



Full wwPDB EM Validation Report ⓘ

Mar 22, 2026 – 12:43 PM UTC

PDB ID : 6AWB / pdb_00006awb
EMDB ID : EMD-7014
Title : Structure of 30S ribosomal subunit and RNA polymerase complex in non-rotated state
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 : 6.70 Å(reported)

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

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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:

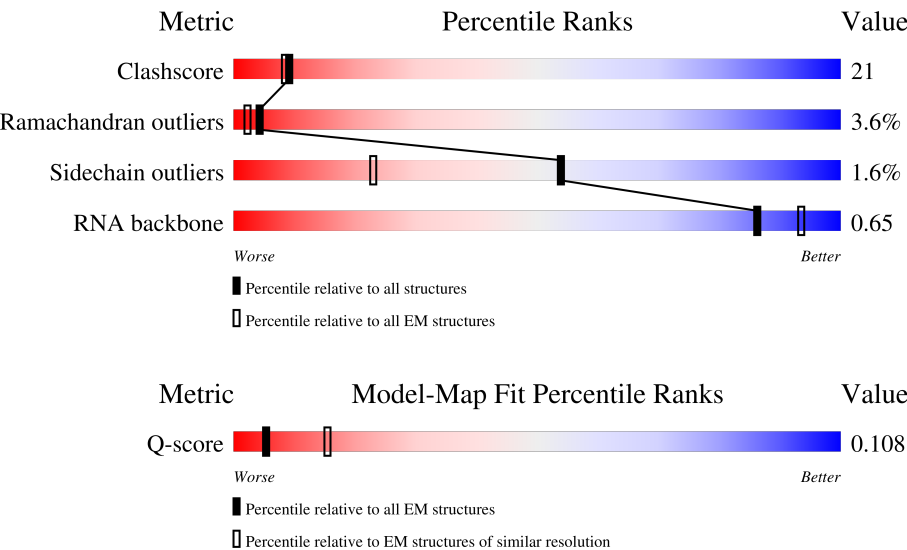
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 6.70 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.



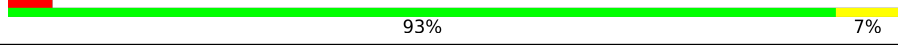
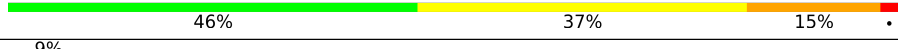
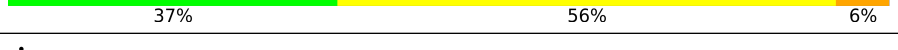
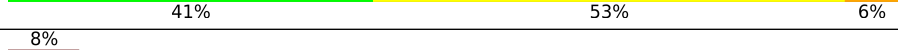
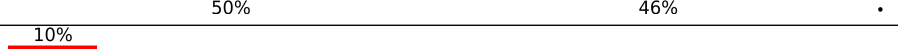
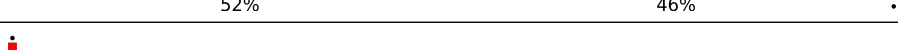
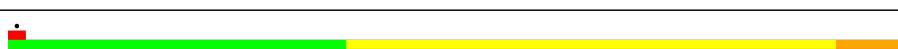
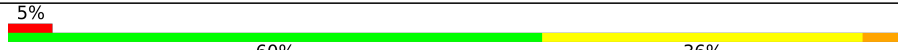
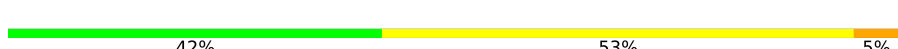
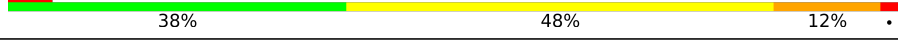
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	523 (6.20 - 7.20)

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...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	03	1340	
4	04	1369	
5	05	76	
6	B	153	
7	E	218	
8	F	206	
9	G	205	
10	H	157	
11	I	100	
12	J	151	
13	K	129	
14	L	127	
15	M	98	
16	N	116	
17	O	123	
18	P	114	
19	Q	100	
20	R	88	
21	S	82	
22	T	80	
23	U	65	
24	V	79	
25	W	85	
26	X	65	

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 75316 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	1443	Total	C	N	O	P	0	0
			30955	13808	5681	10024	1442		

- 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	76	Total	C	N	O	S	0	0
			605	368	115	121	1		

- Molecule 6 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	B	153	Total	C	N	O		
			774	463	154	157	0	0

- Molecule 7 is a protein called 30S ribosomal protein S2.

