYR:CE1	2.48	0.48
3:03:1115:THR:O	3:03:1116:HIS:C	2.53	0.48
4:04:422:LEU:CD1	4:04:471:PRO:HG3	2.43	0.48
4:04:622:ASP:O	4:04:625:MET:HB3	2.13	0.48
12:K:91:LEU:HD12	12:K:92:PRO:HD2	1.95	0.48
14:M:42:LEU:HD11	14:M:73:LEU:CD1	2.43	0.48
20:S:36:VAL:HG13	20:S:36:VAL:O	2.13	0.48
22:U:14:THR:HG21	22:U:51:TYR:HB3	1.94	0.48
1:A:197:A:N6	1:A:221:C:H4'	2.29	0.48
1:A:1237:C:H4'	1:A:1334:G:N2	2.28	0.48
1:A:1340:A:H2'	1:A:1341:U:O4'	2.13	0.48
2:01:172:LEU:N	2:01:172:LEU:HD12	2.28	0.48
3:03:289:VAL:O	3:03:289:VAL:HG22	2.12	0.48
3:03:663:VAL:HG23	3:03:664:GLY:N	2.29	0.48
3:03:851:THR:O	3:03:852:ALA:HB3	2.14	0.48
4:04:717:VAL:HB	4:04:723:TYR:CE2	2.48	0.48
4:04:849:LEU:H	4:04:849:LEU:CD2	2.22	0.48
4:04:1174:ARG:HD3	4:04:1187:GLU:OE2	2.14	0.48
4:04:1234:VAL:O	4:04:1238:GLN:HB2	2.13	0.48
6:E:25:PRO:O	6:E:28:LYS:HB2	2.13	0.48
6:E:38:VAL:O	6:E:39:HIS:CB	2.51	0.48
12:K:1:SER:O	12:K:2:MET:C	2.56	0.48
13:L:49:GLN:N	13:L:50:PRO:HD2	2.28	0.48
22:U:29:LEU:HB3	22:U:68:LEU:HD11	1.96	0.48
24:W:66:ILE:CG2	24:W:71:ALA:HB2	2.44	0.48
1:A:161:A:N6	1:A:347:G:H21	2.12	0.48
1:A:440:C:H3'	1:A:441:A:H5''	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:715:A:H2'	1:A:716:A:C8	2.48	0.48
1:A:824:G:H1'	12:K:2:MET:H	1.78	0.48
1:A:986:U:H2'	1:A:987:G:C8	2.49	0.48
1:A:1354:U:H2'	1:A:1355:G:H8	1.78	0.48
2:01:143:ARG:HH11	2:01:143:ARG:HG3	1.79	0.48
2:02:116:THR:HG23	2:02:116:THR:O	2.13	0.48
3:03:487:LEU:HD12	3:03:492:MET:SD	2.53	0.48
3:03:747:GLY:C	3:03:748:ILE:HD12	2.39	0.48
3:03:1273:MET:HA	3:03:1276:TRP:CE3	2.48	0.48
4:04:544:LEU:HA	4:04:574:VAL:HB	1.95	0.48
4:04:594:GLN:OE1	4:04:600:ALA:HB1	2.13	0.48
4:04:1070:GLY:O	4:04:1074:LEU:HG	2.12	0.48
4:04:1251:LYS:HB2	4:04:1251:LYS:NZ	2.16	0.48
8:G:88:ASN:O	8:G:92:LEU:HD13	2.13	0.48
9:H:47:PHE:HD1	9:H:47:PHE:H	1.60	0.48
12:K:25:THR:HG22	12:K:26:MET:N	2.28	0.48
13:L:66:VAL:HG11	13:L:74:GLN:HB3	1.96	0.48
13:L:98:ARG:HH11	13:L:103:VAL:CG1	2.26	0.48
20:S:71:VAL:O	20:S:75:ILE:HG12	2.13	0.48
25:X:10:GLU:H	25:X:11:PRO:HD3	1.76	0.48
1:A:620:C:O2	8:G:131:ILE:HG13	2.13	0.48
1:A:1259:C:H3'	1:A:1260:G:C5'	2.34	0.48
2:01:40:GLY:O	2:01:44:ARG:HB2	2.13	0.48
2:02:102:LEU:HD11	2:02:110:VAL:HG11	1.96	0.48
3:03:422:LYS:O	3:03:426:ILE:HG13	2.14	0.48
3:03:1066:MET:HA	3:03:1234:LYS:HA	1.95	0.48
4:04:121:PRO:O	4:04:123:ARG:N	2.46	0.48
4:04:474:LEU:HB2	5:05:47:THR:HG23	1.95	0.48
9:H:119:VAL:HG12	9:H:122:VAL:HG13	1.95	0.48
15:N:88:PRO:HA	15:N:92:ARG:HH11	1.78	0.48
1:A:61:G:O2'	1:A:62:U:H5'	2.13	0.48
1:A:219:U:H2'	1:A:220:G:C5'	2.43	0.48
1:A:1273:C:H2'	1:A:1274:A:H5'	1.96	0.48
1:A:1409:C:H2'	1:A:1410:A:C8	2.49	0.48
3:03:19:PRO:HD2	3:03:623:LEU:HD11	1.95	0.48
3:03:205:PRO:O	3:03:208:ILE:HG22	2.14	0.48
3:03:212:ALA:O	3:03:359:ARG:HG3	2.13	0.48
3:03:850:ILE:O	3:03:869:GLY:HA3	2.12	0.48
3:03:1187:PHE:O	3:03:1188:ASP:HB2	2.13	0.48
4:04:215:LYS:O	4:04:215:LYS:HD2	2.13	0.48
6:E:36:ASN:N	6:E:40:ILE:HG13	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:161:LEU:HG	6:E:163:VAL:HG23	1.95	0.48
13:L:117:LEU:HD13	13:L:120:ALA:C	2.38	0.48
13:L:118:ARG:HE	13:L:122:ARG:HG2	1.79	0.48
14:M:54:SER:CB	14:M:58:ASN:HB2	2.43	0.48
17:P:85:TYR:HB2	23:V:72:GLU:HA	1.95	0.48
20:S:10:GLY:HA3	20:S:15:PRO:HA	1.95	0.48
20:S:28:ARG:HH11	20:S:29:ASN:HD22	1.62	0.48
21:T:63:CYS:SG	21:T:64:ARG:N	2.86	0.48
23:V:43:MET:HB2	23:V:61:VAL:HG11	1.95	0.48
1:A:947:G:OP1	17:P:106:ARG:HB2	2.13	0.48
1:A:1297:G:N2	11:J:114:SER:H	2.11	0.48
1:A:1502:A:H5'	1:A:1504:G:N7	2.29	0.48
2:01:107:ILE:HD11	2:01:136:GLU:HG2	1.96	0.48
3:03:322:LEU:O	3:03:322:LEU:HD23	2.13	0.48
3:03:428:VAL:O	3:03:431:LYS:HB3	2.13	0.48
3:03:682:GLY:O	3:03:686:GLN:HG2	2.12	0.48
3:03:836:LEU:HD13	3:03:1054:LEU:HD13	1.96	0.48
3:03:933:VAL:HG12	3:03:1050:VAL:HG12	1.96	0.48
3:03:1315:MET:HE3	3:03:1315:MET:O	2.12	0.48
4:04:644:MET:HE2	4:04:741:ALA:HB2	1.95	0.48
8:G:128:VAL:HG13	8:G:128:VAL:O	2.14	0.48
10:I:46:GLN:HA	10:I:56:LYS:HG2	1.95	0.48
11:J:49:LEU:CD2	11:J:123:LEU:HB3	2.40	0.48
15:N:85:VAL:HG12	15:N:87:GLY:H	1.79	0.48
16:O:110:LYS:N	16:O:110:LYS:HD2	2.29	0.48
1:A:173:U:H3	1:A:198:G:H21	1.62	0.48
2:01:67:GLU:OE1	2:01:171:LEU:HD12	2.13	0.48
2:02:79:LEU:O	2:02:79:LEU:HD13	2.14	0.48
3:03:1099:ASN:HD22	3:03:1100:PRO:CD	2.26	0.48
4:04:307:LEU:HA	4:04:327:LEU:HD12	1.96	0.48
4:04:475:GLU:HA	5:05:20:VAL:CG1	2.43	0.48
4:04:544:LEU:HD11	4:04:575:GLY:HA2	1.95	0.48
15:N:82:GLU:HG2	15:N:108:ASN:OD1	2.13	0.48
1:A:439:U:H5''	8:G:120:LYS:HZ3	1.79	0.48
1:A:782:A:H4'	1:A:1515:G:H4'	1.96	0.48
3:03:529:ARG:NH1	3:03:564:PRO:HG3	2.28	0.48
3:03:985:GLU:HB3	3:03:988:LYS:HB2	1.95	0.48
4:04:308:ASP:HB2	4:04:328:ALA:HB3	1.95	0.48
13:L:112:ARG:HD3	13:L:113:LYS:O	2.13	0.48
14:M:41:PRO:O	14:M:42:LEU:HB2	2.14	0.48
22:U:56:ALA:O	22:U:60:LYS:HD3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1098:C:H2'	1:A:1099:G:O4'	2.14	0.48
3:03:152:SER:HB2	3:03:452:ARG:N	2.29	0.48
3:03:661:VAL:HB	3:03:665:ALA:CB	2.42	0.48
3:03:926:GLY:HA3	3:03:1056:VAL:HG22	1.96	0.48
4:04:60:ARG:CA	4:04:90:VAL:HG22	2.44	0.48
4:04:1029:THR:HG23	4:04:1121:LEU:HD12	1.96	0.48
4:04:1251:LYS:O	4:04:1255:VAL:HG13	2.13	0.48
6:E:24:ASN:N	6:E:25:PRO:HD3	2.29	0.48
6:E:190:ASN:N	6:E:190:ASN:ND2	2.56	0.48
7:F:13:ILE:HG22	7:F:14:VAL:HG23	1.96	0.48
11:J:111:GLY:HA2	11:J:118:ARG:NH2	2.29	0.48
13:L:41:GLU:HG3	13:L:42:THR:N	2.29	0.48
1:A:244:U:H5'	1:A:894:G:N2	2.29	0.47
1:A:1289:A:H61	13:L:71:ILE:HG12	1.79	0.47
3:03:523:GLU:HB3	3:03:527:LYS:HE3	1.95	0.47
3:03:782:VAL:C	3:03:783:LEU:HD22	2.39	0.47
3:03:1207:SER:C	3:03:1209:GLN:N	2.71	0.47
4:04:56:LEU:HA	4:04:62:PHE:HE2	1.78	0.47
4:04:309:ASN:HD22	4:04:315:ALA:H	1.62	0.47
4:04:836:ARG:HG3	4:04:869:CYS:HB3	1.95	0.47
4:04:1198:VAL:HB	4:04:1210:ILE:HG23	1.96	0.47
6:E:10:LEU:O	6:E:11:LYS:C	2.57	0.47
6:E:188:ASP:HB2	6:E:191:SER:OG	2.14	0.47
7:F:8:GLY:HA2	7:F:11:LEU:HG	1.96	0.47
7:F:91:ALA:HA	7:F:96:VAL:O	2.14	0.47
8:G:176:LYS:HZ1	8:G:178:GLU:HB3	1.79	0.47
14:M:35:GLN:OE1	14:M:35:GLN:HA	2.14	0.47
16:O:79:ILE:HG22	16:O:103:CYS:HB2	1.95	0.47
1:A:273:U:H2'	1:A:274:A:H5'	1.97	0.47
1:A:1355:G:H2'	1:A:1356:G:C8	2.49	0.47
2:01:61:ILE:HB	2:01:64:VAL:HG21	1.95	0.47
2:02:179:PRO:HA	2:02:208:ASN:OD1	2.14	0.47
4:04:1029:THR:HG22	4:04:1099:TYR:CD2	2.49	0.47
9:H:159:SER:HB3	9:H:162:GLU:CB	2.44	0.47
10:I:2:ARG:HG2	10:I:2:ARG:HH11	1.79	0.47
11:J:55:LYS:HB3	11:J:59:GLU:HG3	1.95	0.47
15:N:59:PRO:O	15:N:62:ALA:HB3	2.14	0.47
18:Q:26:LEU:HD23	18:Q:30:ILE:HD12	1.96	0.47
1:A:618:C:H42	1:A:622:A:H62	1.60	0.47
1:A:774:G:C2'	1:A:775:G:H5'	2.44	0.47
1:A:1167:A:H2'	1:A:1167:A:N3	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1354:U:H2'	1:A:1355:G:C8	2.49	0.47
2:01:82:LEU:HD13	2:01:173:VAL:HG11	1.96	0.47
3:03:461:GLU:O	3:03:465:ARG:HB2	2.15	0.47
3:03:521:LEU:O	3:03:525:THR:HG22	2.14	0.47
3:03:753:LEU:N	3:03:753:LEU:HD12	2.29	0.47
3:03:759:SER:CB	3:03:763:THR:HB	2.35	0.47
4:04:480:ALA:O	4:04:484:MET:HB2	2.14	0.47
4:04:588:PRO:O	4:04:591:ILE:HG22	2.14	0.47
4:04:805:GLN:HG2	4:04:917:VAL:HG22	1.97	0.47
4:04:1321:SER:HB2	4:04:1349:GLU:OE2	2.14	0.47
7:F:107:LYS:HD3	7:F:143:LEU:HG	1.96	0.47
14:M:21:ALA:HA	14:M:92:LEU:HD22	1.96	0.47
16:O:62:VAL:HG21	16:O:94:TYR:HE2	1.80	0.47
18:Q:37:ASP:H	18:Q:40:ARG:HB2	1.80	0.47
21:T:12:VAL:HB	21:T:23:ALA:HB2	1.95	0.47
24:W:34:VAL:HG11	24:W:78:LEU:HD21	1.95	0.47
1:A:346:G:C2'	1:A:347:G:H5'	2.44	0.47
1:A:878:A:H1'	12:K:3:GLN:HE22	1.79	0.47
3:03:680:LEU:O	3:03:683:ALA:HB3	2.15	0.47
3:03:849:GLU:C	3:03:851:THR:H	2.22	0.47
3:03:1241:ASP:C	3:03:1242:LYS:HD2	2.39	0.47
4:04:55:GLY:H	4:04:58:CYS:HB2	1.78	0.47
4:04:245:LEU:HD12	4:04:245:LEU:N	2.29	0.47
4:04:399:LYS:HA	4:04:402:GLU:HB3	1.97	0.47
4:04:435:GLN:HB2	4:04:457:TYR:OH	2.15	0.47
4:04:644:MET:HB3	4:04:764:ARG:HG2	1.96	0.47
9:H:120:HIS:C	9:H:121:ASN:HD22	2.23	0.47
20:S:19:VAL:HB	20:S:37:GLY:O	2.14	0.47
22:U:26:ILE:C	22:U:28:THR:H	2.21	0.47
23:V:4:LEU:HD23	23:V:4:LEU:N	2.29	0.47
2:02:23:HIS:HB3	2:02:206:GLU:HG2	1.97	0.47
3:03:212:ALA:HB1	3:03:363:LEU:HD21	1.96	0.47
4:04:368:LEU:CD2	4:04:447:ILE:HD12	2.44	0.47
4:04:888:CYS:SG	4:04:890:THR:HB	2.55	0.47
4:04:1222:ARG:HG2	4:04:1222:ARG:NH1	2.29	0.47
4:04:1358:PRO:HB3	4:04:1366:HIS:CD2	2.49	0.47
6:E:18:HIS:O	6:E:40:ILE:N	2.47	0.47
9:H:95:MET:HG2	9:H:124:ALA:HB2	1.96	0.47
14:M:49:PHE:HZ	18:Q:75:LYS:HE3	1.79	0.47
18:Q:63:CYS:HB3	18:Q:68:ARG:H	1.80	0.47
24:W:78:LEU:O	24:W:82:ILE:HG23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:147:G:H2'	1:A:148:G:C8	2.49	0.47
1:A:1279:G:H4'	1:A:1281:C:N4	2.29	0.47
4:04:650:LYS:HE3	4:04:762:ASN:HD22	1.78	0.47
7:F:163:ARG:H	7:F:163:ARG:HD3	1.80	0.47
8:G:46:ARG:HG2	8:G:46:ARG:HH11	1.79	0.47
18:Q:25:GLU:HG3	18:Q:26:LEU:N	2.30	0.47
1:A:65:A:H4'	1:A:66:A:H5'	1.95	0.47
1:A:521:G:H5'	16:O:69:GLU:HB2	1.97	0.47
1:A:656:G:H4'	19:R:61:GLN:NE2	2.30	0.47
1:A:865:A:H2'	1:A:866:C:C6	2.50	0.47
1:A:1188:A:O2'	18:Q:97:LYS:HD2	2.14	0.47
2:01:43:LEU:O	2:01:46:ILE:HG22	2.15	0.47
2:02:191:ARG:HD2	4:04:370:LYS:NZ	2.28	0.47
2:02:195:ARG:HG3	2:02:196:THR:N	2.29	0.47
3:03:143:ARG:HD3	3:03:507:GLY:CA	2.43	0.47
3:03:448:LEU:HD13	3:03:557:ARG:HD2	1.97	0.47
3:03:600:THR:HG22	3:03:602:GLU:HG3	1.95	0.47
3:03:747:GLY:H	3:03:748:ILE:HD12	1.80	0.47
3:03:850:ILE:HD12	3:03:850:ILE:H	1.79	0.47
4:04:47:ARG:HA	4:04:47:ARG:HE	1.79	0.47
4:04:343:LEU:HD22	4:04:343:LEU:N	2.30	0.47
4:04:764:ARG:HD3	4:04:764:ARG:O	2.15	0.47
4:04:1029:THR:HB	4:04:1031:VAL:HG22	1.96	0.47
6:E:136:MET:HE2	6:E:136:MET:CA	2.45	0.47
8:G:3:TYR:HE2	8:G:10:LEU:HD11	1.78	0.47
8:G:164:ARG:HG2	8:G:164:ARG:HH11	1.78	0.47
8:G:170:LEU:HD21	8:G:181:PHE:HD1	1.80	0.47
9:H:97:PRO:HG2	9:H:98:ALA:H	1.80	0.47
11:J:68:VAL:HG23	11:J:99:ALA:HB1	1.95	0.47
12:K:113:ARG:HA	12:K:116:ARG:NH1	2.30	0.47
18:Q:97:LYS:HB2	18:Q:97:LYS:HZ2	1.78	0.47
24:W:38:ILE:C	24:W:40:ALA:H	2.21	0.47
24:W:79:THR:CA	24:W:82:ILE:HG12	2.44	0.47
1:A:62:U:O2'	1:A:379:C:H1'	2.14	0.47
3:03:16:GLY:O	3:03:1155:VAL:HB	2.15	0.47
3:03:615:VAL:HG13	3:03:615:VAL:O	2.15	0.47
3:03:719:LYS:HD2	3:03:719:LYS:N	2.30	0.47
3:03:778:GLU:H	3:03:781:ASP:HB2	1.80	0.47
4:04:691:ASP:O	4:04:695:LYS:HG2	2.14	0.47
7:F:178:ARG:O	7:F:206:ILE:HB	2.15	0.47
10:I:89:VAL:O	10:I:90:MET:HE2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:94:ARG:HH11	11:J:94:ARG:HG3	1.79	0.47
17:P:89:ARG:CB	17:P:96:VAL:HA	2.44	0.47
22:U:34:THR:C	22:U:36:SER:H	2.22	0.47
1:A:811:C:H2'	1:A:812:G:H5'	1.95	0.47
1:A:1330:U:H4'	17:P:22:TYR:CE1	2.50	0.47
1:A:1345:U:H4'	1:A:1346:A:C8	2.50	0.47
2:01:13:LEU:HA	2:01:28:LEU:HA	1.97	0.47
2:02:54:CYS:SG	2:02:148:ARG:HA	2.55	0.47
3:03:46:GLN:OE1	3:03:46:GLN:HA	2.15	0.47
3:03:1124:ILE:O	3:03:1128:ILE:HG13	2.14	0.47
3:03:1263:ALA:HB3	3:03:1264:GLN:OE1	2.15	0.47
4:04:77:ARG:HH21	6:E:18:HIS:CD2	2.31	0.47
4:04:147:ILE:HG13	4:04:147:ILE:O	2.15	0.47
4:04:740:LEU:HD12	4:04:763:PHE:CB	2.45	0.47
4:04:1273:ASP:HB3	4:04:1276:GLU:HB2	1.96	0.47
10:I:74:LEU:HG	10:I:78:PHE:CE2	2.50	0.47
13:L:20:ILE:HD11	13:L:82:ILE:HA	1.96	0.47
13:L:34:LEU:HD23	13:L:39:GLY:HA3	1.96	0.47
24:W:55:PRO:C	24:W:56:ILE:HD12	2.40	0.47
1:A:882:C:O2'	1:A:883:C:H5'	2.15	0.47
2:01:32:GLU:HB2	2:01:35:PHE:HE2	1.80	0.47
2:02:82:LEU:O	2:02:85:LEU:HB2	2.15	0.47
3:03:257:ALA:HB3	3:03:262:TYR:CE2	2.48	0.47
3:03:841:ARG:CB	3:03:848:GLU:HB2	2.45	0.47
3:03:1138:VAL:O	3:03:1142:ARG:HB2	2.14	0.47
3:03:1328:LYS:N	3:03:1328:LYS:HD2	2.30	0.47
4:04:477:GLN:O	4:04:480:ALA:HB3	2.14	0.47
4:04:1163:VAL:HG13	4:04:1200:GLU:HA	1.96	0.47
8:G:73:ASN:O	8:G:77:GLU:HG3	2.15	0.47
8:G:123:MET:HG2	8:G:128:VAL:HA	1.97	0.47
9:H:82:HIS:HB2	9:H:83:PRO:HD2	1.97	0.47
20:S:25:ARG:HH11	20:S:25:ARG:HG2	1.80	0.47
24:W:6:ALA:C	24:W:8:LYS:N	2.73	0.47
1:A:92:U:H3'	1:A:93:U:H5''	1.97	0.46
1:A:580:C:H2'	1:A:581:G:C8	2.51	0.46
1:A:1098:C:OP2	6:E:143:LYS:HG2	2.15	0.46
2:01:52:PRO:HA	2:01:149:GLY:O	2.15	0.46
2:01:167:PRO:O	2:01:169:GLY:N	2.48	0.46
3:03:1327:LEU:O	3:03:1331:ARG:HG3	2.15	0.46
4:04:119:SER:O	4:04:120:LEU:C	2.58	0.46
4:04:1139:PRO:O	4:04:1142:ALA:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:19:PRO:HA	10:I:22:ILE:CG1	2.45	0.46
15:N:110:THR:CG2	15:N:112:VAL:HG13	2.46	0.46
1:A:681:A:H2'	1:A:682:G:C8	2.50	0.46
3:03:26:TYR:HE2	3:03:32:LEU:HD22	1.80	0.46
3:03:271:ALA:HA	3:03:274:ILE:HD12	1.97	0.46
3:03:448:LEU:CD1	3:03:557:ARG:HD2	2.45	0.46
3:03:1285:TYR:O	3:03:1289:GLU:HG2	2.15	0.46
4:04:120:LEU:HB3	4:04:121:PRO:CD	2.39	0.46
4:04:357:VAL:HG12	4:04:359:PRO:HG3	1.97	0.46
4:04:915:ILE:HG13	4:04:916:GLY:N	2.31	0.46
4:04:919:ALA:HB1	4:04:1252:HIS:HB3	1.97	0.46
9:H:104:ILE:HB	9:H:120:HIS:HA	1.96	0.46
11:J:1:PRO:CD	11:J:4:ARG:HB2	2.43	0.46
15:N:27:ASN:O	15:N:56:LYS:HE2	2.16	0.46
15:N:86:LYS:HG2	15:N:112:VAL:HG23	1.97	0.46
16:O:85:ARG:HG3	16:O:85:ARG:NH1	2.29	0.46
20:S:61:VAL:HG22	20:S:67:ILE:HD11	1.97	0.46
22:U:28:THR:HA	22:U:31:ASN:HD22	1.79	0.46
2:01:85:LEU:HD22	2:01:144:ILE:HD13	1.96	0.46
3:03:26:TYR:CE2	3:03:32:LEU:HD22	2.50	0.46
3:03:314:ASN:HD22	3:03:314:ASN:N	2.14	0.46
3:03:757:THR:O	3:03:764:CYS:HA	2.15	0.46
4:04:110:PRO:HB2	4:04:182:ALA:HB3	1.96	0.46
4:04:1090:ILE:HB	4:04:1093:THR:OG1	2.15	0.46
4:04:1298:VAL:HG22	4:04:1298:VAL:O	2.14	0.46
6:E:13:GLY:C	6:E:14:VAL:HG22	2.40	0.46
8:G:170:LEU:HD21	8:G:181:PHE:CD1	2.51	0.46
12:K:113:ARG:HD2	12:K:114:ALA:N	2.31	0.46
14:M:6:ILE:HD13	14:M:87:LEU:HD11	1.97	0.46
15:N:21:HIS:HA	15:N:84:MET:O	2.15	0.46
15:N:86:LYS:HB3	15:N:86:LYS:HZ3	1.79	0.46
15:N:107:THR:HG23	15:N:108:ASN:N	2.30	0.46
16:O:118:VAL:HG12	16:O:119:LYS:O	2.16	0.46
22:U:53:ARG:O	22:U:57:ARG:HG2	2.15	0.46
1:A:570:G:H5'	1:A:820:U:O4'	2.16	0.46
1:A:632:U:H3'	1:A:633:G:H5'	1.97	0.46
3:03:414:ILE:C	3:03:414:ILE:HD12	2.41	0.46
3:03:457:GLY:O	3:03:460:ALA:HB3	2.16	0.46
3:03:1113:LEU:O	3:03:1114:GLU:C	2.58	0.46
4:04:385:LEU:HD13	4:04:400:MET:SD	2.56	0.46
4:04:511:TYR:O	4:04:515:ARG:HB2	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:923:ILE:CD1	4:04:1253:ILE:HA	2.46	0.46
7:F:41:TYR:CE2	7:F:89:VAL:HG11	2.49	0.46
7:F:107:LYS:HB2	7:F:110:LEU:CB	2.45	0.46
12:K:50:VAL:O	12:K:50:VAL:HG22	2.16	0.46
13:L:83:THR:C	13:L:85:ALA:H	2.23	0.46
14:M:12:ALA:HB3	14:M:18:ILE:HD12	1.97	0.46
14:M:24:GLU:O	14:M:27:GLU:HB3	2.15	0.46
18:Q:40:ARG:HD2	18:Q:40:ARG:O	2.15	0.46
20:S:40:ASN:ND2	20:S:42:ILE:HG13	2.30	0.46
1:A:1296:C:H5''	17:P:13:HIS:NE2	2.29	0.46
2:02:90:VAL:HG12	2:02:91:ARG:N	2.30	0.46
3:03:394:ARG:HG3	3:03:394:ARG:HH11	1.81	0.46
4:04:671:GLY:C	4:04:672:LEU:HD12	2.41	0.46
6:E:11:LYS:HA	6:E:11:LYS:CE	2.40	0.46
7:F:82:ASP:O	7:F:86:LEU:HG	2.16	0.46
8:G:2:ARG:HG2	8:G:2:ARG:HH11	1.79	0.46
15:N:84:MET:HE2	15:N:112:VAL:HG11	1.97	0.46
17:P:104:ASN:O	17:P:105:ALA:HB3	2.14	0.46
19:R:78:THR:O	19:R:82:GLU:HB2	2.16	0.46
25:X:16:LEU:HD21	25:X:18:ARG:HB2	1.97	0.46
25:X:16:LEU:HD23	25:X:18:ARG:H	1.80	0.46
1:A:90:C:H2'	1:A:91:U:C5	2.51	0.46
1:A:884:U:H4'	1:A:885:G:H5''	1.97	0.46
1:A:1204:A:H2'	1:A:1205:U:O4'	2.15	0.46
3:03:213:LEU:HD22	3:03:422:LYS:HG2	1.97	0.46
8:G:145:ARG:NH2	8:G:147:LYS:HG3	2.31	0.46
12:K:17:GLN:HE21	12:K:69:ALA:HB1	1.80	0.46
17:P:77:LYS:HB3	17:P:77:LYS:HZ3	1.80	0.46
1:A:51:A:H4'	1:A:52:C:H5''	1.98	0.46
1:A:615:G:H2'	1:A:616:G:H8	1.81	0.46
1:A:662:U:H2'	1:A:663:A:C8	2.51	0.46
2:01:100:LEU:HD12	2:01:100:LEU:N	2.30	0.46
3:03:392:GLU:OE1	3:03:419:ILE:HG23	2.16	0.46
4:04:820:ILE:HD12	4:04:822:MET:HE3	1.98	0.46
7:F:70:ALA:HA	7:F:105:VAL:HG12	1.97	0.46
7:F:89:VAL:O	7:F:92:ASP:HB3	2.15	0.46
8:G:20:LEU:HD12	8:G:21:LYS:N	2.30	0.46
8:G:142:VAL:O	8:G:142:VAL:HG13	2.15	0.46
10:I:19:PRO:HA	10:I:22:ILE:HD12	1.98	0.46
10:I:78:PHE:HD1	10:I:84:VAL:HG21	1.81	0.46
14:M:89:ARG:C	14:M:90:LEU:HD12	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:54:GLN:C	24:W:56:ILE:N	2.74	0.46
1:A:1285:A:H4'	1:A:1286:U:C5'	2.44	0.46
2:01:64:VAL:HG22	2:01:78:ILE:HG21	1.97	0.46
3:03:146:VAL:HG21	3:03:529:ARG:HH21	1.80	0.46
3:03:1125:GLY:HA3	3:03:1179:GLY:HA2	1.98	0.46
3:03:1297:ASP:HB2	3:03:1300:GLY:HA3	1.98	0.46
4:04:78:LEU:HD12	4:04:78:LEU:N	2.30	0.46
4:04:798:ARG:O	4:04:801:VAL:HG22	2.15	0.46
4:04:976:THR:HG22	4:04:1028:ILE:CG1	2.42	0.46
6:E:26:LYS:C	6:E:28:LYS:H	2.22	0.46
11:J:48:THR:O	11:J:51:GLN:HB3	2.15	0.46
12:K:54:THR:O	12:K:56:PRO:HD3	2.16	0.46
14:M:5:ARG:HD3	14:M:79:PRO:HD3	1.97	0.46
16:O:65:TYR:CE2	16:O:67:GLY:HA2	2.50	0.46
24:W:72:ALA:O	24:W:76:ALA:HB3	2.15	0.46
2:01:79:LEU:O	2:01:82:LEU:HB2	2.16	0.46
3:03:624:ASP:O	3:03:626:GLU:N	2.39	0.46
4:04:504:GLN:C	4:04:506:VAL:H	2.24	0.46
8:G:53:GLN:HE22	9:H:111:ARG:NH1	2.14	0.46
17:P:89:ARG:HB2	17:P:96:VAL:HA	1.98	0.46
1:A:69:G:H2'	1:A:70:U:C6	2.51	0.46
1:A:1392:G:H2'	1:A:1393:U:C6	2.51	0.46
2:02:33:ARG:HD3	2:02:33:ARG:N	2.31	0.46
3:03:795:ALA:O	3:03:796:LEU:C	2.59	0.46
4:04:85:CYS:HB3	4:04:88:CYS:O	2.15	0.46
4:04:289:ASP:HA	4:04:292:VAL:CG2	2.42	0.46
4:04:975:ILE:HD12	4:04:1001:ALA:HB3	1.98	0.46
4:04:1282:TYR:O	4:04:1285:VAL:HG12	2.16	0.46
9:H:35:LEU:HD12	9:H:48:GLY:O	2.16	0.46
9:H:67:ARG:HG3	9:H:67:ARG:HH11	1.81	0.46
11:J:142:ARG:HH11	11:J:142:ARG:HG3	1.81	0.46
18:Q:2:LYS:HB2	18:Q:5:MET:HB2	1.97	0.46
24:W:19:HIS:ND1	24:W:19:HIS:O	2.48	0.46
24:W:69:ASN:HA	24:W:72:ALA:HB3	1.97	0.46
1:A:745:G:H4'	1:A:836:G:N2	2.31	0.45
1:A:1379:G:H2'	1:A:1380:U:C6	2.51	0.45
2:01:166:ARG:N	2:01:167:PRO:CD	2.79	0.45
2:02:111:THR:HG22	2:02:129:VAL:HG22	1.97	0.45
2:02:197:ASP:C	2:02:198:LEU:HD22	2.41	0.45
3:03:1288:GLN:NE2	4:04:1356:LEU:HD21	2.31	0.45
4:04:143:SER:CB	4:04:159:ILE:HB	2.40	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:1:ALA:CB	8:G:67:LEU:HD11	2.41	0.45
11:J:49:LEU:C	11:J:49:LEU:HD12	2.41	0.45
12:K:15:ASN:HA	12:K:18:ALA:CB	2.46	0.45
13:L:29:ILE:O	13:L:29:ILE:HG23	2.16	0.45
1:A:9:G:N2	1:A:10:A:C4	2.84	0.45
1:A:44:A:H2'	1:A:45:G:H5'	1.99	0.45
2:02:159:ILE:HG23	2:02:172:LEU:HD21	1.97	0.45
3:03:211:ARG:NH2	3:03:351:LEU:HD22	2.31	0.45
3:03:1239:VAL:HB	3:03:1243:MET:HG2	1.97	0.45
3:03:1252:SER:HB2	3:03:1257:GLN:O	2.16	0.45
4:04:504:GLN:HB2	4:04:506:VAL:HG12	1.98	0.45
4:04:845:ALA:HA	4:04:883:ARG:NH1	2.31	0.45
4:04:894:VAL:HG12	4:04:895:CYS:N	2.31	0.45
4:04:1089:LEU:N	4:04:1089:LEU:HD12	2.30	0.45
12:K:46:GLU:O	12:K:47:ASP:O	2.34	0.45
15:N:109:ILE:N	15:N:109:ILE:CD1	2.79	0.45
1:A:626:G:H2'	1:A:627:G:C8	2.51	0.45
1:A:826:C:H1'	12:K:11:THR:HG22	1.97	0.45
3:03:556:GLY:H	3:03:660:VAL:HG23	1.81	0.45
3:03:688:GLN:OE1	3:03:1235:LEU:HD23	2.17	0.45
4:04:368:LEU:HD23	4:04:447:ILE:HD12	1.98	0.45
4:04:1157:ALA:HB2	4:04:1210:ILE:HD11	1.97	0.45
7:F:9:ILE:HG23	7:F:10:ARG:HG3	1.99	0.45
8:G:123:MET:HG3	8:G:145:ARG:HB2	1.98	0.45
9:H:104:ILE:HG23	9:H:104:ILE:O	2.17	0.45
13:L:105:ARG:O	13:L:106:ASP:HB3	2.16	0.45
21:T:64:ARG:HD3	21:T:65:PRO:O	2.15	0.45
1:A:701:U:H5''	1:A:703:G:H1'	1.98	0.45
3:03:18:ARG:HH12	3:03:623:LEU:H	1.64	0.45
3:03:276:GLN:HG2	3:03:276:GLN:O	2.17	0.45
3:03:520:PRO:HB2	3:03:708:VAL:HG12	1.98	0.45
3:03:540:ARG:HG3	3:03:540:ARG:HH11	1.80	0.45
3:03:832:HIS:HE2	3:03:1238:LEU:CD2	2.28	0.45
3:03:1064:ASP:H	3:03:1076:ILE:HG22	1.81	0.45
3:03:1313:HIS:O	3:03:1314:GLN:HB2	2.16	0.45
4:04:255:LEU:HD22	4:04:255:LEU:N	2.32	0.45
4:04:597:GLY:O	4:04:601:ILE:HG22	2.16	0.45
4:04:735:ALA:O	4:04:738:ARG:HB3	2.17	0.45
4:04:797:THR:HA	4:04:800:LEU:HB2	1.98	0.45
11:J:25:PHE:HE1	11:J:103:ILE:HB	1.80	0.45
11:J:78:ARG:HD2	11:J:78:ARG:N	2.24	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:81:GLY:C	12:K:82:LEU:HD12	2.42	0.45
17:P:78:ARG:HH21	23:V:64:GLU:HG3	1.80	0.45
1:A:878:A:OP1	12:K:81:GLY:HA3	2.17	0.45
2:01:50:SER:OG	2:02:35:PHE:HE1	1.99	0.45
2:02:143:ARG:HG2	2:02:143:ARG:HH11	1.82	0.45
3:03:684:ASN:O	3:03:687:ARG:HG3	2.16	0.45
3:03:1119:MET:HE3	3:03:1122:LYS:HB3	1.97	0.45
4:04:812:ASP:C	4:04:895:CYS:HB2	2.42	0.45
4:04:885:VAL:HG21	4:04:1255:VAL:HG12	1.99	0.45
4:04:1322:ALA:C	4:04:1324:SER:H	2.25	0.45
8:G:151:GLN:C	8:G:153:ARG:H	2.24	0.45
11:J:69:ARG:CG	11:J:95:ARG:HB3	2.46	0.45
13:L:46:VAL:HA	13:L:49:GLN:HG3	1.97	0.45
14:M:47:GLU:HB2	14:M:67:ILE:HB	1.99	0.45
20:S:16:PHE:HA	20:S:41:PRO:HD2	1.99	0.45
22:U:72:ASP:OD2	22:U:73:ARG:HG2	2.15	0.45
1:A:552:U:H2'	1:A:553:A:C8	2.51	0.45
1:A:637:C:H2'	1:A:638:U:C6	2.52	0.45
1:A:1225:A:H2'	1:A:1225:A:N3	2.32	0.45
1:A:1268:G:H1'	1:A:1326:U:O2'	2.16	0.45
2:01:56:VAL:HG12	2:01:86:LYS:HA	1.99	0.45
2:02:182:ARG:HD3	2:02:182:ARG:C	2.41	0.45
3:03:587:LEU:HD23	3:03:588:GLU:N	2.31	0.45
3:03:885:GLY:HA2	3:03:917:SER:OG	2.17	0.45
3:03:1138:VAL:HG21	3:03:1166:ASP:OD1	2.16	0.45
4:04:71:LEU:HD13	4:04:71:LEU:C	2.42	0.45
4:04:205:LEU:HD13	4:04:205:LEU:O	2.16	0.45
4:04:356:THR:OG1	4:04:357:VAL:N	2.49	0.45
4:04:485:MET:CB	4:04:488:ASN:HD22	2.26	0.45
4:04:583:VAL:HG13	4:04:587:LEU:HD23	1.98	0.45
4:04:785:ASP:O	4:04:786:THR:C	2.57	0.45
6:E:116:ASP:O	6:E:120:GLN:HG2	2.17	0.45
8:G:2:ARG:HE	8:G:4:LEU:HD21	1.81	0.45
13:L:34:LEU:HD23	13:L:39:GLY:CA	2.46	0.45
24:W:28:ARG:O	24:W:32:LYS:HG2	2.16	0.45
1:A:864:A:OP2	9:H:90:GLY:HA3	2.17	0.45
2:01:48:LEU:HD21	2:01:183:ILE:HB	1.98	0.45
3:03:517:GLN:HB3	3:03:759:SER:OG	2.16	0.45
3:03:679:ALA:O	3:03:683:ALA:N	2.50	0.45
3:03:1285:TYR:CG	4:04:475:GLU:HB3	2.52	0.45
4:04:125:GLY:HA2	4:04:135:ILE:HD12	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:1098:GLN:HG3	4:04:1098:GLN:O	2.16	0.45
6:E:104:TRP:C	6:E:106:THR:H	2.23	0.45
6:E:138:THR:O	6:E:141:LEU:HB3	2.17	0.45
9:H:87:VAL:O	9:H:87:VAL:HG13	2.17	0.45
12:K:76:ARG:HH11	12:K:76:ARG:HG3	1.82	0.45
13:L:38:PHE:HA	13:L:41:GLU:HB3	1.98	0.45
14:M:52:LEU:N	14:M:52:LEU:HD12	2.32	0.45
17:P:22:TYR:HD2	17:P:65:GLU:HA	1.81	0.45
20:S:28:ARG:HE	20:S:29:ASN:HD22	1.65	0.45
1:A:612:C:H5'	8:G:80:ARG:HH11	1.82	0.45
1:A:668:G:O2'	19:R:47:LYS:HB2	2.17	0.45
1:A:917:G:H2'	1:A:918:A:H8	1.81	0.45
1:A:1055:A:OP1	1:A:1055:A:H3'	2.17	0.45
1:A:1522:U:H2'	1:A:1523:G:H8	1.82	0.45
3:03:79:VAL:HG23	3:03:80:PHE:N	2.32	0.45
3:03:671:LEU:HD23	3:03:1187:PHE:CZ	2.52	0.45
4:04:60:ARG:HH11	4:04:60:ARG:HG3	1.81	0.45
4:04:114:ILE:HD11	4:04:311:ARG:H	1.81	0.45
4:04:250:ARG:HH11	4:04:250:ARG:HG3	1.82	0.45
4:04:656:GLU:C	4:04:658:GLU:H	2.25	0.45
7:F:31:ASN:N	7:F:31:ASN:HD22	2.15	0.45
8:G:51:GLY:O	8:G:54:LEU:HB3	2.16	0.45
9:H:60:GLN:O	9:H:64:GLU:HG2	2.16	0.45
13:L:82:ILE:O	13:L:86:LEU:HB2	2.16	0.45
15:N:80:ASN:HA	15:N:105:ARG:O	2.16	0.45
1:A:292:G:N2	1:A:608:A:H61	1.92	0.45
1:A:946:A:H2'	1:A:947:G:C8	2.52	0.45
1:A:1162:C:H2'	1:A:1163:A:H8	1.81	0.45
2:02:58:GLU:HB2	2:02:145:LYS:HD3	1.98	0.45
3:03:198:ILE:HG22	3:03:199:ASP:H	1.82	0.45
3:03:678:ARG:HB3	3:03:1071:GLY:HA3	1.98	0.45
3:03:697:LYS:HD3	3:03:697:LYS:N	2.26	0.45
3:03:840:SER:OG	3:03:1046:VAL:HA	2.17	0.45
6:E:42:ASN:HD21	6:E:45:LYS:CB	2.26	0.45
10:I:51:ILE:HD12	10:I:86:ARG:HH21	1.82	0.45
13:L:11:ARG:HG2	13:L:11:ARG:HH11	1.82	0.45
13:L:75:ALA:O	13:L:79:ARG:HG2	2.16	0.45
15:N:110:THR:HG22	15:N:111:ASP:N	2.32	0.45
17:P:68:LEU:O	17:P:72:ILE:HG12	2.17	0.45
18:Q:92:ILE:HD12	18:Q:92:ILE:N	2.32	0.45
1:A:443:C:H2'	1:A:444:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:770:C:H2'	1:A:771:G:H8	1.82	0.45
2:01:61:ILE:HB	2:01:64:VAL:CG2	2.47	0.45
3:03:207:THR:HA	3:03:210:LEU:HD12	1.99	0.45
3:03:836:LEU:HD21	3:03:921:PRO:CD	2.45	0.45
3:03:1235:LEU:HD12	3:03:1235:LEU:N	2.32	0.45
6:E:11:LYS:HG3	6:E:15:HIS:CG	2.51	0.45
6:E:125:THR:CG2	6:E:129:LEU:HD22	2.45	0.45
7:F:11:LEU:HB3	7:F:17:TRP:NE1	2.32	0.45
18:Q:78:LEU:HD13	18:Q:82:LYS:HB3	1.98	0.45
25:X:9:ASN:N	25:X:9:ASN:HD22	2.13	0.45
1:A:670:G:H2'	1:A:671:G:H8	1.82	0.44
1:A:1261:A:H2'	1:A:1262:C:H5'	1.99	0.44
2:01:56:VAL:O	2:01:56:VAL:HG13	2.17	0.44
3:03:1122:LYS:HG2	3:03:1229:TYR:CE2	2.52	0.44
3:03:1252:SER:CB	3:03:1257:GLN:HB2	2.47	0.44
4:04:199:GLU:O	4:04:203:GLU:HG3	2.17	0.44
4:04:789:LYS:HD2	4:04:789:LYS:HA	1.74	0.44
6:E:91:PHE:O	6:E:150:GLY:HA3	2.17	0.44
7:F:24:ASN:ND2	7:F:25:THR:N	2.63	0.44
7:F:126:ARG:HD3	7:F:126:ARG:N	2.31	0.44
9:H:112:ALA:HA	9:H:115:GLU:OE1	2.17	0.44
19:R:63:ARG:O	19:R:67:ASP:HB2	2.18	0.44
20:S:40:ASN:HD22	20:S:43:ALA:HA	1.80	0.44
1:A:667:G:H2'	1:A:668:G:C8	2.52	0.44
2:01:28:LEU:O	2:01:200:LYS:HA	2.17	0.44
3:03:40:GLU:HG2	3:03:41:GLN:N	2.31	0.44
3:03:217:THR:HG22	3:03:314:ASN:OD1	2.17	0.44
3:03:400:VAL:HG11	3:03:452:ARG:HH12	1.81	0.44
3:03:788:SER:HB3	3:03:795:ALA:O	2.17	0.44
4:04:125:GLY:HA2	4:04:135:ILE:CD1	2.46	0.44
4:04:688:ALA:O	4:04:692:ARG:HG3	2.17	0.44
4:04:865:HIS:HB3	4:04:901:ARG:NE	2.32	0.44
4:04:1287:ILE:HG13	4:04:1288:ALA:N	2.31	0.44
5:05:21:LEU:O	5:05:24:ALA:HB3	2.17	0.44
6:E:178:ASN:C	6:E:179:LEU:HD12	2.42	0.44
7:F:5:HIS:HA	7:F:6:PRO:HD3	1.88	0.44
9:H:105:ILE:HD12	9:H:105:ILE:H	1.81	0.44
10:I:29:ILE:HG21	10:I:64:VAL:HG21	1.98	0.44
13:L:112:ARG:HE	18:Q:100:TRP:CD1	2.35	0.44
13:L:121:ARG:HG3	13:L:121:ARG:HH11	1.83	0.44
1:A:50:A:C4'	1:A:51:A:H5'	2.45	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:U:O2'	1:A:274:A:H5'	2.17	0.44
1:A:346:G:H2'	1:A:347:G:H5'	1.98	0.44
1:A:1393:U:H2'	1:A:1395:C:H5	1.82	0.44
2:02:102:LEU:C	2:02:102:LEU:HD13	2.41	0.44
2:02:224:LEU:HD23	2:02:224:LEU:C	2.42	0.44
3:03:209:ILE:HG23	3:03:210:LEU:N	2.33	0.44
3:03:877:VAL:HG21	3:03:928:VAL:HG13	1.98	0.44
3:03:1210:ILE:HG22	3:03:1211:ARG:N	2.32	0.44
4:04:795:TYR:O	4:04:798:ARG:HB3	2.17	0.44
4:04:903:LEU:HG	4:04:904:ALA:N	2.29	0.44
4:04:1309:ILE:HG13	4:04:1310:THR:N	2.31	0.44
6:E:107:VAL:O	6:E:107:VAL:HG12	2.18	0.44
11:J:65:LEU:HA	11:J:68:VAL:HG22	1.98	0.44
15:N:60:PHE:O	15:N:64:VAL:HG23	2.17	0.44
16:O:40:THR:O	16:O:41:PRO:O	2.34	0.44
16:O:82:ARG:HB2	16:O:97:VAL:CG2	2.48	0.44
23:V:16:LYS:O	23:V:20:LYS:HG3	2.17	0.44
23:V:39:ILE:HD12	23:V:65:MET:HB3	1.98	0.44
1:A:880:C:H2'	1:A:881:G:C8	2.51	0.44
3:03:663:VAL:O	3:03:667:LEU:HB2	2.17	0.44
4:04:127:LEU:HD13	4:04:223:LEU:HD23	1.99	0.44
6:E:136:MET:HA	6:E:136:MET:CE	2.46	0.44
7:F:139:ASN:O	7:F:143:LEU:HB2	2.18	0.44
13:L:64:ILE:HD13	13:L:78:ILE:HG23	1.99	0.44
15:N:53:GLY:N	15:N:56:LYS:HG3	2.29	0.44
18:Q:71:GLY:C	18:Q:79:SER:HA	2.42	0.44
24:W:9:ARG:HG2	24:W:9:ARG:HH11	1.82	0.44
24:W:54:GLN:HA	24:W:57:VAL:HG12	1.99	0.44
24:W:79:THR:HG22	24:W:83:ASN:ND2	2.32	0.44
1:A:62:U:H4'	1:A:378:G:N2	2.32	0.44
1:A:136:C:H2'	1:A:137:U:H5'	1.99	0.44
1:A:583:A:H61	16:O:8:ARG:NH2	2.15	0.44
1:A:920:U:H2'	1:A:921:U:C6	2.53	0.44
1:A:1066:C:O2'	1:A:1067:A:H5'	2.17	0.44
2:01:80:GLU:HA	2:01:83:LEU:HB2	2.00	0.44
3:03:1274:GLU:O	3:03:1278:LEU:HD23	2.18	0.44
3:03:1309:VAL:HG21	4:04:394:ILE:HD12	1.99	0.44
4:04:57:PHE:CD2	4:04:252:LEU:HD22	2.53	0.44
4:04:505:ASP:HA	4:04:508:LEU:HB2	1.99	0.44
4:04:557:LYS:HD3	4:04:611:ILE:O	2.17	0.44
4:04:586:GLY:HA3	4:04:612:LEU:HD22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:793:SER:O	4:04:797:THR:HG23	2.18	0.44
4:04:1041:ILE:N	4:04:1041:ILE:CD1	2.76	0.44
6:E:60:ILE:HD11	6:E:184:PHE:CE2	2.52	0.44
7:F:71:ARG:O	7:F:75:VAL:HG23	2.18	0.44
8:G:75:TYR:OH	8:G:200:VAL:HG23	2.17	0.44
8:G:80:ARG:HH11	8:G:80:ARG:HG2	1.82	0.44
9:H:9:GLU:OE1	9:H:9:GLU:N	2.51	0.44
13:L:112:ARG:HH11	13:L:114:LYS:HG2	1.81	0.44
16:O:43:LYS:HG3	16:O:44:PRO:HD3	1.98	0.44
22:U:54:GLN:OE1	22:U:54:GLN:HA	2.17	0.44
24:W:66:ILE:HG22	24:W:71:ALA:HB2	1.98	0.44
1:A:185:U:O2	24:W:58:ASP:HB3	2.17	0.44
3:03:888:THR:O	3:03:914:LYS:HG2	2.18	0.44
3:03:1079:ILE:HG23	3:03:1079:ILE:O	2.18	0.44
4:04:483:LEU:HD23	5:05:16:ARG:HD3	1.99	0.44
4:04:842:ARG:O	4:04:864:LEU:HB2	2.18	0.44
7:F:35:ASP:HA	7:F:38:VAL:HG22	1.99	0.44
7:F:134:LYS:NZ	9:H:56:PRO:HG3	2.33	0.44
8:G:127:ARG:N	8:G:127:ARG:HD2	2.32	0.44
10:I:19:PRO:HA	10:I:22:ILE:CD1	2.48	0.44
17:P:7:ASN:ND2	17:P:9:PRO:HD3	2.32	0.44
1:A:1425:U:H2'	1:A:1426:G:H8	1.83	0.44
2:01:60:GLU:HB2	2:01:170:ARG:HD2	1.99	0.44
4:04:247:PRO:C	4:04:249:LEU:N	2.76	0.44
4:04:349:TYR:HE1	4:04:379:PRO:HG2	1.83	0.44
4:04:965:SER:HB3	4:04:973:LEU:HD11	2.00	0.44
4:04:1306:LEU:HD23	4:04:1307:LEU:N	2.32	0.44
10:I:47:LEU:HD21	10:I:57:ALA:CB	2.45	0.44
11:J:38:ALA:O	11:J:42:VAL:HG23	2.17	0.44
11:J:90:VAL:HG13	11:J:95:ARG:HG2	1.98	0.44
12:K:87:ARG:HG3	12:K:88:LYS:N	2.32	0.44
16:O:88:ASP:C	16:O:89:LEU:HD12	2.43	0.44
22:U:64:TYR:C	22:U:65:LEU:HD12	2.43	0.44
23:V:18:VAL:O	23:V:22:VAL:HG23	2.18	0.44
1:A:314:C:O2'	1:A:315:A:H5'	2.18	0.44
1:A:357:G:H5''	1:A:367:U:OP2	2.18	0.44
1:A:358:U:H2'	1:A:359:G:H8	1.82	0.44
1:A:599:C:H5''	12:K:87:ARG:CB	2.45	0.44
1:A:631:C:H3'	1:A:632:U:H5'	2.00	0.44
3:03:702:THR:HG23	3:03:704:MET:H	1.82	0.44
3:03:1254:VAL:HG13	3:03:1255:THR:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:586:GLY:HA3	4:04:612:LEU:HB2	1.98	0.44
7:F:151:GLU:O	7:F:198:LYS:HB2	2.17	0.44
10:I:93:LYS:HB3	10:I:93:LYS:HZ3	1.81	0.44
13:L:72:SER:HA	13:L:75:ALA:CB	2.47	0.44
17:P:13:HIS:HA	17:P:42:VAL:O	2.18	0.44
21:T:61:ARG:NH1	21:T:61:ARG:CB	2.81	0.44
1:A:1356:G:H2'	1:A:1357:A:C8	2.53	0.44
1:A:1376:U:O2'	1:A:1377:A:H5'	2.18	0.44
4:04:281:ARG:O	4:04:285:LEU:HD13	2.18	0.44
4:04:1077:ALA:HB1	4:04:1079:LYS:HE3	2.00	0.44
4:04:1216:ALA:HB3	4:04:1219:ASP:OD2	2.18	0.44
6:E:157:LEU:HD23	6:E:157:LEU:N	2.30	0.44
11:J:136:LYS:O	11:J:140:VAL:HG23	2.18	0.44
14:M:72:ARG:HG2	14:M:72:ARG:HH11	1.83	0.44
16:O:83:GLY:HA2	16:O:94:TYR:HD1	1.82	0.44
23:V:8:PRO:CA	23:V:38:THR:HG21	2.48	0.44
23:V:30:LEU:HD12	23:V:30:LEU:N	2.32	0.44
1:A:177:G:O2'	1:A:1447:A:H2'	2.18	0.43
1:A:511:C:O2'	1:A:512:U:H5'	2.18	0.43
1:A:867:G:H21	1:A:873:A:H2	1.64	0.43
1:A:1320:C:O2'	23:V:72:GLU:HG2	2.17	0.43
2:02:195:ARG:HG3	2:02:196:THR:H	1.82	0.43
3:03:722:GLY:H	3:03:777:VAL:CG2	2.31	0.43
3:03:777:VAL:HB	3:03:781:ASP:HB3	2.00	0.43
3:03:806:PRO:HA	3:03:811:ASN:HD21	1.81	0.43
4:04:268:LEU:O	4:04:272:VAL:HG23	2.18	0.43
4:04:615:LYS:HB2	4:04:616:PRO:HD3	2.00	0.43
4:04:739:GLN:HB3	4:04:744:ARG:HD2	2.00	0.43
4:04:1215:GLU:HG3	4:04:1220:ILE:HD11	2.00	0.43
4:04:1307:LEU:HD12	4:04:1307:LEU:N	2.32	0.43
6:E:23:TRP:NE1	6:E:25:PRO:CG	2.81	0.43
8:G:196:GLU:N	8:G:196:GLU:OE1	2.50	0.43
16:O:24:GLU:C	16:O:26:CYS:N	2.76	0.43
18:Q:52:ARG:N	18:Q:52:ARG:HD2	2.33	0.43
23:V:28:LYS:O	23:V:30:LEU:HD12	2.18	0.43