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

- Molecule 8 is a protein called 30S ribosomal protein S3.

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

- Molecule 9 is a protein called 30S ribosomal protein S4.

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

- Molecule 10 is a protein called 30S ribosomal protein S5.

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

- Molecule 11 is a protein called 30S ribosomal protein S6.

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

- Molecule 12 is a protein called 30S ribosomal protein S7.

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

- Molecule 13 is a protein called 30S ribosomal protein S8.

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

- Molecule 14 is a protein called 30S ribosomal protein S9.

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

- Molecule 15 is a protein called 30S ribosomal protein S10.

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

- Molecule 16 is a protein called 30S ribosomal protein S11.

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

- Molecule 17 is a protein called 30S ribosomal protein S12.

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

- Molecule 18 is a protein called 30S ribosomal protein S13.

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

- Molecule 19 is a protein called 30S ribosomal protein S14.

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

- Molecule 20 is a protein called 30S ribosomal protein S15.

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

- Molecule 21 is a protein called 30S ribosomal protein S16.

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

- Molecule 22 is a protein called 30S ribosomal protein S17.

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

- Molecule 23 is a protein called 30S ribosomal protein S18.

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

- Molecule 24 is a protein called 30S ribosomal protein S19.

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

- Molecule 25 is a protein called 30S ribosomal protein S20.

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

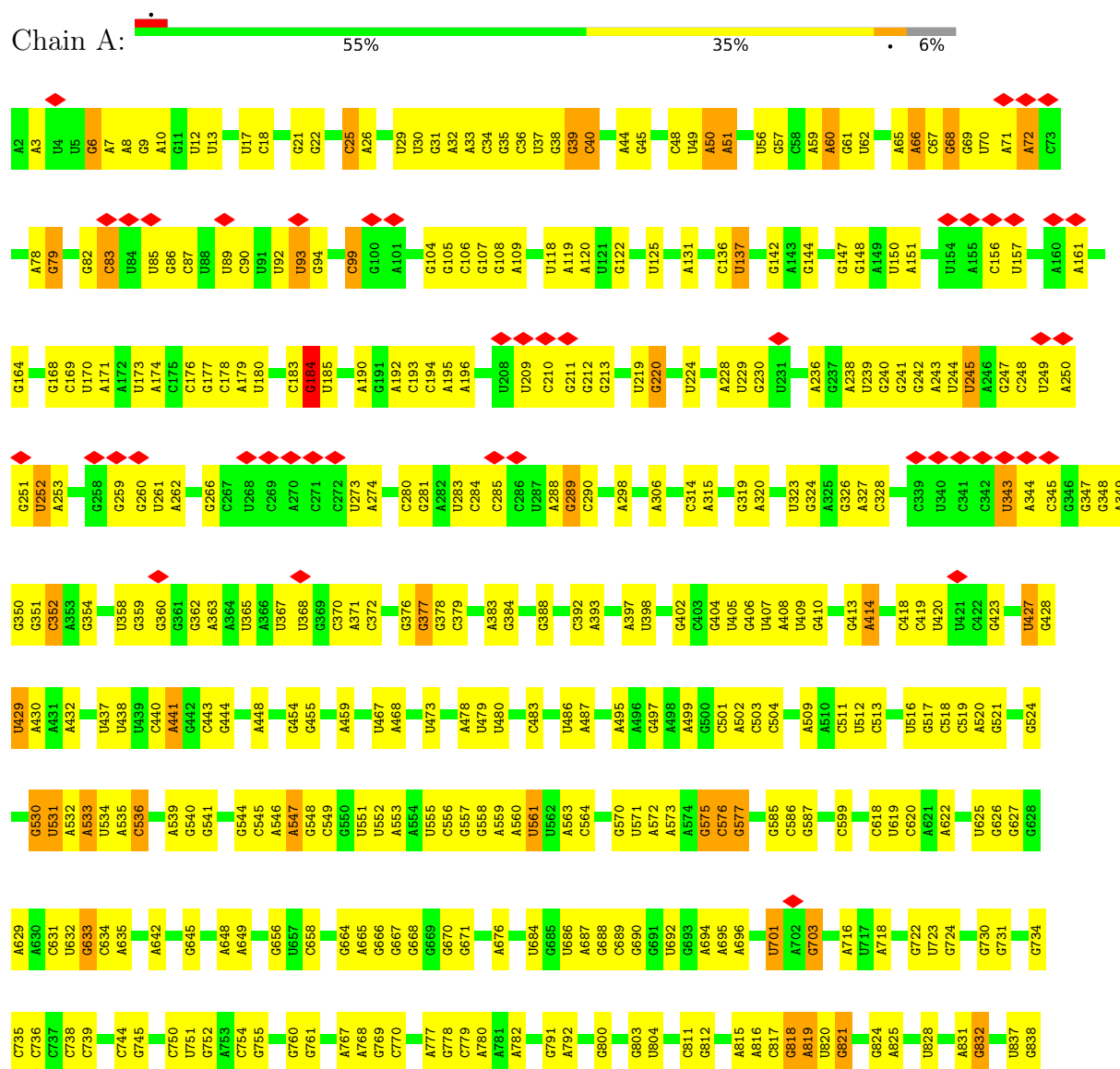
- Molecule 26 is a protein called 30S ribosomal protein S21.