24:W:50:PHE:O	24:W:54:GLN:HG3	2.18	0.43
1:A:358:U:H2'	1:A:359:G:C8	2.53	0.43
1:A:877:G:H21	12:K:3:GLN:NE2	2.15	0.43
2:01:41:ASN:HA	2:01:44:ARG:HB3	2.00	0.43
3:03:144:VAL:HG11	3:03:527:LYS:HG2	2.00	0.43
3:03:194:LEU:HD21	3:03:432:LEU:HD23	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:499:SER:C	3:03:501:ALA:H	2.26	0.43
3:03:850:ILE:O	3:03:850:ILE:HG22	2.17	0.43
3:03:1246:ARG:HD3	3:03:1246:ARG:C	2.43	0.43
4:04:156:ARG:HD3	4:04:157:GLN:HG2	2.00	0.43
4:04:253:VAL:HA	4:04:254:PRO:HD3	1.88	0.43
4:04:381:ILE:O	4:04:385:LEU:HG	2.18	0.43
4:04:515:ARG:HE	4:04:717:VAL:CG2	2.31	0.43
4:04:601:ILE:O	4:04:604:MET:HB3	2.18	0.43
4:04:661:VAL:HG12	4:04:685:ILE:HD11	2.00	0.43
6:E:45:LYS:HD3	6:E:45:LYS:HA	1.84	0.43
6:E:129:LEU:HD23	6:E:129:LEU:N	2.33	0.43
7:F:19:SER:HB2	7:F:21:TRP:HE1	1.83	0.43
7:F:21:TRP:HB3	7:F:58:ARG:HB3	1.99	0.43
8:G:123:MET:HE2	8:G:145:ARG:CA	2.48	0.43
11:J:28:ILE:HG21	11:J:101:ARG:HA	2.01	0.43
21:T:69:THR:HG22	21:T:69:THR:O	2.18	0.43
1:A:228:A:O2'	20:S:2:VAL:HG11	2.19	0.43
2:02:9:LEU:HD13	2:02:192:VAL:HG21	1.99	0.43
3:03:65:ASN:HB3	3:03:105:TYR:HD2	1.83	0.43
3:03:176:ILE:HB	3:03:184:LEU:HB3	1.99	0.43
3:03:502:VAL:HG13	3:03:503:LYS:CD	2.38	0.43
3:03:722:GLY:H	3:03:777:VAL:HG22	1.83	0.43
3:03:811:ASN:HA	3:03:815:SER:HB3	2.00	0.43
3:03:1146:GLN:OE1	3:03:1146:GLN:HA	2.17	0.43
4:04:20:ILE:HD12	4:04:20:ILE:N	2.32	0.43
4:04:21:LYS:O	4:04:21:LYS:HG3	2.18	0.43
4:04:137:ARG:HD2	4:04:159:ILE:CD1	2.49	0.43
4:04:154:LEU:N	4:04:154:LEU:HD12	2.33	0.43
4:04:363:LEU:HA	4:04:450:HIS:CD2	2.52	0.43
4:04:1220:ILE:HB	4:04:1229:VAL:HG23	2.01	0.43
8:G:44:LYS:HA	8:G:45:PRO:HD3	1.88	0.43
9:H:101:GLY:O	9:H:102:THR:C	2.60	0.43
15:N:110:THR:HG22	15:N:112:VAL:HG13	2.00	0.43
16:O:2:THR:O	16:O:5:GLN:HB3	2.18	0.43
16:O:62:VAL:HG21	16:O:94:TYR:CE2	2.52	0.43
17:P:13:HIS:HB3	17:P:41:ASP:HA	2.00	0.43
25:X:10:GLU:N	25:X:11:PRO:CD	2.81	0.43
1:A:204:G:H1'	1:A:465:A:N1	2.33	0.43
1:A:503:C:O2'	1:A:504:C:H5'	2.19	0.43
1:A:670:G:H2'	1:A:671:G:C8	2.53	0.43
1:A:946:A:H1'	1:A:1333:A:C2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:02:10:LYS:N	2:02:10:LYS:HD2	2.33	0.43
2:02:95:LYS:HD3	2:02:98:VAL:HB	2.00	0.43
3:03:72:SER:OG	3:03:73:TYR:N	2.51	0.43
3:03:833:ILE:HG12	3:03:1055:ALA:HB2	1.99	0.43
4:04:56:LEU:N	4:04:56:LEU:HD12	2.33	0.43
4:04:778:GLY:O	4:04:781:LYS:HB3	2.18	0.43
6:E:75:ALA:HB1	6:E:207:ILE:HD11	2.00	0.43
13:L:57:VAL:HB	13:L:58:GLU:OE1	2.18	0.43
17:P:90:HIS:HB2	17:P:96:VAL:CG1	2.48	0.43
1:A:1069:C:H4'	1:A:1192:C:O2	2.18	0.43
2:01:46:ILE:HG23	2:01:47:LEU:N	2.34	0.43
3:03:194:LEU:HD23	3:03:194:LEU:C	2.43	0.43
3:03:890:LYS:HB2	3:03:890:LYS:HZ2	1.83	0.43
3:03:1156:ARG:HD2	3:03:1156:ARG:O	2.18	0.43
4:04:308:ASP:HB2	4:04:328:ALA:CB	2.49	0.43
4:04:1238:GLN:O	4:04:1242:ARG:HG3	2.18	0.43
6:E:118:GLU:HG3	6:E:122:GLN:NE2	2.29	0.43
7:F:107:LYS:HD2	7:F:110:LEU:HD22	2.00	0.43
7:F:115:VAL:O	7:F:119:ILE:HG13	2.19	0.43
13:L:62:LEU:HD13	13:L:64:ILE:HG13	1.99	0.43
1:A:538:G:OP1	16:O:110:LYS:HB2	2.18	0.43
3:03:153:PRO:HB2	3:03:401:GLY:CA	2.47	0.43
3:03:283:LYS:HB2	3:03:283:LYS:HZ2	1.83	0.43
3:03:853:ASP:CG	3:03:854:ILE:N	2.76	0.43
3:03:1331:ARG:HG2	3:03:1331:ARG:NH1	2.33	0.43
4:04:66:LYS:HE2	4:04:69:GLU:HG2	2.00	0.43
4:04:84:ILE:HG13	4:04:84:ILE:O	2.18	0.43
4:04:197:GLU:O	4:04:201:LEU:HG	2.19	0.43
4:04:510:LEU:O	4:04:513:MET:HB3	2.18	0.43
4:04:1145:PHE:CE1	4:04:1256:ILE:HG21	2.54	0.43
4:04:1251:LYS:CB	4:04:1251:LYS:NZ	2.78	0.43
6:E:19:GLN:OE1	6:E:19:GLN:HA	2.19	0.43
6:E:157:LEU:HD13	6:E:179:LEU:HD23	2.01	0.43
7:F:22:PHE:HB3	14:M:97:ASP:HB2	2.00	0.43
1:A:19:A:OP1	9:H:131:ASN:HB2	2.19	0.43
1:A:694:A:H2	1:A:788:U:H5'	1.83	0.43
1:A:885:G:H2'	1:A:886:G:C8	2.53	0.43
1:A:905:U:H2'	1:A:906:A:H5'	2.01	0.43
2:02:42:ALA:O	2:02:46:ILE:HG13	2.19	0.43
3:03:956:ALA:O	3:03:960:LEU:HD23	2.19	0.43
3:03:1233:LEU:C	3:03:1233:LEU:HD13	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:130:MET:CG	4:04:131:PRO:HD2	2.44	0.43
4:04:646:ILE:HA	4:04:647:PRO:HD3	1.82	0.43
6:E:21:ARG:HA	6:E:23:TRP:CD1	2.53	0.43
6:E:65:GLY:O	6:E:66:LYS:O	2.36	0.43
9:H:56:PRO:O	9:H:60:GLN:HG2	2.18	0.43
21:T:26:ARG:HG2	21:T:26:ARG:HH11	1.84	0.43
2:01:64:VAL:CG2	2:01:78:ILE:HG21	2.49	0.43
2:02:192:VAL:O	2:02:193:GLU:C	2.62	0.43
3:03:525:THR:O	3:03:529:ARG:HD3	2.18	0.43
4:04:174:ASP:O	4:04:175:GLU:C	2.62	0.43
4:04:180:MET:HG2	4:04:293:ARG:HH11	1.83	0.43
8:G:124:VAL:C	8:G:126:GLY:H	2.25	0.43
10:I:18:VAL:H	10:I:19:PRO:HD3	1.83	0.43
10:I:45:ARG:HB2	10:I:59:TYR:HD2	1.83	0.43
15:N:35:ASP:HB2	15:N:39:ASN:HB2	2.00	0.43
16:O:51:VAL:HG12	16:O:65:TYR:HA	2.00	0.43
18:Q:25:GLU:HG3	18:Q:26:LEU:H	1.84	0.43
18:Q:79:SER:O	18:Q:83:VAL:HG23	2.18	0.43
20:S:47:GLU:CD	20:S:47:GLU:H	2.27	0.43
1:A:59:A:H1'	1:A:354:G:N2	2.34	0.43
1:A:356:A:H4'	1:A:367:U:H5	1.83	0.43
1:A:509:A:H5'	8:G:54:LEU:HD23	2.01	0.43
1:A:594:U:O2'	1:A:595:A:H5'	2.19	0.43
1:A:1106:G:H5''	7:F:171:ARG:HB2	2.00	0.43
2:01:66:HIS:HB2	3:03:929:ILE:HG22	2.01	0.43
2:01:101:THR:HB	2:01:116:THR:OG1	2.19	0.43
3:03:32:LEU:N	3:03:32:LEU:HD12	2.34	0.43
3:03:729:ALA:O	3:03:755:LYS:HG3	2.18	0.43
3:03:1304:MET:HE3	3:03:1315:MET:CB	2.48	0.43
4:04:97:VAL:HG12	4:04:101:ARG:NH1	2.33	0.43
4:04:755:ILE:HG22	4:04:757:THR:N	2.26	0.43
4:04:800:LEU:O	4:04:803:VAL:HG12	2.19	0.43
5:05:38:LEU:H	5:05:38:LEU:CD1	2.31	0.43
8:G:96:ARG:HG2	8:G:98:ASP:OD1	2.18	0.43
12:K:77:VAL:HG11	12:K:124:ILE:HD12	2.00	0.43
14:M:8:ILE:HB	14:M:74:VAL:CG2	2.49	0.43
21:T:61:ARG:HB3	21:T:61:ARG:CZ	2.48	0.43
25:X:37:PHE:CE1	25:X:39:GLU:HB3	2.54	0.43
25:X:47:ARG:C	25:X:47:ARG:HD3	2.43	0.43
1:A:26:A:H61	1:A:558:G:H1'	1.84	0.43
1:A:779:C:H2'	1:A:780:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1210:C:C2'	1:A:1211:U:H5'	2.49	0.43
2:02:33:ARG:H	2:02:33:ARG:CD	2.32	0.43
3:03:103:VAL:HG23	3:03:103:VAL:O	2.19	0.43
4:04:67:ASP:OD1	4:04:95:THR:HG22	2.18	0.43
4:04:114:ILE:HG23	4:04:115:TRP:N	2.34	0.43
6:E:59:LYS:C	6:E:61:ALA:H	2.27	0.43
10:I:52:ASN:N	10:I:52:ASN:ND2	2.63	0.43
15:N:78:ILE:O	15:N:78:ILE:HG13	2.18	0.43
24:W:70:LYS:NZ	24:W:70:LYS:HB2	2.33	0.43
1:A:744:C:H2'	1:A:745:G:H8	1.83	0.42
1:A:1393:U:H5'	1:A:1502:A:OP1	2.18	0.42
2:02:73:GLY:O	2:02:134:THR:HG22	2.19	0.42
2:02:77:ASP:O	2:02:81:ILE:HG13	2.19	0.42
3:03:73:TYR:CE2	3:03:75:LEU:HD21	2.54	0.42
3:03:146:VAL:HG11	3:03:531:SER:HB2	2.00	0.42
3:03:386:GLU:O	3:03:390:PHE:HB2	2.19	0.42
3:03:720:ARG:HD3	3:03:742:TYR:CD2	2.54	0.42
3:03:727:VAL:HG13	3:03:732:ILE:HG12	1.99	0.42
3:03:779:ARG:HG2	3:03:779:ARG:HH11	1.82	0.42
4:04:92:VAL:O	4:04:92:VAL:HG23	2.19	0.42
4:04:421:VAL:HG22	4:04:439:PRO:HD3	1.99	0.42
4:04:779:ALA:O	4:04:780:ARG:C	2.61	0.42
4:04:848:VAL:HG21	4:04:880:VAL:HG13	2.00	0.42
6:E:9:MET:HE2	6:E:9:MET:CA	2.49	0.42
7:F:42:LEU:HD11	7:F:46:LEU:HD12	2.00	0.42
7:F:55:VAL:HG23	7:F:66:THR:HB	2.01	0.42
7:F:79:LYS:HB2	7:F:81:GLU:OE1	2.19	0.42
9:H:75:LEU:H	9:H:75:LEU:HD23	1.84	0.42
11:J:45:ALA:HB2	11:J:116:ALA:HA	2.01	0.42
13:L:105:ARG:O	13:L:105:ARG:HD3	2.19	0.42
18:Q:55:SER:HB3	18:Q:59:GLN:HG2	2.01	0.42
23:V:11:ASP:HB3	23:V:13:HIS:CD2	2.53	0.42
1:A:71:A:H3'	1:A:72:A:C5'	2.49	0.42
1:A:629:A:H2'	1:A:630:A:O4'	2.18	0.42
1:A:932:C:OP2	11:J:2:ARG:HD2	2.20	0.42
3:03:151:ARG:HB3	3:03:177:ILE:CD1	2.37	0.42
3:03:635:THR:HA	3:03:643:SER:O	2.19	0.42
3:03:636:CYS:HB2	3:03:645:PHE:HD2	1.83	0.42
3:03:1064:ASP:CG	3:03:1234:LYS:HE3	2.44	0.42
4:04:23:ALA:HA	4:04:1339:GLY:HA2	2.00	0.42
4:04:227:PHE:O	4:04:231:GLY:N	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:357:VAL:HG12	4:04:359:PRO:HD3	2.01	0.42
4:04:385:LEU:HB3	4:04:391:ALA:HB2	2.01	0.42
4:04:487:THR:O	4:04:614:LEU:HD11	2.19	0.42
6:E:21:ARG:HG2	6:E:21:ARG:HH11	1.83	0.42
10:I:77:THR:O	10:I:81:ASN:HB2	2.18	0.42
11:J:56:SER:OG	11:J:59:GLU:HG2	2.19	0.42
11:J:67:ASN:O	11:J:134:VAL:HG23	2.19	0.42
15:N:122:PRO:HB2	15:N:123:PRO:HD2	2.00	0.42
18:Q:55:SER:HA	18:Q:57:SER:N	2.34	0.42
22:U:15:ALA:HB2	22:U:48:ARG:HH12	1.82	0.42
23:V:38:THR:HA	23:V:69:LYS:HD3	2.01	0.42
1:A:128:G:O2'	1:A:129:A:H5'	2.19	0.42
1:A:168:G:O2'	1:A:169:C:H5'	2.19	0.42
1:A:257:G:O2'	1:A:258:G:H5'	2.19	0.42
1:A:1503:A:O2'	1:A:1504:G:H5'	2.18	0.42
3:03:46:GLN:O	3:03:47:TYR:C	2.61	0.42
3:03:525:THR:CG2	3:03:687:ARG:HB3	2.45	0.42
3:03:690:VAL:HG12	3:03:1234:LYS:HB3	1.99	0.42
3:03:763:THR:HG22	3:03:764:CYS:N	2.29	0.42
3:03:1112:ILE:CG2	4:04:641:ILE:N	2.82	0.42
3:03:1272:GLU:HA	3:03:1275:VAL:CG2	2.49	0.42
4:04:1141:VAL:HA	4:04:1144:LEU:HD12	2.01	0.42
4:04:1273:ASP:CG	4:04:1274:PHE:H	2.26	0.42
9:H:96:GLN:HE21	9:H:97:PRO:HD2	1.83	0.42
11:J:10:LYS:HD2	11:J:10:LYS:HA	1.86	0.42
12:K:45:ILE:HD11	12:K:60:LEU:HB3	2.01	0.42
12:K:86:LYS:HG3	12:K:124:ILE:HD13	2.01	0.42
12:K:120:LEU:HD12	12:K:120:LEU:C	2.44	0.42
13:L:25:GLY:HA3	13:L:58:GLU:HA	2.01	0.42
14:M:102:LEU:HD23	14:M:102:LEU:H	1.83	0.42
18:Q:68:ARG:HD3	18:Q:79:SER:CB	2.50	0.42
19:R:63:ARG:HG2	19:R:63:ARG:HH11	1.84	0.42
21:T:11:VAL:HA	21:T:22:VAL:HG23	2.01	0.42
23:V:4:LEU:HD21	23:V:9:PHE:HE2	1.84	0.42
25:X:49:LYS:O	25:X:49:LYS:HD2	2.20	0.42
1:A:254:G:O2'	1:A:255:G:H5'	2.19	0.42
1:A:1486:G:H2'	1:A:1487:G:H8	1.85	0.42
2:01:150:ARG:HD2	2:01:150:ARG:C	2.44	0.42
2:02:100:LEU:CD2	2:02:121:VAL:HG21	2.42	0.42
3:03:29:SER:HB2	3:03:30:ILE:HD12	2.01	0.42
3:03:401:GLY:O	3:03:405:PHE:CD2	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:1103:VAL:C	3:03:1105:SER:N	2.75	0.42
3:03:1211:ARG:HB3	3:03:1224:PRO:HG3	2.01	0.42
4:04:189:LEU:HD13	4:04:234:PRO:O	2.20	0.42
4:04:220:ARG:HH11	4:04:220:ARG:HG2	1.84	0.42
4:04:291:ILE:O	4:04:294:ASN:HB3	2.19	0.42
6:E:60:ILE:HD11	6:E:184:PHE:HE2	1.83	0.42
8:G:18:LEU:HB3	8:G:63:ILE:CG1	2.42	0.42
9:H:75:LEU:HD23	9:H:75:LEU:N	2.35	0.42
19:R:66:LEU:HD22	19:R:77:TYR:HE1	1.85	0.42
19:R:81:ILE:O	19:R:85:GLY:HA2	2.19	0.42
24:W:57:VAL:HG13	24:W:58:ASP:N	2.34	0.42
1:A:219:U:H3'	1:A:220:G:H5''	2.01	0.42
1:A:372:C:N4	1:A:389:A:H62	2.07	0.42
1:A:735:C:H5''	22:U:57:ARG:HH12	1.84	0.42
1:A:1409:C:H2'	1:A:1410:A:H8	1.83	0.42
2:02:19:VAL:O	2:02:19:VAL:HG12	2.17	0.42
2:02:219:ARG:O	2:02:223:ILE:HG13	2.18	0.42
3:03:209:ILE:CG2	3:03:210:LEU:N	2.81	0.42
3:03:666:SER:O	3:03:702:THR:HG21	2.19	0.42
3:03:1242:LYS:HD2	3:03:1242:LYS:N	2.34	0.42
4:04:1089:LEU:HD12	4:04:1089:LEU:H	1.85	0.42
7:F:87:ARG:HG3	7:F:98:ALA:HB3	2.01	0.42
7:F:183:TYR:OH	7:F:198:LYS:HD2	2.19	0.42
8:G:112:GLU:O	8:G:115:GLN:HB3	2.19	0.42
8:G:138:PRO:HA	8:G:181:PHE:CD2	2.54	0.42
1:A:184:G:O2'	1:A:224:U:H4'	2.20	0.42
1:A:653:U:H3	12:K:27:PRO:HB3	1.84	0.42
1:A:750:C:H1'	19:R:22:GLY:HA3	2.00	0.42
1:A:981:U:C3'	1:A:982:U:H5''	2.42	0.42
2:01:9:LEU:H	2:01:9:LEU:CD2	2.33	0.42
2:02:82:LEU:HD23	2:02:85:LEU:HD12	2.01	0.42
2:02:154:PRO:HG3	4:04:541:LEU:CD2	2.48	0.42
3:03:153:PRO:HB2	3:03:401:GLY:HA2	2.01	0.42
3:03:520:PRO:O	3:03:524:ILE:HG13	2.20	0.42
3:03:984:VAL:O	3:03:984:VAL:HG13	2.20	0.42
3:03:1284:ALA:O	3:03:1287:LEU:HB3	2.20	0.42
4:04:78:LEU:H	4:04:78:LEU:CD1	2.32	0.42
4:04:234:PRO:HA	4:04:237:MET:HE2	2.01	0.42
4:04:895:CYS:SG	4:04:898:CYS:HB2	2.60	0.42
6:E:221:VAL:C	6:E:223:GLU:H	2.28	0.42
7:F:135:ARG:HH11	7:F:135:ARG:HG3	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:14:GLN:HG2	10:I:83:ALA:HB2	2.01	0.42
10:I:47:LEU:HD11	10:I:57:ALA:HB2	2.01	0.42
11:J:20:GLU:HA	11:J:23:ALA:CB	2.49	0.42
11:J:29:LEU:HD12	11:J:104:VAL:HG13	2.01	0.42
13:L:129:ARG:HG2	13:L:129:ARG:HH11	1.84	0.42
18:Q:20:PHE:CE2	18:Q:54:SER:HB3	2.49	0.42
19:R:87:ARG:HA	19:R:87:ARG:HE	1.84	0.42
1:A:837:U:H2'	1:A:838:G:C8	2.52	0.42
1:A:883:C:H2'	1:A:884:U:C6	2.55	0.42
1:A:883:C:O2'	1:A:884:U:H5'	2.20	0.42
1:A:992:U:H3'	1:A:1042:A:OP2	2.19	0.42
1:A:1024:G:O2'	1:A:1025:U:H5'	2.20	0.42
3:O3:753:LEU:HB3	3:O3:755:LYS:HG2	2.02	0.42
3:O3:936:ARG:CB	3:O3:1048:LYS:HE2	2.49	0.42
4:O4:515:ARG:HH21	4:O4:717:VAL:HG23	1.83	0.42
4:O4:763:PHE:CZ	4:O4:767:LEU:HD21	2.54	0.42
4:O4:1241:TYR:O	4:O4:1245:GLY:N	2.53	0.42
6:E:39:HIS:O	6:E:40:ILE:CG1	2.67	0.42
8:G:138:PRO:HA	8:G:181:PHE:HD2	1.84	0.42
8:G:167:PRO:C	8:G:169:TRP:N	2.75	0.42
12:K:34:ALA:HB1	12:K:109:VAL:HB	2.01	0.42
16:O:64:SER:HA	16:O:92:VAL:HG13	2.01	0.42
18:Q:68:ARG:HH22	18:Q:80:ARG:NH2	2.16	0.42
20:S:27:ALA:O	20:S:29:ASN:N	2.53	0.42
20:S:39:PHE:CE2	20:S:74:LEU:HD22	2.55	0.42
21:T:30:HIS:CE1	21:T:32:ILE:HD12	2.54	0.42
1:A:877:G:N2	12:K:3:GLN:HE21	2.17	0.42
1:A:885:G:H2'	1:A:886:G:H8	1.83	0.42
2:O1:218:ARG:HD2	2:O1:218:ARG:C	2.45	0.42
2:O2:178:SER:C	2:O2:180:VAL:H	2.26	0.42
3:O3:86:GLN:HB2	3:O3:757:THR:HG21	2.01	0.42
3:O3:1034:ARG:HH11	3:O3:1038:GLN:HE21	1.68	0.42
4:O4:481:ARG:HA	4:O4:485:MET:HB2	2.02	0.42
6:E:109:GLN:O	6:E:112:LYS:HB3	2.20	0.42
12:K:77:VAL:HG22	12:K:127:TYR:CE2	2.54	0.42
13:L:53:LEU:HD12	13:L:97:LEU:HD12	2.02	0.42
16:O:89:LEU:HD12	16:O:89:LEU:N	2.35	0.42
19:R:7:THR:O	19:R:11:VAL:HG23	2.19	0.42
1:A:269:C:O5'	1:A:1466:C:H4'	2.19	0.42
1:A:500:G:H2'	1:A:501:C:C6	2.55	0.42
1:A:961:U:H2'	1:A:962:C:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:994:A:N1	1:A:1216:A:H4'	2.35	0.42
1:A:1162:C:H2'	1:A:1163:A:C8	2.55	0.42
2:01:92:VAL:HA	2:01:120:ASP:O	2.19	0.42
2:02:162:GLU:C	2:02:164:ASP:H	2.28	0.42
3:03:137:VAL:HG22	3:03:142:GLU:HG3	2.02	0.42
3:03:198:ILE:HG22	3:03:199:ASP:N	2.34	0.42
3:03:677:ASN:O	3:03:680:LEU:HB3	2.19	0.42
3:03:1184:THR:HA	3:03:1185:PRO:HD3	1.76	0.42
4:04:37:GLU:HB2	4:04:104:HIS:CE1	2.55	0.42
4:04:1259:GLN:O	4:04:1262:ARG:HG3	2.19	0.42
6:E:40:ILE:CG2	6:E:41:ILE:H	2.30	0.42
6:E:114:LEU:HD22	6:E:148:LEU:HD23	2.02	0.42
7:F:146:LYS:HB2	7:F:202:PHE:HD2	1.84	0.42
8:G:140:ASP:CG	8:G:141:VAL:H	2.28	0.42
12:K:14:ARG:HH21	12:K:75:GLN:HB3	1.85	0.42
12:K:30:LYS:HG3	12:K:31:LEU:N	2.34	0.42
15:N:88:PRO:HG2	25:X:29:LEU:HD22	2.01	0.42
17:P:24:VAL:HG23	17:P:28:ARG:HB3	2.01	0.42
18:Q:22:LYS:C	18:Q:24:ALA:N	2.73	0.42
19:R:9:LYS:O	19:R:12:SER:HB3	2.20	0.42
23:V:15:LEU:HA	23:V:18:VAL:HB	2.02	0.42
1:A:337:G:H2'	1:A:338:A:C8	2.55	0.42
1:A:770:C:H2'	1:A:771:G:C8	2.55	0.42
3:03:102:LEU:HG	3:03:104:ILE:HD11	2.02	0.42
3:03:722:GLY:O	3:03:777:VAL:HG22	2.20	0.42
4:04:91:GLU:HG3	4:04:91:GLU:O	2.20	0.42
4:04:268:LEU:HB3	4:04:306:LEU:HD23	2.01	0.42
4:04:552:ILE:CD1	4:04:568:SER:HB3	2.50	0.42
4:04:811:GLU:O	4:04:895:CYS:HA	2.20	0.42
4:04:1258:ARG:HA	4:04:1261:LEU:HG	2.01	0.42
4:04:1344:LEU:HG	4:04:1344:LEU:O	2.19	0.42
9:H:113:VAL:HA	9:H:116:VAL:HG22	2.02	0.42
11:J:31:VAL:HG22	11:J:32:ASP:N	2.35	0.42
18:Q:12:ARG:HH11	18:Q:12:ARG:HG3	1.85	0.42
24:W:53:MET:O	24:W:57:VAL:HG12	2.20	0.42
1:A:303:A:O2'	1:A:304:U:H5'	2.19	0.41
1:A:949:A:H2'	1:A:950:U:C6	2.55	0.41
2:01:9:LEU:HD21	2:01:198:LEU:HD21	2.01	0.41
2:01:74:VAL:O	3:03:729:ALA:HB2	2.19	0.41
2:01:180:VAL:HA	2:01:206:GLU:O	2.20	0.41
2:01:213:PRO:O	2:01:216:ALA:HB3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:02:191:ARG:HH11	4:04:370:LYS:NZ	2.17	0.41
3:03:30:ILE:HD13	3:03:528:ARG:HD2	2.02	0.41
3:03:759:SER:HB3	3:03:763:THR:CB	2.39	0.41
4:04:292:VAL:HG23	4:04:293:ARG:HG3	2.02	0.41