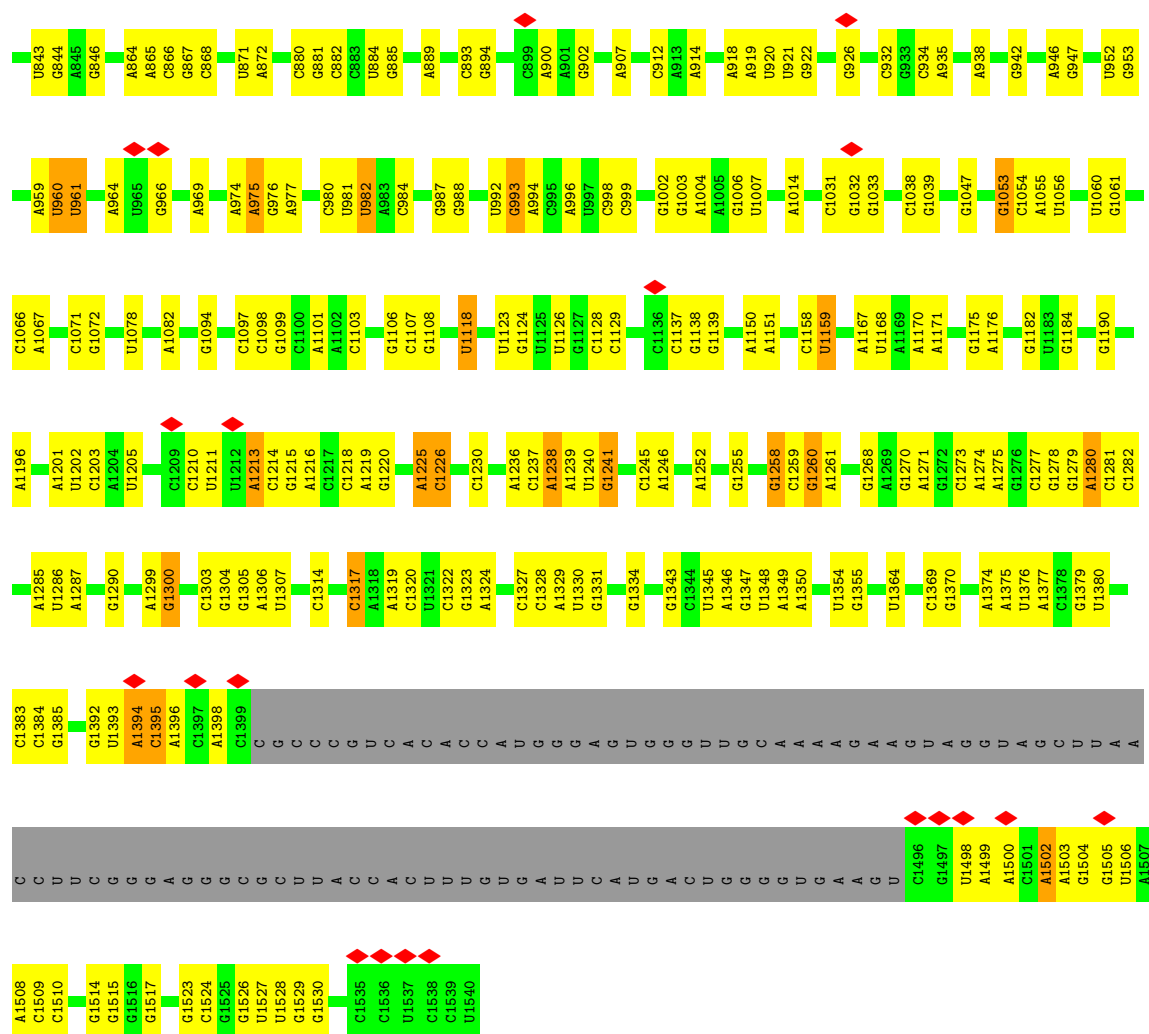
Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

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.

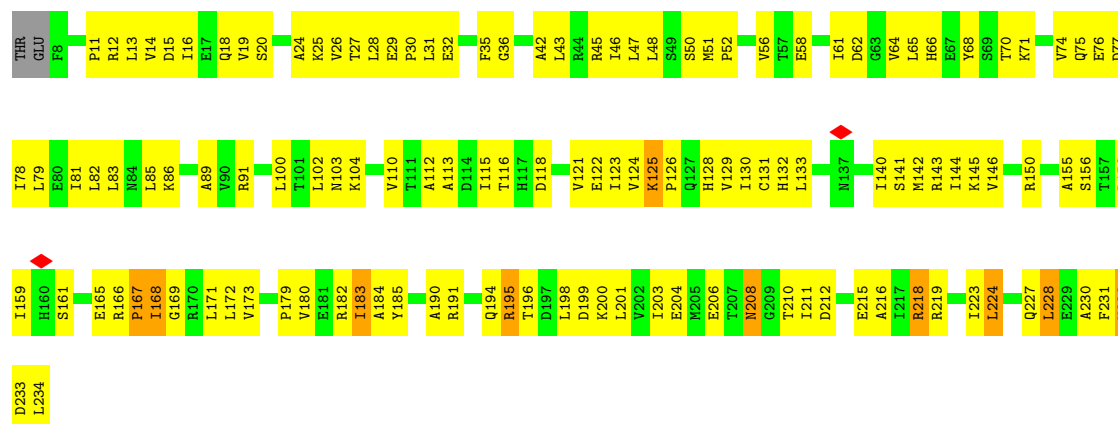
• Molecule 1: 16S rRNA





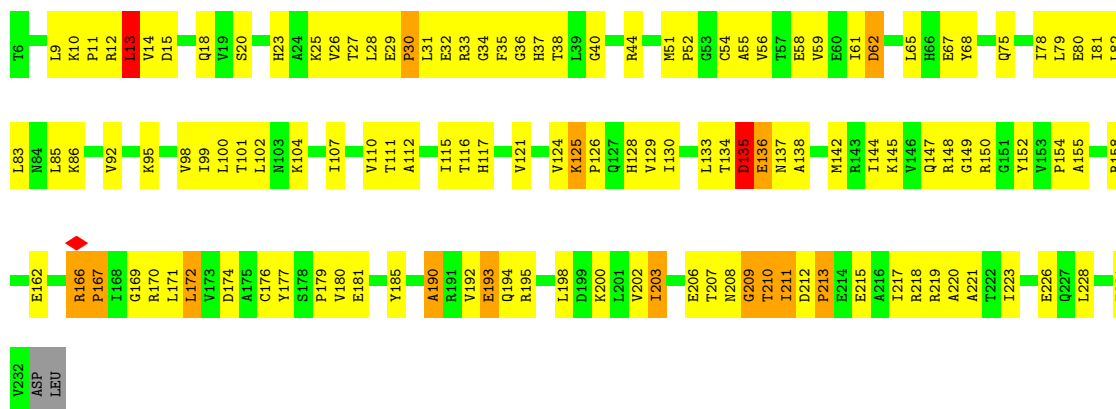
• Molecule 2: DNA-directed RNA polymerase subunit alpha