4:04:786:THR:OG1	4:04:787:ALA:N	2.53	0.41
4:04:1209:VAL:HG23	4:04:1209:VAL:O	2.20	0.41
4:04:1319:PHE:H	4:04:1319:PHE:HD1	1.67	0.41
6:E:83:ALA:HB2	6:E:214:LEU:HB3	2.02	0.41
9:H:68:ARG:HD3	9:H:68:ARG:C	2.45	0.41
9:H:130:THR:HG23	9:H:130:THR:O	2.19	0.41
10:I:11:HIS:C	10:I:13:ASP:N	2.77	0.41
10:I:23:GLU:O	10:I:27:ALA:HB2	2.19	0.41
11:J:24:LYS:O	11:J:28:ILE:HG13	2.19	0.41
13:L:95:SER:O	13:L:98:ARG:HB2	2.19	0.41
16:O:26:CYS:O	16:O:27:PRO:C	2.63	0.41
16:O:64:SER:C	16:O:92:VAL:HG13	2.44	0.41
18:Q:87:ALA:CA	18:Q:92:ILE:HD13	2.50	0.41
25:X:12:PHE:CG	25:X:13:ASP:N	2.87	0.41
25:X:44:GLU:O	25:X:48:ALA:HB3	2.20	0.41
1:A:211:G:C2'	1:A:212:G:H5'	2.50	0.41
1:A:419:C:H2'	1:A:420:U:O4'	2.21	0.41
1:A:439:U:H5''	8:G:120:LYS:HZ1	1.84	0.41
1:A:606:G:O5'	1:A:607:A:H5'	2.21	0.41
1:A:918:A:H2'	1:A:919:A:O4'	2.20	0.41
1:A:1024:G:C2'	1:A:1025:U:H5'	2.50	0.41
1:A:1175:G:H2'	1:A:1176:A:C8	2.54	0.41
1:A:1504:G:OP1	1:A:1507:A:H4'	2.20	0.41
3:03:295:LYS:HB3	3:03:335:THR:HB	2.01	0.41
3:03:1017:GLN:O	3:03:1021:LEU:HG	2.20	0.41
3:03:1176:LEU:C	3:03:1178:LYS:H	2.28	0.41
3:03:1223:ARG:O	3:03:1224:PRO:C	2.63	0.41
4:04:481:ARG:HG3	4:04:481:ARG:NH1	2.33	0.41
4:04:788:LEU:N	4:04:788:LEU:HD12	2.35	0.41
4:04:1255:VAL:HG23	4:04:1256:ILE:N	2.35	0.41
6:E:16:PHE:HB3	6:E:43:LEU:HA	2.01	0.41
22:U:52:GLN:OE1	22:U:52:GLN:HA	2.20	0.41
1:A:296:U:H2'	1:A:297:G:O4'	2.21	0.41
1:A:440:C:H2'	1:A:441:A:C5'	2.48	0.41
1:A:668:G:H4'	19:R:47:LYS:HB3	2.02	0.41
2:01:28:LEU:O	2:01:200:LYS:HG3	2.20	0.41
2:01:48:LEU:CD2	2:01:183:ILE:HB	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:02:78:ILE:HA	2:02:81:ILE:HD12	2.01	0.41
3:03:32:LEU:HD12	3:03:32:LEU:H	1.85	0.41
3:03:97:ARG:HB3	3:03:121:GLU:CA	2.48	0.41
3:03:424:ASP:O	3:03:428:VAL:HG23	2.20	0.41
3:03:550:VAL:HB	4:04:780:ARG:NH1	2.36	0.41
3:03:901:LEU:HD23	3:03:901:LEU:HA	1.89	0.41
4:04:141:PHE:CD2	4:04:297:ARG:HG2	2.56	0.41
4:04:437:PHE:HZ	4:04:453:VAL:HG11	1.85	0.41
4:04:835:LEU:HD11	4:04:880:VAL:HB	2.02	0.41
4:04:861:ASN:OD1	4:04:861:ASN:O	2.38	0.41
5:05:13:ILE:HB	5:05:19:LEU:HD13	2.02	0.41
6:E:18:HIS:C	6:E:40:ILE:HA	2.45	0.41
7:F:110:LEU:HG	7:F:203:LYS:HZ2	1.82	0.41
8:G:140:ASP:CG	8:G:141:VAL:N	2.78	0.41
12:K:77:VAL:HG11	12:K:124:ILE:CD1	2.51	0.41
21:T:10:ARG:HH21	21:T:25:GLU:HG3	1.86	0.41
24:W:9:ARG:HG2	24:W:9:ARG:NH1	2.35	0.41
1:A:8:A:O2'	1:A:9:G:C8	2.73	0.41
3:03:211:ARG:CZ	3:03:351:LEU:HD22	2.51	0.41
3:03:730:SER:O	3:03:753:LEU:HD13	2.21	0.41
3:03:902:LEU:C	3:03:904:ALA:H	2.28	0.41
3:03:1075:VAL:O	3:03:1075:VAL:HG23	2.20	0.41
4:04:165:TYR:O	4:04:169:LEU:HG	2.19	0.41
4:04:605:LEU:HD12	4:04:605:LEU:N	2.35	0.41
4:04:694:SER:C	4:04:696:ALA:H	2.27	0.41
4:04:697:MET:O	4:04:701:LEU:HB2	2.19	0.41
4:04:1231:ARG:HG2	4:04:1231:ARG:NH1	2.34	0.41
4:04:1323:ALA:HA	4:04:1328:THR:HA	2.03	0.41
4:04:1343:GLU:O	4:04:1344:LEU:HB3	2.20	0.41
6:E:168:HIS:HB3	6:E:169:GLU:OE2	2.19	0.41
8:G:158:LEU:HD23	8:G:158:LEU:C	2.46	0.41
10:I:2:ARG:HD3	10:I:68:GLN:HB3	2.02	0.41
12:K:95:MET:CB	12:K:98:LEU:HB2	2.49	0.41
15:N:55:ARG:HA	15:N:58:THR:CG2	2.51	0.41
15:N:92:ARG:NH2	25:X:20:LYS:HD3	2.35	0.41
21:T:3:LYS:NZ	21:T:3:LYS:HB3	2.35	0.41
23:V:11:ASP:HB3	23:V:13:HIS:HD2	1.84	0.41
1:A:589:U:H5''	12:K:29:SER:HB2	2.00	0.41
1:A:1038:C:H2'	1:A:1039:G:C8	2.56	0.41
1:A:1298:U:C5	11:J:113:LYS:HA	2.55	0.41
2:01:9:LEU:HD23	2:01:9:LEU:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:381:ALA:O	3:03:382:GLU:C	2.63	0.41
3:03:723:VAL:HA	3:03:776:PRO:HA	2.01	0.41
3:03:1064:ASP:H	3:03:1076:ILE:CG2	2.32	0.41
3:03:1205:PRO:O	3:03:1206:THR:C	2.64	0.41
4:04:114:ILE:HG23	4:04:115:TRP:HD1	1.83	0.41
4:04:333:GLY:HA3	4:04:338:PHE:HB2	2.01	0.41
4:04:550:VAL:HG21	4:04:572:THR:HG22	2.02	0.41
4:04:905:ARG:HE	4:04:907:HIS:HB2	1.85	0.41
4:04:1079:LYS:HE2	4:04:1098:GLN:HB3	2.02	0.41
4:04:1361:THR:O	4:04:1364:ALA:HB3	2.20	0.41
6:E:50:PHE:O	6:E:53:ALA:HB3	2.20	0.41
14:M:18:ILE:HA	14:M:96:VAL:HG21	2.02	0.41
14:M:92:LEU:HD12	14:M:92:LEU:N	2.35	0.41
15:N:55:ARG:HA	15:N:58:THR:HG23	2.01	0.41
21:T:11:VAL:N	21:T:22:VAL:HG23	2.35	0.41
24:W:57:VAL:C	24:W:59:ARG:H	2.28	0.41
24:W:84:LYS:HB2	24:W:84:LYS:HZ3	1.85	0.41
25:X:10:GLU:HA	25:X:12:PHE:HE1	1.85	0.41
25:X:10:GLU:N	25:X:11:PRO:HD3	2.35	0.41
1:A:1285:A:H5'	1:A:1286:U:C5	2.55	0.41
1:A:1309:G:P	17:P:86:ARG:HH21	2.43	0.41
1:A:1339:A:H2'	1:A:1340:A:O4'	2.21	0.41
1:A:1516:G:H2'	1:A:1518:A:OP2	2.20	0.41
2:01:218:ARG:HH11	2:01:218:ARG:HG3	1.85	0.41
2:02:100:LEU:N	2:02:100:LEU:HD12	2.35	0.41
3:03:10:ARG:HG3	3:03:10:ARG:HH11	1.85	0.41
3:03:53:PHE:O	3:03:57:PHE:HB2	2.21	0.41
3:03:122:VAL:HG13	3:03:124:MET:HG3	2.01	0.41
3:03:178:PRO:HD3	3:03:183:TRP:HA	2.02	0.41
3:03:686:GLN:C	3:03:688:GLN:H	2.28	0.41
3:03:1100:PRO:O	3:03:1104:PRO:HD3	2.21	0.41
3:03:1328:LYS:NZ	4:04:99:ARG:O	2.53	0.41
4:04:147:ILE:HD11	4:04:177:ASP:OD2	2.20	0.41
4:04:414:GLU:HG2	5:05:43:ASN:ND2	2.36	0.41
4:04:734:ALA:HA	4:04:737:ILE:HD12	2.03	0.41
4:04:1053:LEU:HD12	4:04:1053:LEU:N	2.35	0.41
6:E:39:HIS:O	6:E:40:ILE:HG13	2.20	0.41
12:K:46:GLU:O	12:K:47:ASP:C	2.62	0.41
13:L:11:ARG:HG2	13:L:76:GLY:HA3	2.02	0.41
13:L:98:ARG:HG2	13:L:103:VAL:CB	2.40	0.41
14:M:40:ILE:HA	14:M:41:PRO:HD2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:49:PHE:CZ	18:Q:75:LYS:HE3	2.56	0.41
1:A:9:G:O2'	1:A:10:A:H5'	2.21	0.41
1:A:1053:G:H4'	1:A:1054:C:H3'	2.01	0.41
1:A:1175:G:H2'	1:A:1176:A:H8	1.84	0.41
2:01:72:GLU:CD	2:01:72:GLU:H	2.29	0.41
2:01:160:HIS:O	2:01:161:SER:HB3	2.21	0.41
3:03:257:ALA:CB	3:03:262:TYR:HE2	2.32	0.41
3:03:1103:VAL:N	3:03:1104:PRO:CD	2.84	0.41
3:03:1287:LEU:O	3:03:1291:LEU:HG	2.20	0.41
4:04:196:GLN:O	4:04:200:GLN:HG3	2.21	0.41
4:04:200:GLN:HA	4:04:203:GLU:HG3	2.02	0.41
4:04:923:ILE:HD12	4:04:1256:ILE:HG13	2.02	0.41
6:E:34:ALA:HB3	6:E:43:LEU:HD13	2.02	0.41
6:E:76:ALA:O	6:E:80:VAL:HG23	2.21	0.41
7:F:55:VAL:CG2	7:F:66:THR:HB	2.51	0.41
11:J:25:PHE:HD1	11:J:100:MET:HB3	1.86	0.41
1:A:106:C:H2'	1:A:107:G:O4'	2.20	0.41
1:A:419:C:C5'	1:A:513:C:H4'	2.51	0.41
1:A:977:A:H4'	1:A:980:C:H41	1.86	0.41
2:02:143:ARG:HG2	2:02:143:ARG:NH1	2.36	0.41
3:03:133:ASN:HA	3:03:713:GLY:HA3	2.02	0.41
3:03:141:THR:HB	3:03:760:ASN:ND2	2.36	0.41
3:03:233:ARG:O	3:03:236:LYS:HG2	2.20	0.41
3:03:697:LYS:HA	3:03:698:PRO:HD3	1.87	0.41
3:03:861:ALA:HA	3:03:864:LYS:CE	2.47	0.41
3:03:1305:TYR:HE1	4:04:379:PRO:HG3	1.86	0.41
4:04:78:LEU:O	4:04:81:ARG:HD2	2.21	0.41
4:04:137:ARG:HD2	4:04:159:ILE:HD12	2.03	0.41
4:04:958:ILE:CG2	4:04:982:LEU:HD11	2.51	0.41
7:F:52:SER:HB2	7:F:68:HIS:O	2.21	0.41
7:F:62:SER:HA	7:F:96:VAL:HB	2.02	0.41
9:H:93:VAL:HG22	9:H:126:ALA:CA	2.44	0.41
10:I:64:VAL:HG22	10:I:65:GLU:N	2.36	0.41
11:J:78:ARG:HH11	11:J:78:ARG:HG3	1.85	0.41
12:K:28:SER:HB2	12:K:58:LEU:CB	2.36	0.41
12:K:74:ILE:HG13	12:K:127:TYR:O	2.21	0.41
16:O:2:THR:HB	16:O:5:GLN:HB3	2.03	0.41
24:W:48:LYS:HD2	24:W:48:LYS:C	2.45	0.41
1:A:118:U:H2'	1:A:119:A:H5'	2.03	0.41
1:A:242:G:C2'	1:A:243:A:H5'	2.51	0.41
1:A:768:A:H2'	1:A:769:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1186:G:O3'	13:L:114:LYS:HD3	2.20	0.41
1:A:1323:G:H2'	1:A:1324:A:C8	2.56	0.41
2:01:150:ARG:HH11	2:01:150:ARG:HG2	1.85	0.41
3:03:146:VAL:CG1	3:03:531:SER:HB2	2.51	0.41
3:03:230:PHE:HB2	3:03:333:ILE:O	2.21	0.41
3:03:435:ILE:O	3:03:435:ILE:HG22	2.21	0.41
3:03:1107:MET:N	3:03:1107:MET:SD	2.93	0.41
3:03:1126:ASP:O	3:03:1129:ASN:HB3	2.21	0.41
3:03:1146:GLN:O	3:03:1150:ASP:HB2	2.21	0.41
3:03:1305:TYR:C	3:03:1307:ASN:H	2.29	0.41
4:04:99:ARG:HH11	4:04:99:ARG:HG3	1.85	0.41
4:04:513:MET:O	4:04:575:GLY:HA3	2.19	0.41
4:04:694:SER:C	4:04:696:ALA:N	2.76	0.41
4:04:917:VAL:O	4:04:921:GLN:HG2	2.21	0.41
4:04:1123:ARG:HH11	4:04:1123:ARG:HG2	1.85	0.41
6:E:20:THR:HB	6:E:38:VAL:HG13	2.03	0.41
6:E:23:TRP:NE1	6:E:25:PRO:HG2	2.35	0.41
6:E:23:TRP:CD2	6:E:25:PRO:HG3	2.56	0.41
6:E:28:LYS:O	6:E:29:PRO:C	2.64	0.41
6:E:29:PRO:C	6:E:31:ILE:H	2.29	0.41
6:E:56:GLU:O	6:E:60:ILE:HG12	2.20	0.41
6:E:130:THR:HG21	6:E:132:LYS:CD	2.47	0.41
7:F:173:PRO:HB2	7:F:176:THR:OG1	2.21	0.41
8:G:18:LEU:HD21	8:G:59:LYS:HG3	2.03	0.41
11:J:12:LEU:HD12	11:J:13:PRO:HD2	2.03	0.41
11:J:90:VAL:HG13	11:J:95:ARG:CG	2.51	0.41
12:K:97:GLY:C	12:K:98:LEU:HD12	2.45	0.41
14:M:22:THR:O	14:M:26:VAL:HG23	2.20	0.41
14:M:78:GLU:HA	14:M:79:PRO:HD2	1.98	0.41
14:M:88:MET:C	14:M:90:LEU:H	2.27	0.41
21:T:47:ASP:HB3	21:T:74:LEU:HD21	2.02	0.41
2:02:56:VAL:HG22	2:02:146:VAL:HG22	2.02	0.41
3:03:216:THR:HG22	3:03:217:THR:N	2.36	0.41
3:03:255:ILE:HD12	3:03:263:VAL:CB	2.51	0.41
3:03:563:THR:HA	3:03:564:PRO:HD2	1.89	0.41
4:04:31:ARG:NH2	4:04:241:VAL:HG22	2.36	0.41
4:04:527:LEU:HD12	4:04:528:THR:H	1.85	0.41
4:04:552:ILE:HD12	4:04:568:SER:HB3	2.03	0.41
4:04:850:LYS:HG2	4:04:857:LEU:HD23	2.03	0.41
4:04:1173:ARG:HG2	4:04:1174:ARG:N	2.35	0.41
6:E:31:ILE:HG13	6:E:33:GLY:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:96:GLN:HG2	9:H:123:LEU:HD12	2.03	0.41
11:J:144:ALA:C	11:J:146:ALA:H	2.28	0.41
18:Q:32:ASP:C	18:Q:34:ASN:H	2.28	0.41
22:U:34:THR:C	22:U:36:SER:N	2.78	0.41
24:W:48:LYS:HD2	24:W:48:LYS:O	2.21	0.41
1:A:463:U:H3	1:A:469:C:H42	1.68	0.40
1:A:958:A:N1	23:V:53:GLY:HA3	2.36	0.40
1:A:1227:A:OP2	17:P:109:LYS:HE2	2.21	0.40
1:A:1507:A:H2'	1:A:1508:A:C8	2.56	0.40
3:03:292:ILE:O	3:03:294:GLY:N	2.51	0.40
3:03:555:TYR:CD1	3:03:660:VAL:HG21	2.56	0.40
3:03:688:GLN:HB3	3:03:1236:ASN:H	1.86	0.40
3:03:698:PRO:HD3	3:03:795:ALA:HB2	2.04	0.40
3:03:901:LEU:HA	3:03:904:ALA:HB3	2.03	0.40
3:03:1108:ASN:ND2	3:03:1111:GLN:HE21	2.19	0.40
4:04:504:GLN:C	4:04:506:VAL:N	2.77	0.40
4:04:749:LYS:C	4:04:751:ASP:H	2.27	0.40
4:04:923:ILE:HD11	4:04:1253:ILE:HA	2.02	0.40
4:04:1295:ASN:HB3	4:04:1298:VAL:HG12	2.02	0.40
8:G:27:ILE:C	8:G:27:ILE:HD12	2.45	0.40
8:G:80:ARG:HD2	8:G:80:ARG:C	2.45	0.40
8:G:104:MET:CE	8:G:170:LEU:HD13	2.51	0.40
15:N:74:LYS:H	15:N:74:LYS:CD	2.29	0.40
17:P:76:ILE:HG22	17:P:80:MET:SD	2.61	0.40
20:S:66:THR:C	20:S:67:ILE:HD12	2.46	0.40
22:U:56:ALA:O	22:U:60:LYS:HB2	2.21	0.40
24:W:7:LYS:HD2	24:W:7:LYS:C	2.46	0.40
1:A:348:G:H2'	1:A:349:A:H8	1.87	0.40
1:A:419:C:H5'	1:A:513:C:H4'	2.03	0.40
1:A:1522:U:H2'	1:A:1523:G:C8	2.55	0.40
2:01:39:LEU:HD21	2:02:227:GLN:HB3	2.03	0.40
3:03:211:ARG:HD3	3:03:357:ASN:HA	2.03	0.40
3:03:310:ILE:CG2	3:03:321:LEU:HD22	2.51	0.40
3:03:881:ASP:O	3:03:920:VAL:HG23	2.21	0.40
3:03:1064:ASP:O	3:03:1075:VAL:HA	2.21	0.40
4:04:105:ILE:HD12	4:04:242:LEU:HD23	2.03	0.40
4:04:246:PRO:HA	4:04:247:PRO:HD3	1.98	0.40
4:04:745:GLY:C	4:04:746:LEU:HD12	2.45	0.40
4:04:1323:ALA:CB	4:04:1328:THR:HG23	2.51	0.40
6:E:14:VAL:HG12	6:E:16:PHE:CZ	2.56	0.40
6:E:15:HIS:NE2	6:E:47:VAL:HA	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:19:PRO:O	10:I:22:ILE:HB	2.20	0.40
11:J:28:ILE:O	11:J:104:VAL:HG11	2.21	0.40
11:J:77:ARG:HB2	11:J:86:VAL:HG21	2.03	0.40
19:R:55:LEU:O	19:R:56:LEU:C	2.64	0.40
21:T:61:ARG:CB	21:T:61:ARG:HH11	2.34	0.40
22:U:53:ARG:O	22:U:56:ALA:HB3	2.20	0.40
23:V:43:MET:SD	23:V:48:ILE:HD13	2.61	0.40
1:A:184:G:OP1	1:A:225:C:H4'	2.22	0.40
1:A:360:G:H2'	1:A:361:G:H8	1.87	0.40
1:A:1158:C:H4'	6:E:132:LYS:HB3	2.03	0.40
3:03:239:MET:HB2	3:03:287:VAL:HG21	2.03	0.40
3:03:600:THR:CG2	3:03:602:GLU:HG3	2.51	0.40
3:03:699:LEU:HD13	3:03:1122:LYS:HB2	2.02	0.40
3:03:949:GLU:HG2	3:03:1036:ILE:HB	2.02	0.40
3:03:1064:ASP:OD2	3:03:1234:LYS:HE3	2.21	0.40
3:03:1256:GLN:HE22	3:03:1298:VAL:HB	1.86	0.40
4:04:31:ARG:CZ	4:04:241:VAL:HG22	2.52	0.40
4:04:126:LEU:HD12	4:04:126:LEU:C	2.47	0.40
4:04:180:MET:HG2	4:04:293:ARG:NH1	2.36	0.40
4:04:404:GLU:HG2	4:04:409:TRP:HE1	1.86	0.40
4:04:780:ARG:O	4:04:781:LYS:C	2.64	0.40
8:G:23:GLY:HA3	8:G:160:LEU:HD21	2.03	0.40
17:P:3:ILE:C	17:P:3:ILE:HD12	2.45	0.40
19:R:87:ARG:HA	19:R:87:ARG:NE	2.36	0.40
20:S:20:VAL:HA	20:S:35:ARG:HA	2.03	0.40
21:T:82:VAL:OXT	21:T:82:VAL:HG23	2.20	0.40
25:X:12:PHE:N	25:X:12:PHE:CD1	2.90	0.40
25:X:47:ARG:HD3	25:X:48:ALA:N	2.37	0.40
1:A:219:U:H2'	1:A:220:G:C4'	2.51	0.40
1:A:827:U:O4'	12:K:15:ASN:HB3	2.22	0.40
1:A:1372:U:OP1	13:L:72:SER:HB3	2.21	0.40
2:01:102:LEU:HD11	2:01:110:VAL:HG11	2.02	0.40
2:01:166:ARG:HB2	2:01:167:PRO:HD3	2.03	0.40
3:03:756:TYR:CE1	3:03:766:ASN:HB2	2.56	0.40
3:03:832:HIS:NE2	3:03:1238:LEU:HD22	2.34	0.40
3:03:1099:ASN:C	3:03:1101:LEU:H	2.30	0.40
4:04:1124:ILE:HA	4:04:1125:PRO:HD3	1.78	0.40
8:G:71:PHE:HE1	8:G:93:LEU:HD21	1.85	0.40
10:I:5:GLU:HA	10:I:63:ASN:HA	2.03	0.40
10:I:24:ARG:HG3	10:I:24:ARG:HH11	1.85	0.40
13:L:27:ILE:HD12	13:L:34:LEU:HD12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:548:G:H2'	1:A:549:C:C6	2.56	0.40
1:A:903:G:H2'	1:A:904:U:C6	2.56	0.40
1:A:1344:C:O2'	1:A:1345:U:H5'	2.22	0.40
1:A:1451:U:H3'	1:A:1452:C:H5'	2.02	0.40
2:02:67:GLU:HA	2:02:79:LEU:HD23	2.04	0.40
3:03:45:GLY:HA2	3:03:50:GLU:HB3	2.03	0.40
3:03:225:PHE:CZ	3:03:345:PRO:HA	2.57	0.40
3:03:448:LEU:HB2	3:03:608:ALA:CB	2.52	0.40
3:03:521:LEU:HB2	3:03:794:LEU:HD21	2.03	0.40
3:03:530:ILE:HB	3:03:573:ASN:O	2.22	0.40
3:03:715:THR:HG23	3:03:717:VAL:HG13	2.03	0.40
4:04:242:LEU:HD21	4:04:272:VAL:HG11	2.03	0.40
4:04:422:LEU:HD23	4:04:484:MET:HE1	2.03	0.40
4:04:858:VAL:CG2	4:04:864:LEU:HD21	2.46	0.40
4:04:910:ASN:N	4:04:910:ASN:HD22	2.19	0.40
4:04:1223:LEU:HD13	4:04:1223:LEU:C	2.47	0.40
7:F:34:SER:C	7:F:36:PHE:H	2.30	0.40
8:G:96:ARG:O	8:G:100:VAL:HG23	2.21	0.40
13:L:7:GLY:CA	13:L:85:ALA:HB2	2.50	0.40
14:M:15:HIS:CG	14:M:16:ARG:H	2.40	0.40
15:N:127:ARG:OXT	15:N:127:ARG:HD2	2.22	0.40
16:O:17:LYS:HB2	16:O:17:LYS:HZ2	1.86	0.40
17:P:64:VAL:HG23	17:P:66:GLY:H	1.85	0.40
24:W:79:THR:O	24:W:82:ILE:HG12	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	01	225/229 (98%)	193 (86%)	24 (11%)	8 (4%)	2 20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	02	225/229 (98%)	179 (80%)	35 (16%)	11 (5%)	1	16
3	03	1323/1340 (99%)	1036 (78%)	233 (18%)	54 (4%)	2	18
4	04	1339/1369 (98%)	1099 (82%)	206 (15%)	34 (2%)	4	26
5	05	57/59 (97%)	48 (84%)	9 (16%)	0	100	100
6	E	216/218 (99%)	156 (72%)	37 (17%)	23 (11%)	0	6
7	F	204/206 (99%)	180 (88%)	22 (11%)	2 (1%)	12	49
8	G	203/205 (99%)	151 (74%)	42 (21%)	10 (5%)	1	16
9	H	155/157 (99%)	120 (77%)	30 (19%)	5 (3%)	3	21
10	I	98/100 (98%)	78 (80%)	18 (18%)	2 (2%)	6	31
11	J	149/151 (99%)	118 (79%)	26 (17%)	5 (3%)	3	21
12	K	127/129 (98%)	105 (83%)	17 (13%)	5 (4%)	2	19
13	L	125/127 (98%)	101 (81%)	18 (14%)	6 (5%)	2	16
14	M	96/98 (98%)	82 (85%)	10 (10%)	4 (4%)	2	17
15	N	114/116 (98%)	92 (81%)	16 (14%)	6 (5%)	1	15
16	O	121/123 (98%)	88 (73%)	23 (19%)	10 (8%)	0	9
17	P	112/114 (98%)	90 (80%)	17 (15%)	5 (4%)	2	17
18	Q	98/100 (98%)	66 (67%)	24 (24%)	8 (8%)	0	9
19	R	86/88 (98%)	72 (84%)	12 (14%)	2 (2%)	5	28
20	S	80/82 (98%)	58 (72%)	16 (20%)	6 (8%)	1	10
21	T	78/80 (98%)	61 (78%)	10 (13%)	7 (9%)	0	8
22	U	63/65 (97%)	46 (73%)	13 (21%)	4 (6%)	1	13
23	V	77/79 (98%)	60 (78%)	15 (20%)	2 (3%)	4	25
24	W	83/85 (98%)	69 (83%)	13 (16%)	1 (1%)	10	44
25	X	63/65 (97%)	45 (71%)	10 (16%)	8 (13%)	0	4
All	All	5517/5614 (98%)	4393 (80%)	896 (16%)	228 (4%)	4	18