Chain 01: 42% 52%



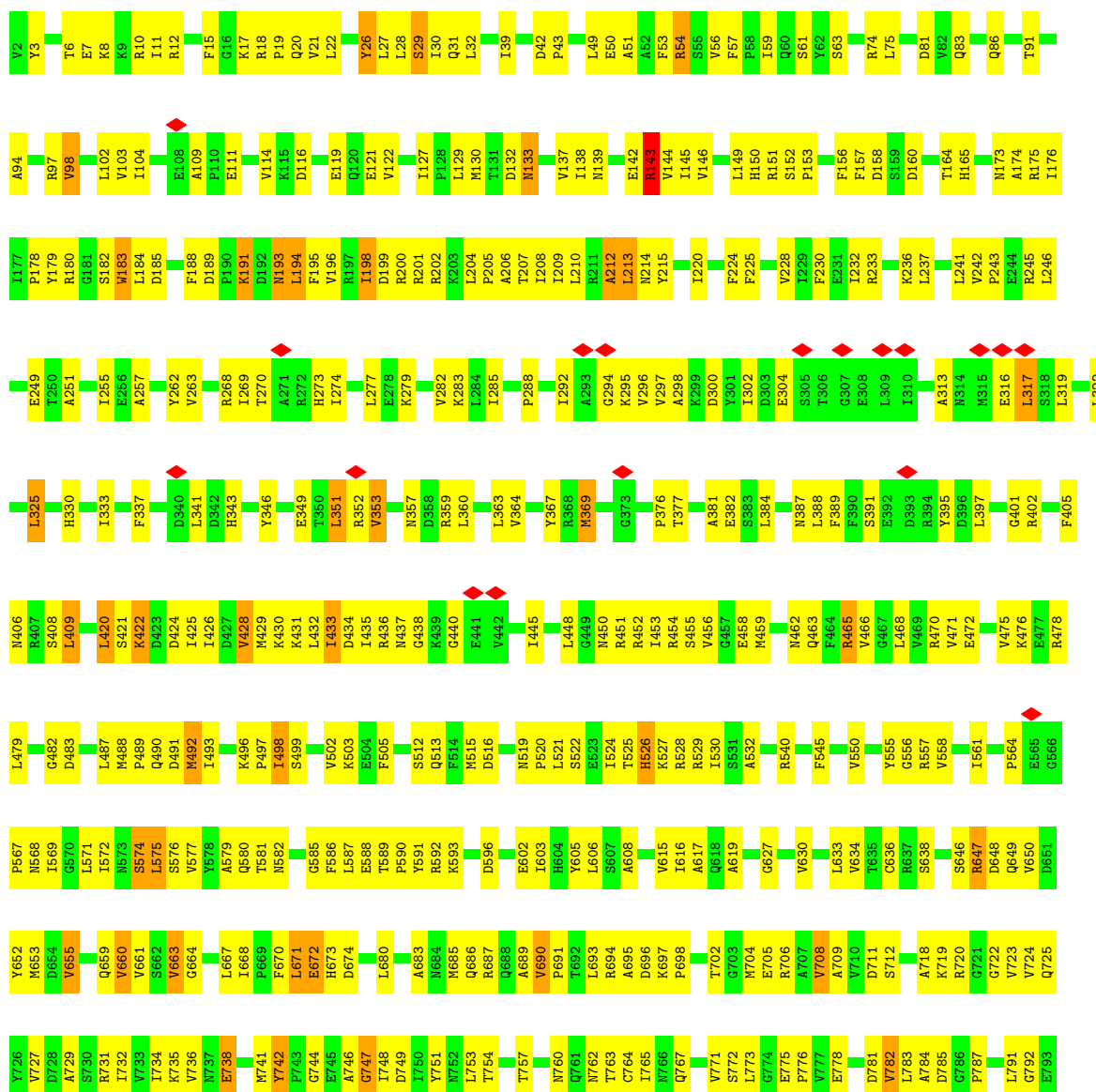
• Molecule 2: DNA-directed RNA polymerase subunit alpha

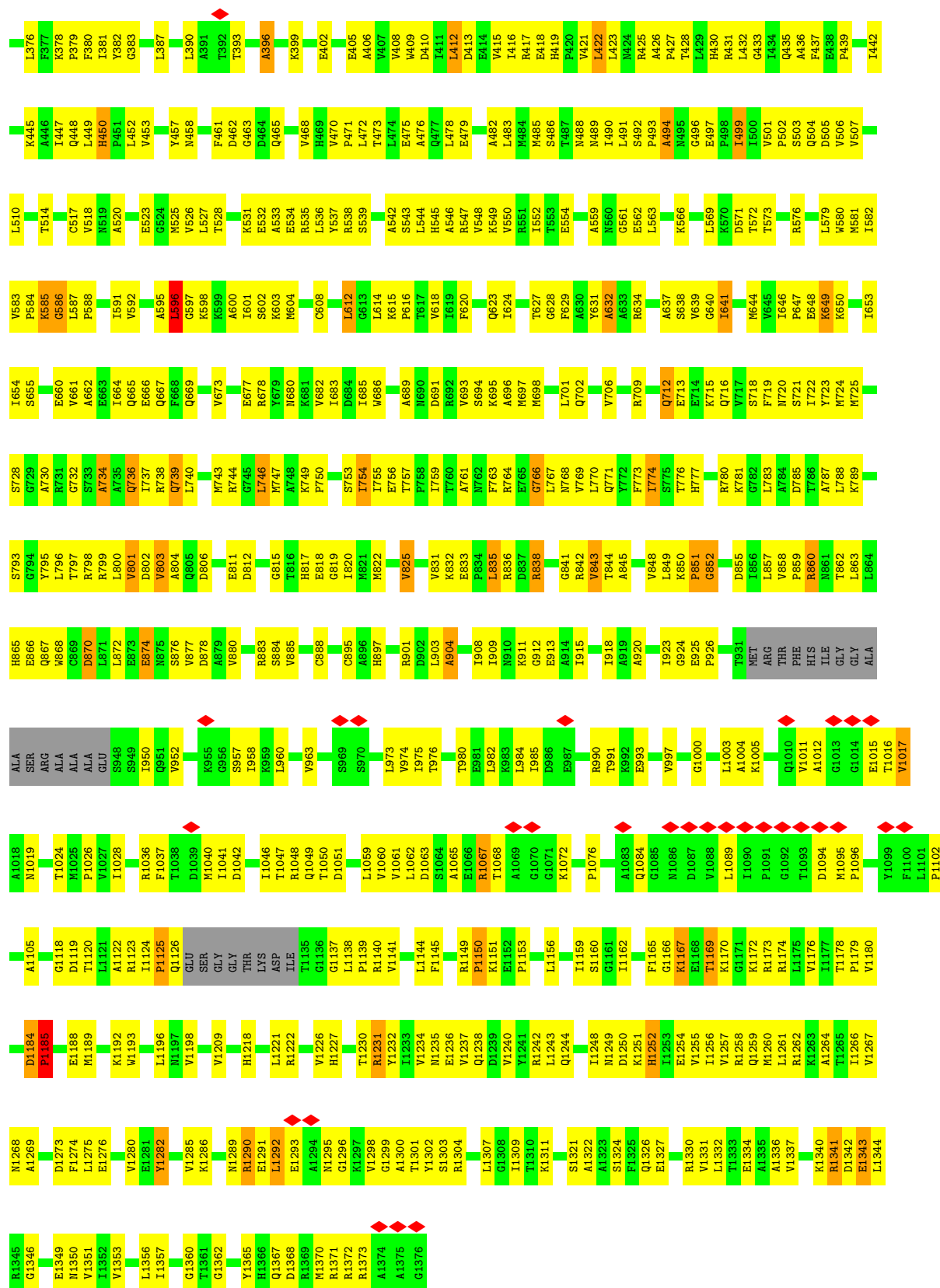
Chain 02: 44% 48% 6%

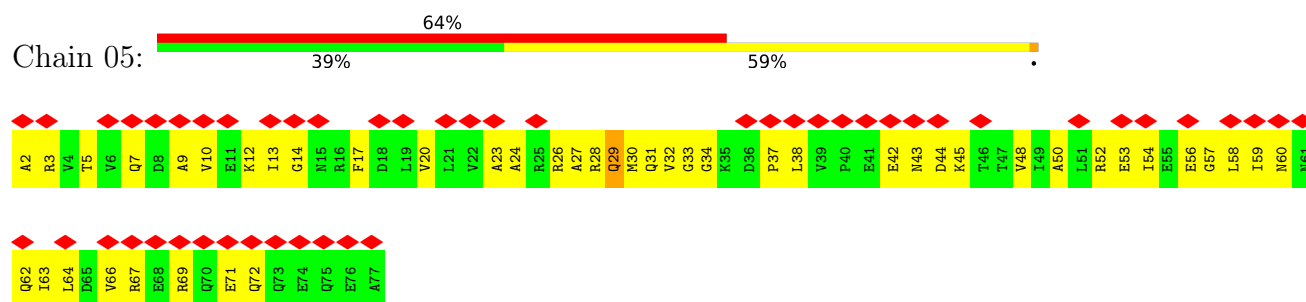


• Molecule 3: DNA-directed RNA polymerase subunit beta

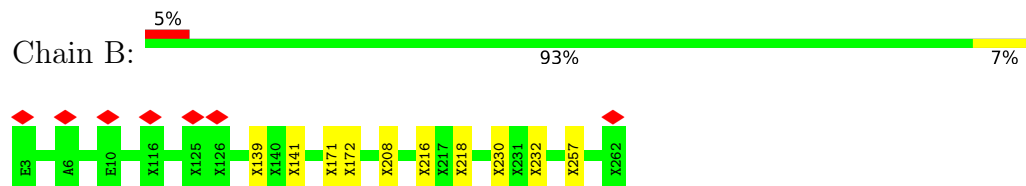
Chain 03: 49% 44% 5% •







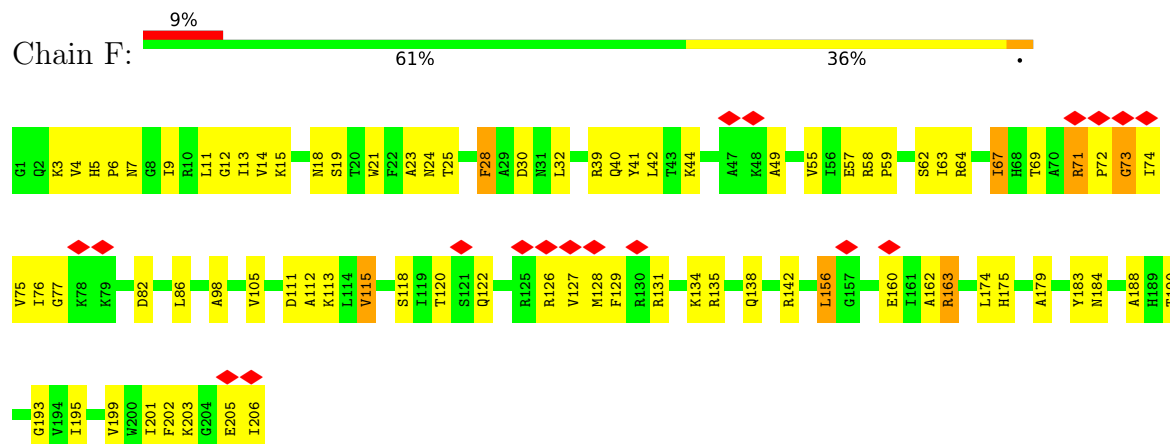
- Molecule 6: 30S ribosomal protein S1



- Molecule 7: 30S ribosomal protein S2