All (228) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	01	161	SER
2	01	168	ILE
2	02	138	ALA
2	02	168	ILE
3	03	596	ASP

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Mol	Chain	Res	Type
3	03	655	VAL
3	03	841	ARG
3	03	917	SER
3	03	1188	ASP
4	04	338	PHE
4	04	345	LYS
4	04	1343	GLU
6	E	11	LYS
6	E	12	ALA
6	E	14	VAL
6	E	19	GLN
6	E	21	ARG
6	E	30	PHE
6	E	39	HIS
6	E	40	ILE
6	E	41	ILE
6	E	88	ASP
6	E	201	PRO
8	G	33	ILE
12	K	3	GLN
12	K	47	ASP
12	K	125	ILE
16	O	23	LEU
16	O	27	PRO
17	P	14	ALA
17	P	26	LYS
20	S	26	ASN
20	S	54	LEU
20	S	69	ASP
21	T	19	SER
21	T	81	ALA
22	U	20	GLU
2	02	13	LEU
2	02	196	THR
3	03	65	ASN
3	03	271	ALA
3	03	284	LEU
3	03	293	ALA
3	03	329	GLY
3	03	625	GLU
3	03	820	GLU
3	03	936	ARG

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Mol	Chain	Res	Type
3	03	1208	GLY
3	03	1317	PRO
4	04	286	ALA
4	04	357	VAL
4	04	495	ASN
4	04	781	LYS
4	04	1167	LYS
4	04	1250	ASP
4	04	1328	THR
6	E	18	HIS
6	E	33	GLY
6	E	43	LEU
6	E	64	LYS
6	E	151	ILE
7	F	126	ARG
8	G	31	CYS
8	G	39	GLN
8	G	45	PRO
8	G	182	LYS
9	H	102	THR
12	K	53	ASP
13	L	71	ILE
14	M	58	ASN
15	N	118	ASN
15	N	120	CYS
16	O	35	ARG
16	O	41	PRO
16	O	104	SER
18	Q	69	PRO
21	T	4	ILE
21	T	48	GLU
21	T	50	ASN
22	U	35	GLU
22	U	46	GLY
25	X	9	ASN
25	X	16	LEU
25	X	38	TYR
2	01	33	ARG
2	01	72	GLU
2	01	94	GLY
2	02	32	GLU
2	02	62	ASP