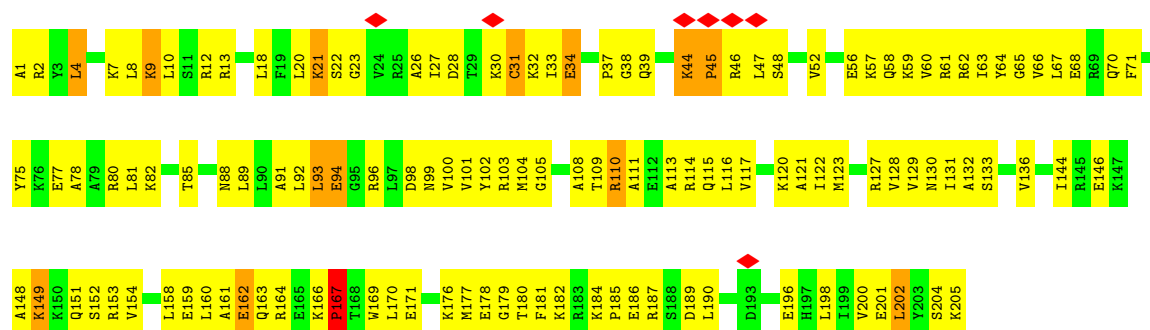


- Molecule 8: 30S ribosomal protein S3



- Molecule 9: 30S ribosomal protein S4

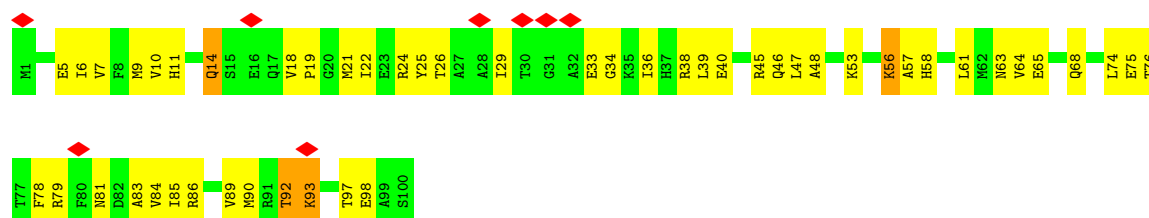




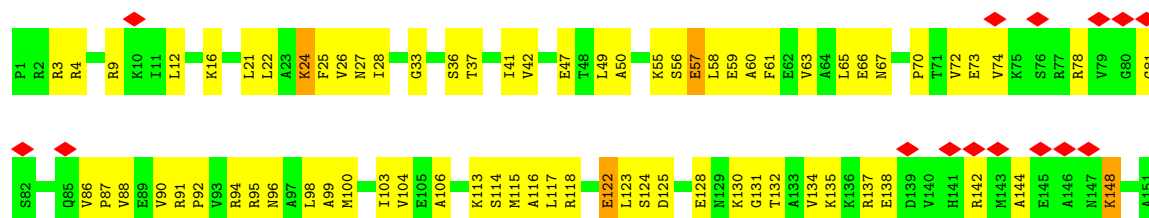
• Molecule 10: 30S ribosomal protein S5



• Molecule 11: 30S ribosomal protein S6

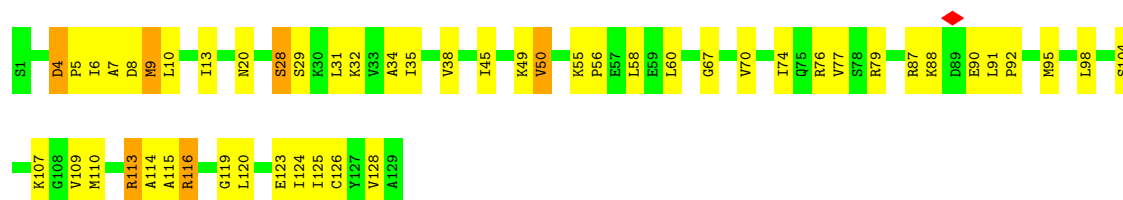


• Molecule 12: 30S ribosomal protein S7