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Mol	Chain	Res	Type
2	02	167	PRO
2	02	193	GLU
3	03	45	GLY
3	03	110	PRO
3	03	383	SER
3	03	384	LEU
3	03	518	ASN
3	03	534	GLY
3	03	821	ARG
3	03	853	ASP
3	03	942	ASP
3	03	1158	LYS
3	03	1203	ASP
4	04	47	ARG
4	04	339	ARG
4	04	490	ILE
4	04	596	LEU
4	04	1084	GLN
4	04	1150	PRO
4	04	1169	THR
4	04	1341	ARG
4	04	1347	LEU
6	E	27	MET
6	E	45	LYS
6	E	66	LYS
8	G	47	LEU
9	H	77	ASN
10	I	33	GLU
11	J	2	ARG
13	L	25	GLY
13	L	102	PHE
13	L	124	PRO
14	M	41	PRO
15	N	93	GLU
15	N	126	ARG
18	Q	21	ALA
18	Q	23	ARG
18	Q	61	ASN
19	R	46	LYS
19	R	57	ARG
20	S	43	ALA
22	U	37	GLY

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Mol	Chain	Res	Type
25	X	11	PRO
25	X	25	LYS
25	X	43	THR
2	02	96	ASP
3	03	29	SER
3	03	67	GLU
3	03	398	SER
3	03	756	TYR
3	03	796	LEU
3	03	813	GLU
3	03	822	VAL
3	03	895	LEU
3	03	941	LYS
3	03	1067	ALA
3	03	1131	MET
3	03	1152	GLY
3	03	1239	VAL
3	03	1296	ASP
3	03	1314	GLN
4	04	49	PHE
4	04	113	HIS
4	04	122	SER
4	04	313	GLY
4	04	1000	GLY
4	04	1170	LYS
6	E	22	TYR
6	E	25	PRO
6	E	29	PRO
8	G	190	LEU
9	H	23	THR
10	I	56	LYS
11	J	110	ARG
13	L	128	LYS
14	M	42	LEU
14	M	75	ASP
16	O	33	CYS
16	O	88	ASP
17	P	11	HIS
17	P	106	ARG
18	Q	2	LYS
18	Q	26	LEU
20	S	28	ARG

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Mol	Chain	Res	Type
21	T	71	SER
21	T	79	GLU
23	V	14	LEU
2	01	164	ASP
2	01	195	ARG
3	03	30	ILE
3	03	842	ASP
3	03	1237	HIS
4	04	641	ILE
4	04	825	VAL
4	04	962	ASN
4	04	1076	PRO
8	G	167	PRO
8	G	203	TYR
9	H	99	SER
11	J	16	LYS
11	J	145	GLU
13	L	121	ARG
15	N	38	GLY
15	N	40	ALA
16	O	15	VAL
16	O	70	GLY
18	Q	8	ARG
24	W	17	ARG
2	02	33	ARG
2	02	63	GLY
3	03	63	SER
3	03	743	PRO
3	03	850	ILE
3	03	1218	GLY
4	04	815	GLY
4	04	998	PRO
4	04	1326	GLN
6	E	164	ILE
8	G	194	ILE
25	X	24	GLU
3	03	747	GLY
3	03	879	GLY
7	F	144	GLY
18	Q	44	VAL
3	03	1223	ARG
4	04	1207	GLY

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Mol	Chain	Res	Type
25	X	10	GLU
3	03	507	GLY
3	03	660	VAL
4	04	344	GLY
16	O	117	GLY
2	01	14	VAL
3	03	1071	GLY
12	K	122	GLY
20	S	49	GLY
23	V	29	PRO
9	H	24	VAL
11	J	13	PRO
17	P	23	GLY

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	01	194/197 (98%)	192 (99%)	2 (1%)	68	78
2	02	194/197 (98%)	193 (100%)	1 (0%)	81	83
3	03	1098/1155 (95%)	1084 (99%)	14 (1%)	61	74
4	04	1103/1141 (97%)	1093 (99%)	10 (1%)	70	79
5	05	49/49 (100%)	49 (100%)	0	100	100
6	E	180/180 (100%)	171 (95%)	9 (5%)	22	43
7	F	170/170 (100%)	168 (99%)	2 (1%)	63	75
8	G	172/172 (100%)	167 (97%)	5 (3%)	37	58
9	H	119/119 (100%)	119 (100%)	0	100	100
10	I	87/87 (100%)	86 (99%)	1 (1%)	65	76
11	J	124/124 (100%)	123 (99%)	1 (1%)	73	80
12	K	104/104 (100%)	104 (100%)	0	100	100
13	L	105/105 (100%)	104 (99%)	1 (1%)	68	78
14	M	86/86 (100%)	86 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	N	89/89 (100%)	85 (96%)	4 (4%)	24	46
16	O	103/103 (100%)	99 (96%)	4 (4%)	28	49
17	P	92/92 (100%)	91 (99%)	1 (1%)	65	76
18	Q	83/83 (100%)	81 (98%)	2 (2%)	43	64
19	R	76/76 (100%)	75 (99%)	1 (1%)	61	74
20	S	65/65 (100%)	63 (97%)	2 (3%)	35	56
21	T	74/74 (100%)	74 (100%)	0	100	100
22	U	56/56 (100%)	55 (98%)	1 (2%)	51	68
23	V	70/70 (100%)	70 (100%)	0	100	100
24	W	65/65 (100%)	62 (95%)	3 (5%)	24	45
25	X	55/55 (100%)	52 (94%)	3 (6%)	19	41
All	All	4613/4714 (98%)	4546 (98%)	67 (2%)	55	72

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	01	133	LEU
2	01	150	ARG
2	02	79	LEU
3	03	75	LEU
3	03	149	LEU
3	03	378	ARG
3	03	521	LEU
3	03	763	THR
3	03	766	ASN
3	03	791	LEU
3	03	850	ILE
3	03	890	LYS
3	03	903	ARG
3	03	1107	MET
3	03	1151	LEU
3	03	1160	ASP
3	03	1198	LEU
4	04	132	LEU
4	04	217	LEU
4	04	248	ASP
4	04	343	LEU
4	04	510	LEU

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Mol	Chain	Res	Type
4	04	536	LEU
4	04	955	LYS
4	04	1041	ILE
4	04	1251	LYS
4	04	1332	LEU
6	E	14	VAL
6	E	16	PHE
6	E	18	HIS
6	E	35	ARG
6	E	39	HIS
6	E	48	PRO
6	E	139	ARG
6	E	190	ASN
6	E	212	LEU
7	F	2	GLN
7	F	163	ARG
8	G	20	LEU
8	G	80	ARG
8	G	167	PRO
8	G	190	LEU
8	G	196	GLU
10	I	14	GLN
11	J	24	LYS
13	L	128	LYS
15	N	109	ILE
15	N	117	HIS
15	N	124	LYS
15	N	126	ARG
16	O	27	PRO
16	O	48	LEU
16	O	49	ARG
16	O	107	LYS
17	P	16	ILE
18	Q	59	GLN
18	Q	97	LYS
19	R	9	LYS
20	S	25	ARG
20	S	67	ILE
22	U	48	ARG
24	W	67	HIS
24	W	70	LYS
24	W	84	LYS

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Mol	Chain	Res	Type
25	X	11	PRO
25	X	35	ARG
25	X	49	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (123) such sidechains are listed below:

Mol	Chain	Res	Type
2	01	128	HIS
2	01	137	ASN
2	01	227	GLN
2	02	23	HIS
2	02	37	HIS
2	02	103	ASN
2	02	186	ASN
3	03	31	GLN
3	03	69	GLN
3	03	214	ASN
3	03	314	ASN
3	03	437	ASN
3	03	517	GLN
3	03	604	HIS
3	03	620	ASN
3	03	658	GLN
3	03	673	HIS
3	03	688	GLN
3	03	834	GLN
3	03	1017	GLN
3	03	1038	GLN
3	03	1080	ASN
3	03	1099	ASN
3	03	1111	GLN
3	03	1237	HIS
3	03	1288	GLN
3	03	1312	ASN
3	03	1336	ASN
4	04	153	ASN
4	04	157	GLN
4	04	266	ASN
4	04	276	ASN
4	04	300	GLN
4	04	309	ASN
4	04	320	ASN

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Mol	Chain	Res	Type
4	04	335	GLN
4	04	365	GLN
4	04	435	GLN
4	04	458	ASN
4	04	488	ASN
4	04	489	ASN
4	04	606	ASN
4	04	690	ASN
4	04	739	GLN
4	04	762	ASN
4	04	768	ASN
4	04	771	GLN
4	04	861	ASN
4	04	865	HIS
4	04	910	ASN
4	04	921	GLN
4	04	1098	GLN
4	04	1126	GLN
4	04	1197	ASN
4	04	1235	ASN
4	04	1244	GLN
4	04	1249	ASN
6	E	36	ASN
6	E	39	HIS
6	E	93	ASN
6	E	94	HIS
6	E	122	GLN
6	E	146	ASN
6	E	190	ASN
7	F	2	GLN
7	F	5	HIS
7	F	24	ASN
7	F	31	ASN
7	F	122	GLN
7	F	139	ASN
7	F	184	ASN
8	G	40	HIS
8	G	53	GLN
8	G	58	GLN
8	G	88	ASN
8	G	115	GLN
8	G	195	ASN

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Mol	Chain	Res	Type
9	H	72	ASN
9	H	96	GLN
9	H	121	ASN
9	H	134	ASN
9	H	145	ASN
9	H	147	ASN
10	I	3	HIS
10	I	17	GLN
10	I	52	ASN
10	I	94	HIS
11	J	8	GLN
11	J	27	ASN
11	J	96	ASN
11	J	121	ASN
11	J	141	HIS
12	K	3	GLN
12	K	37	ASN
13	L	4	GLN
13	L	74	GLN
13	L	109	GLN
14	M	56	HIS
14	M	58	ASN
15	N	100	ASN
16	O	58	ASN
17	P	7	ASN
17	P	90	HIS
19	R	36	ASN
19	R	50	HIS
19	R	61	GLN
20	S	18	GLN
20	S	29	ASN
20	S	40	ASN
21	T	30	HIS
21	T	50	ASN
22	U	31	ASN
22	U	74	HIS
23	V	13	HIS
23	V	51	HIS
24	W	2	ASN
24	W	12	GLN
24	W	54	GLN
24	W	60	GLN

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Mol	Chain	Res	Type
24	W	74	HIS
24	W	81	GLN
24	W	83	ASN
25	X	9	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1538/1539 (99%)	182 (11%)	3 (0%)

All (182) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	9	G
1	A	22	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	40	C
1	A	48	C
1	A	49	U
1	A	50	A
1	A	51	A
1	A	60	A
1	A	61	G
1	A	66	A
1	A	68	G
1	A	70	U
1	A	71	A
1	A	72	A
1	A	83	C
1	A	85	U
1	A	86	G
1	A	89	U
1	A	90	C
1	A	94	G
1	A	95	C
1	A	99	C
1	A	137	U
1	A	144	G

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Mol	Chain	Res	Type
1	A	174	A
1	A	177	G
1	A	180	U
1	A	183	C
1	A	184	G
1	A	185	U
1	A	209	U
1	A	210	C
1	A	220	G
1	A	245	U
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C
1	A	280	C
1	A	281	G
1	A	289	G
1	A	306	A
1	A	328	C
1	A	344	A
1	A	345	C
1	A	352	C
1	A	372	C
1	A	377	G
1	A	388	G
1	A	397	A
1	A	398	U
1	A	406	G
1	A	413	G
1	A	414	A
1	A	423	G
1	A	427	U
1	A	429	U
1	A	441	A
1	A	448	A
1	A	467	U
1	A	468	A
1	A	479	U
1	A	480	U
1	A	486	U
1	A	487	A
1	A	495	A

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Mol	Chain	Res	Type
1	A	496	A
1	A	497	G
1	A	500	G
1	A	513	C
1	A	518	C
1	A	524	G
1	A	530	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	534	U
1	A	535	A
1	A	536	C
1	A	547	A
1	A	559	A
1	A	560	A
1	A	561	U
1	A	563	A
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	C
1	A	577	G
1	A	615	G
1	A	633	G
1	A	642	A
1	A	665	A
1	A	703	G
1	A	723	U
1	A	724	G
1	A	755	G
1	A	777	A
1	A	817	C
1	A	818	G
1	A	819	A
1	A	821	G
1	A	832	G
1	A	843	U
1	A	846	G
1	A	871	U
1	A	873	A
1	A	902	G

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Mol	Chain	Res	Type
1	A	926	G
1	A	934	C
1	A	935	A
1	A	945	G
1	A	960	U
1	A	961	U
1	A	966	G
1	A	969	A
1	A	975	A
1	A	977	A
1	A	982	U
1	A	984	C
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1004	A
1	A	1031	C
1	A	1032	G
1	A	1033	G
1	A	1054	C
1	A	1055	A
1	A	1094	G
1	A	1101	A
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1159	U
1	A	1168	U
1	A	1182	G
1	A	1184	G
1	A	1196	A
1	A	1201	A
1	A	1213	A
1	A	1215	G
1	A	1225	A
1	A	1226	C
1	A	1238	A
1	A	1240	U
1	A	1241	G
1	A	1258	G
1	A	1260	G
1	A	1261	A

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Mol	Chain	Res	Type
1	A	1275	A
1	A	1278	G
1	A	1280	A
1	A	1282	C
1	A	1287	A
1	A	1300	G
1	A	1303	C
1	A	1317	C
1	A	1346	A
1	A	1347	G
1	A	1364	U
1	A	1374	A
1	A	1379	G
1	A	1394	A
1	A	1395	C
1	A	1397	C
1	A	1398	A
1	A	1400	C
1	A	1441	A
1	A	1446	A
1	A	1452	C
1	A	1492	A
1	A	1498	U
1	A	1502	A
1	A	1506	U
1	A	1517	G
1	A	1529	G
1	A	1530	G

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	69	G
1	A	343	U
1	A	1399	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

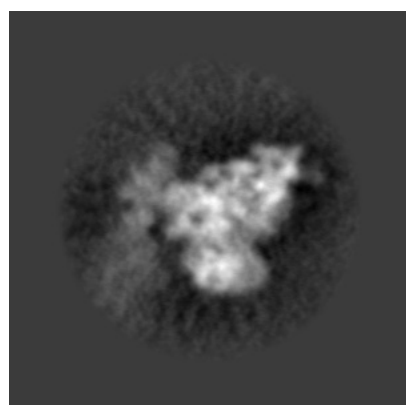
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7016. These allow visual inspection of the internal detail of the map and identification of artifacts.

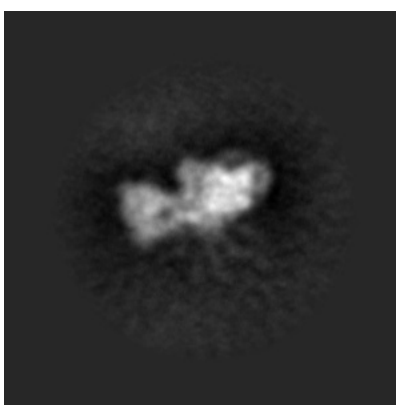
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

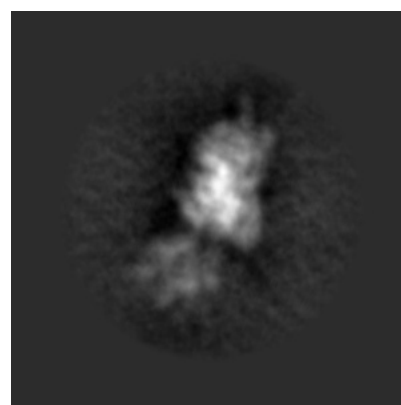
6.1.1 Primary map



X



Y

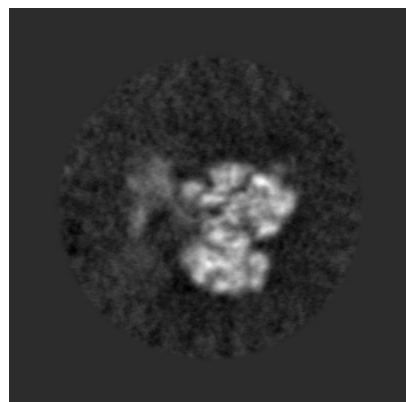


Z

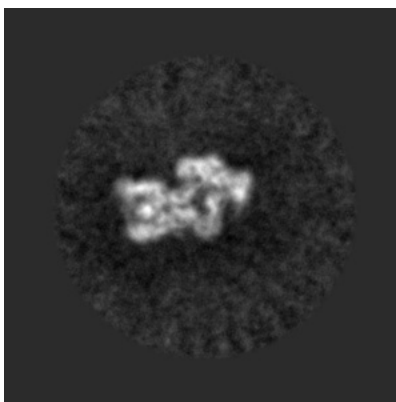
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

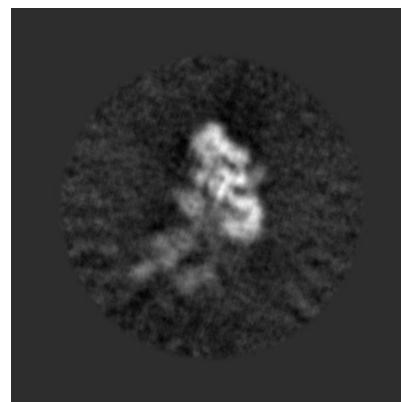
6.2.1 Primary map



X Index: 140



Y Index: 140

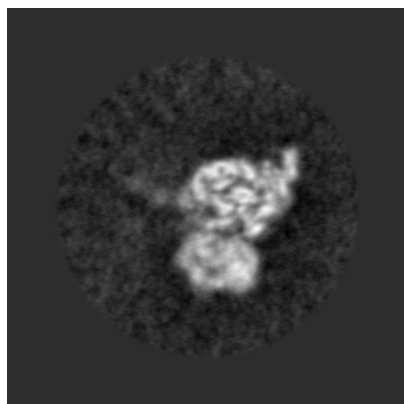


Z Index: 140

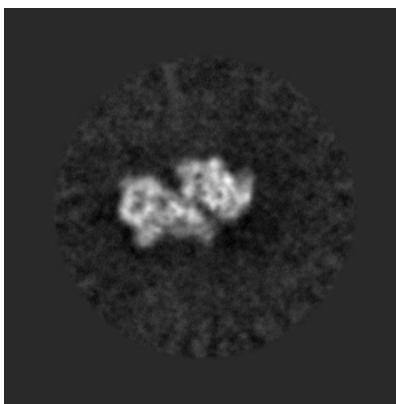
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

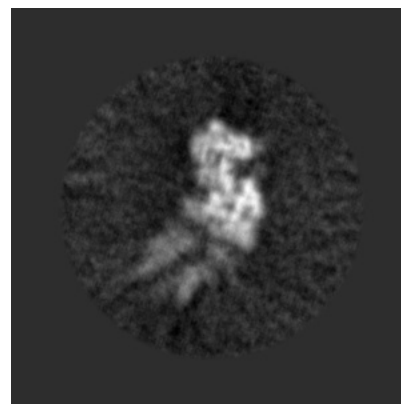
6.3.1 Primary map



X Index: 148



Y Index: 147

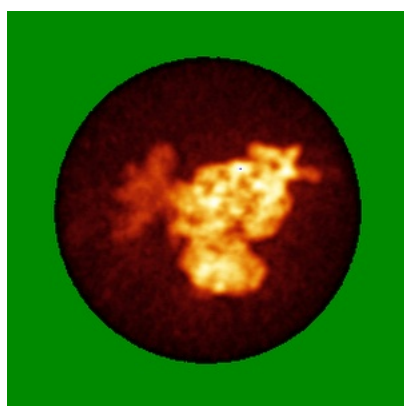


Z Index: 147

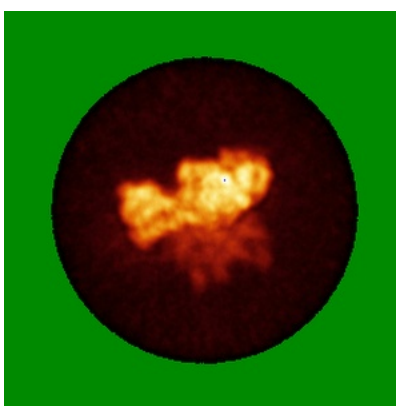
The images above show the largest variance slices of the map in three orthogonal directions.

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

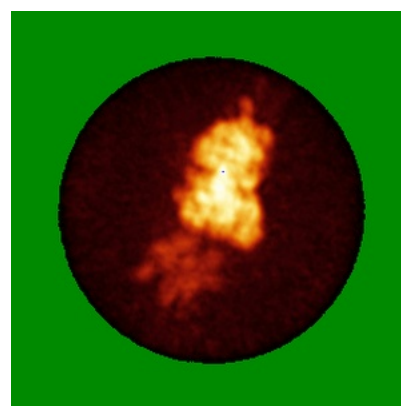
6.4.1 Primary map



X



Y

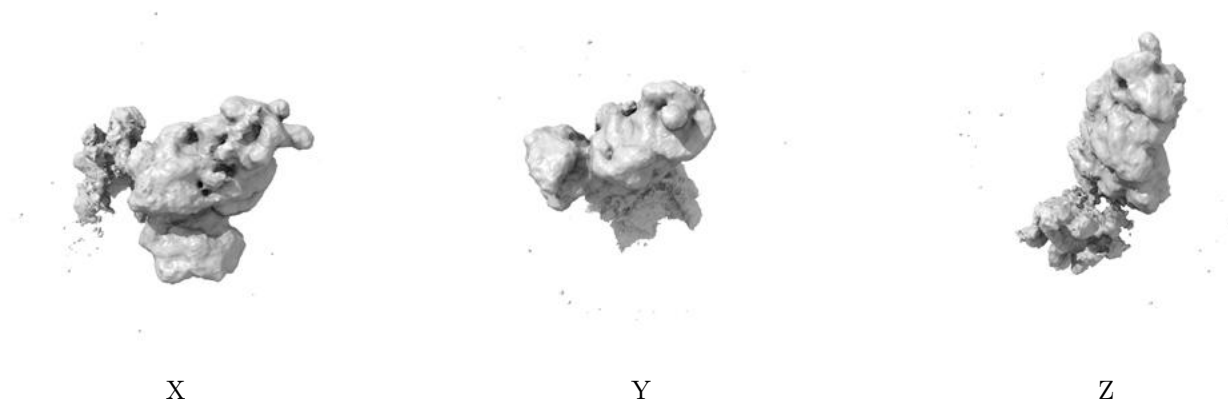


Z

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



The images above show the 3D surface view of the map at the recommended contour level 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

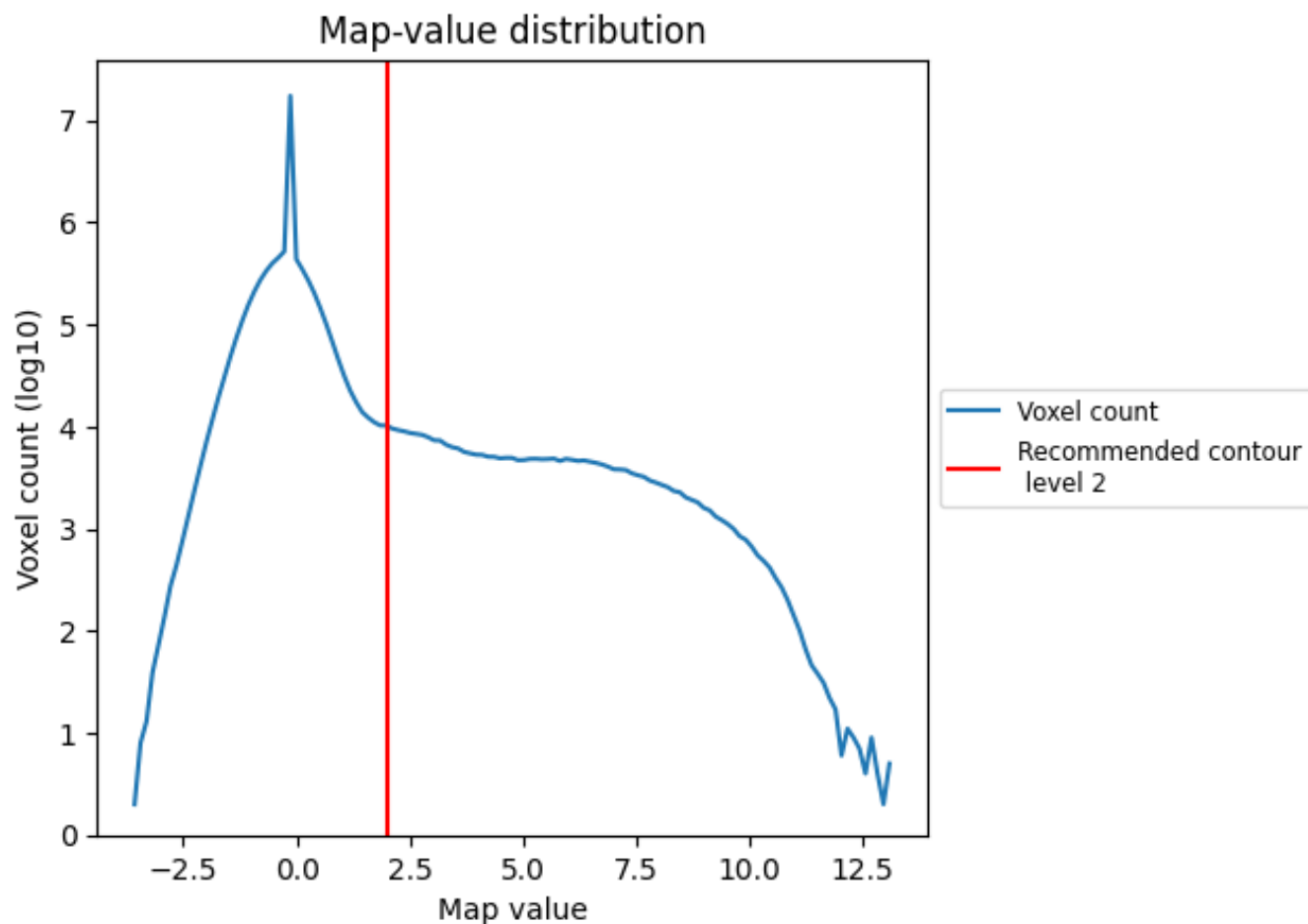
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

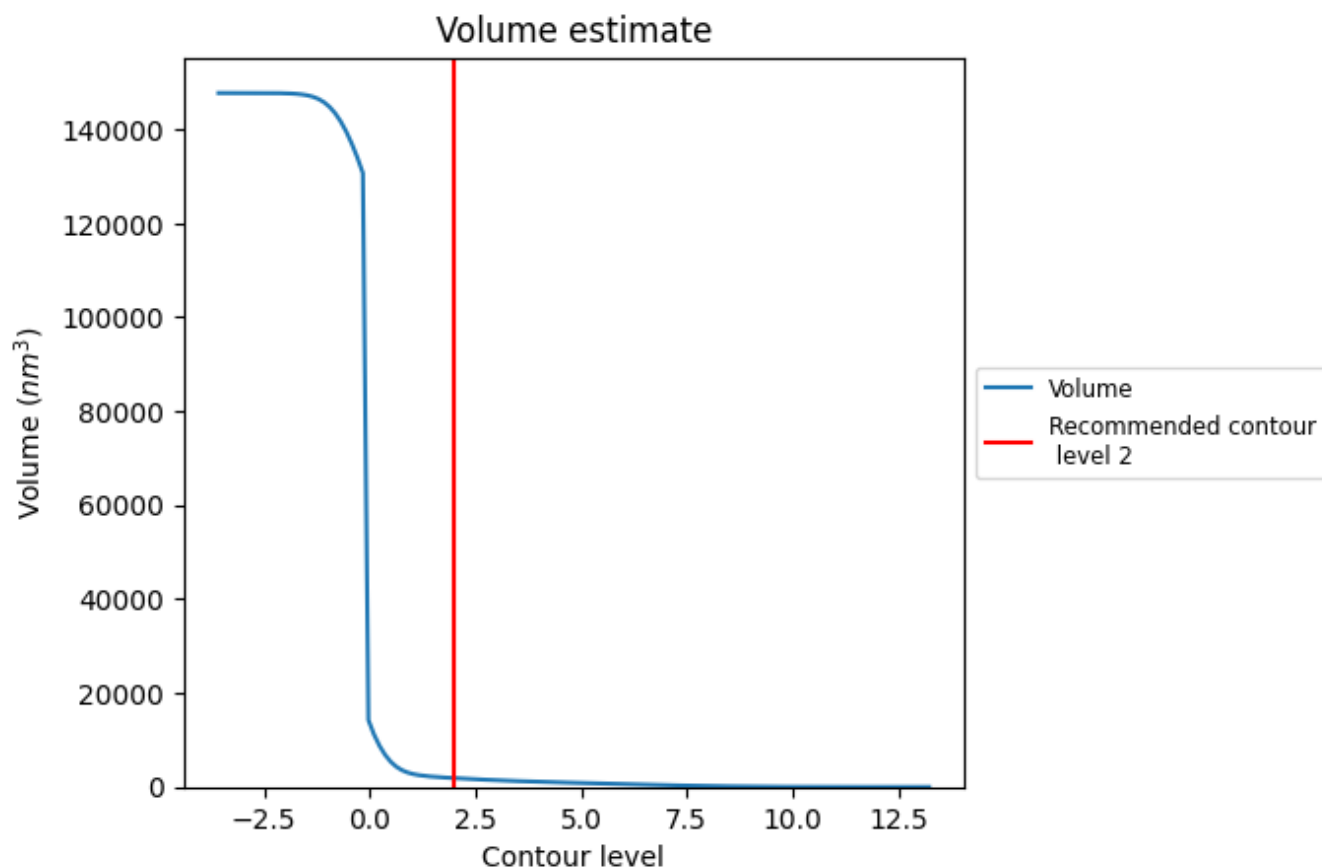
This section contains the results of statistical analysis of the map.

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.

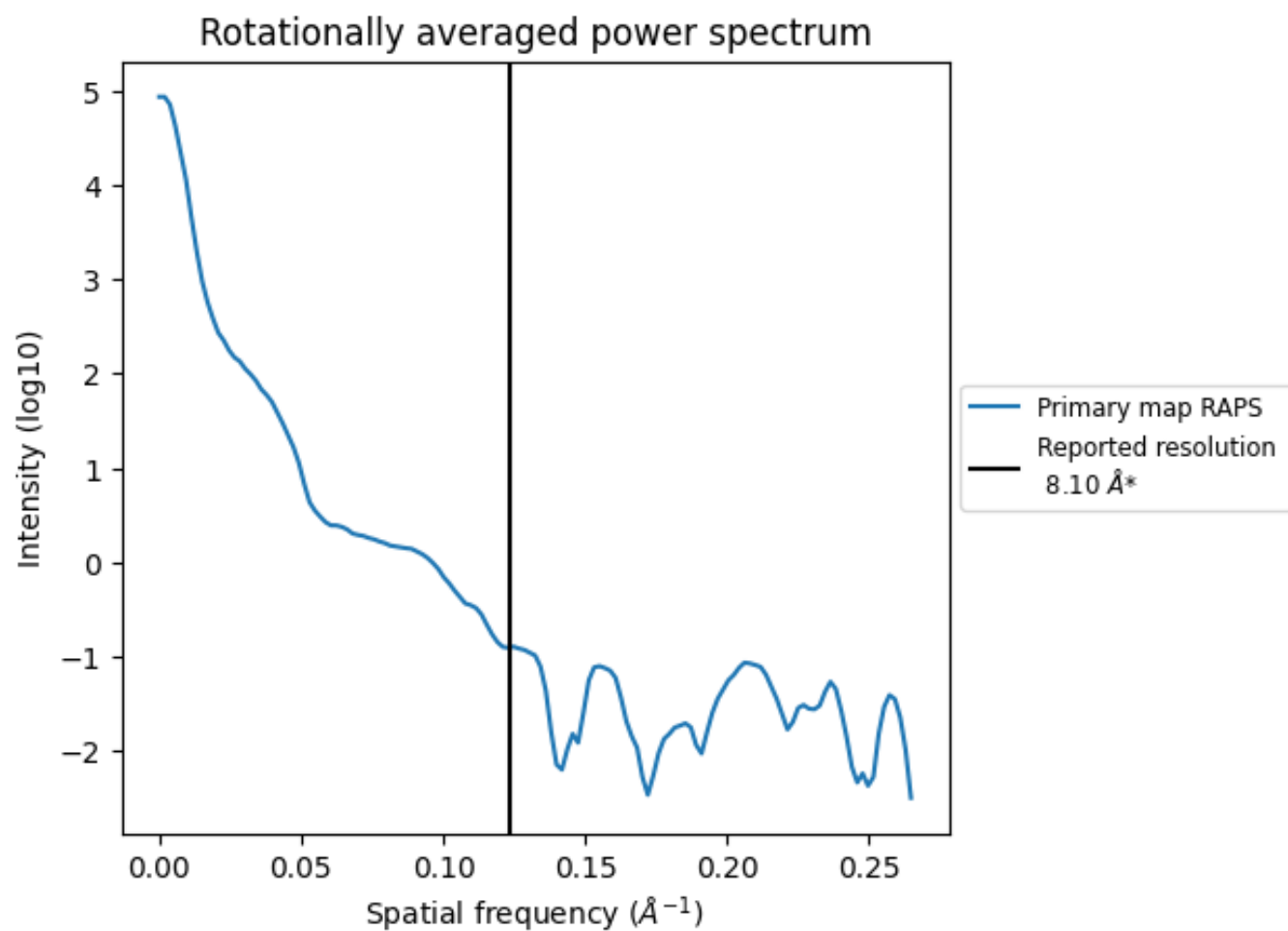
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1882 nm^3 ; this corresponds to an approximate mass of 1700 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 0.123 Å⁻¹

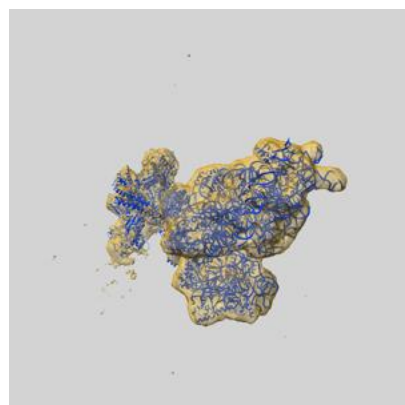
8 Fourier-Shell correlation

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

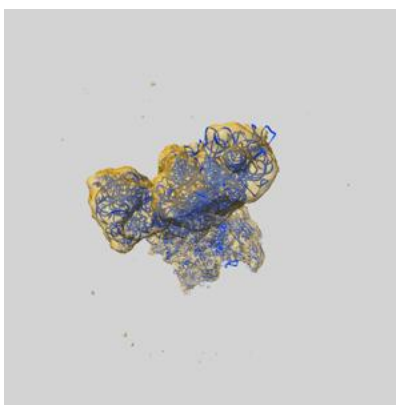
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7016 and PDB model 6AWD. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

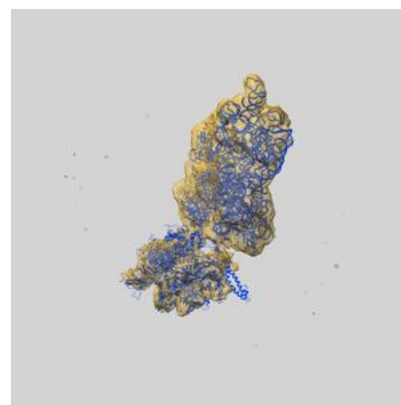
9.1 Map-model overlay [i](#)



X



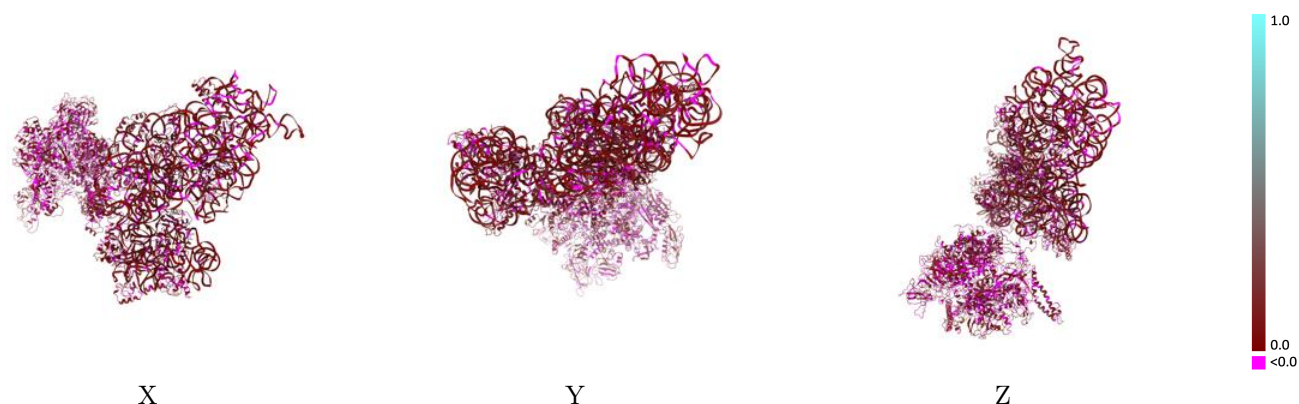
Y



Z

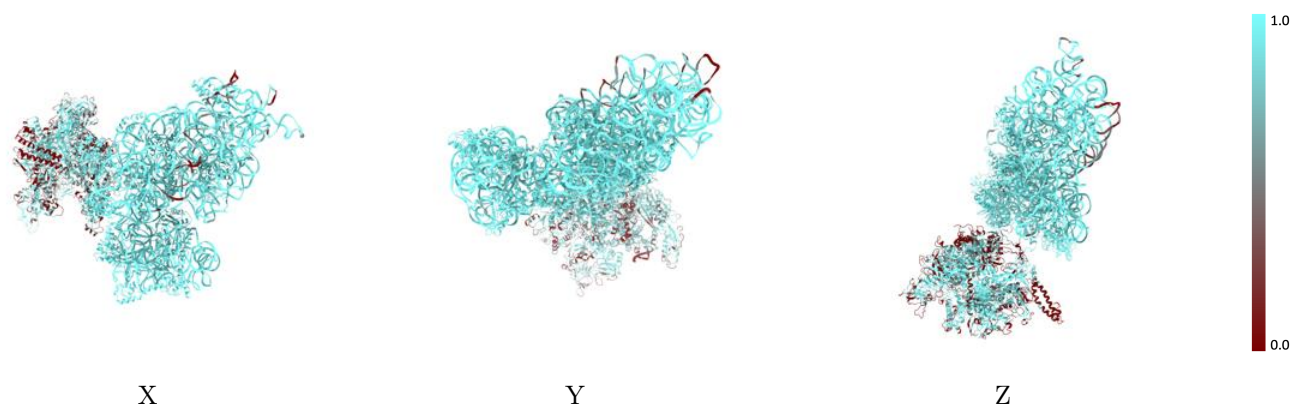
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



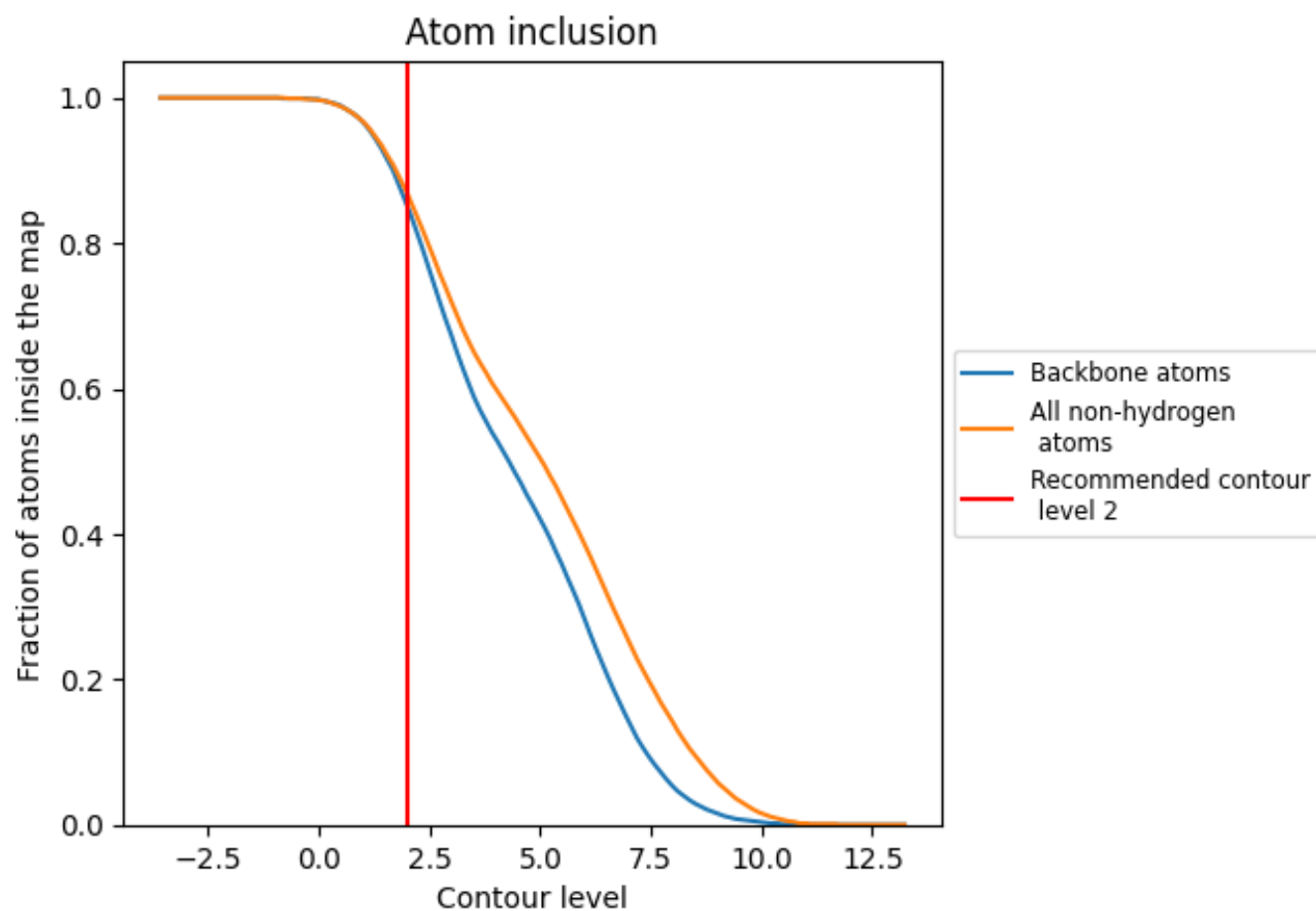
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 87% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8680	 0.0700
01	 0.7340	 0.0450
02	 0.6820	 0.0520
03	 0.6420	 0.0520
04	 0.6410	 0.0530
05	 0.1430	 0.0260
A	 0.9640	 0.0820
E	 0.9680	 0.0910
F	 0.9960	 0.0960
G	 0.9960	 0.0570
H	 0.9980	 0.0960
I	 0.9950	 0.0990
J	 0.9920	 0.0570
K	 0.9990	 0.0910
L	 0.9980	 0.0490
M	 0.9990	 0.0710
N	 0.9990	 0.0750
O	 0.9760	 0.0720
P	 0.9930	 0.0620
Q	 1.0000	 0.0320
R	 1.0000	 0.0850
S	 0.9920	 0.0700
T	 0.9970	 0.0910
U	 1.0000	 0.0750
V	 0.9940	 0.0430
W	 0.9860	 0.0690
X	 0.9420	 0.0230