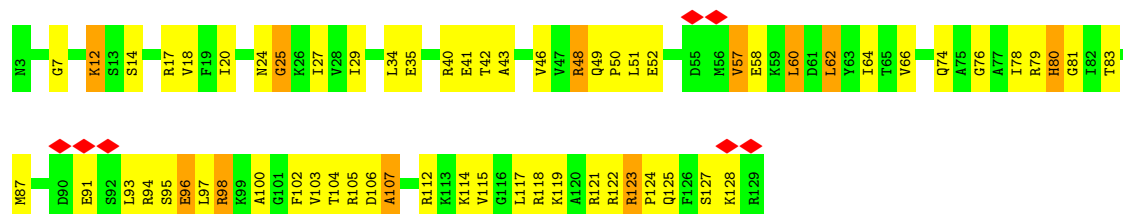


• Molecule 13: 30S ribosomal protein S8

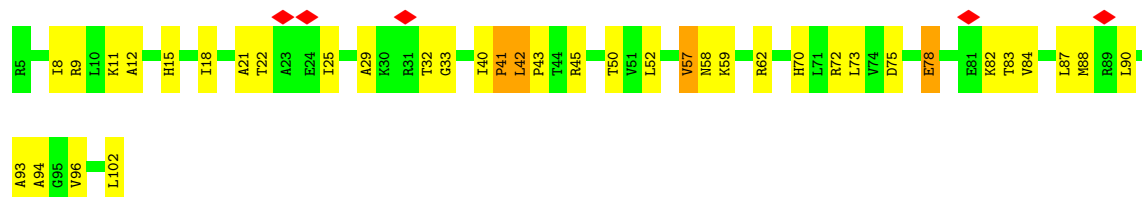




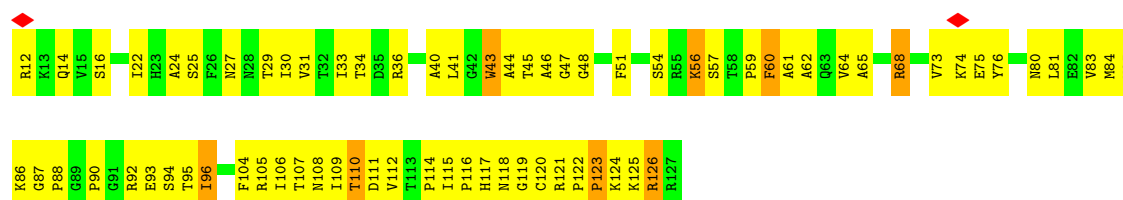
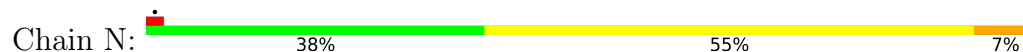
• Molecule 14: 30S ribosomal protein S9



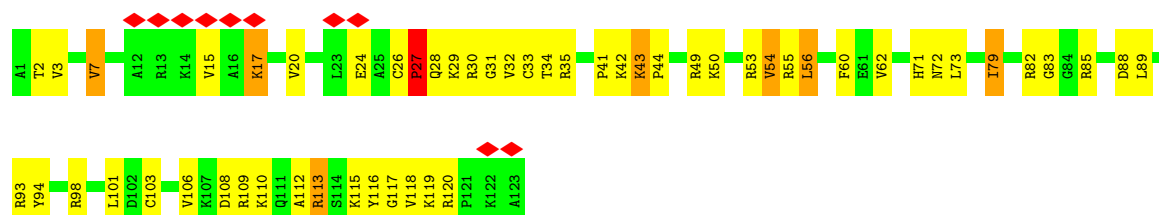
• Molecule 15: 30S ribosomal protein S10



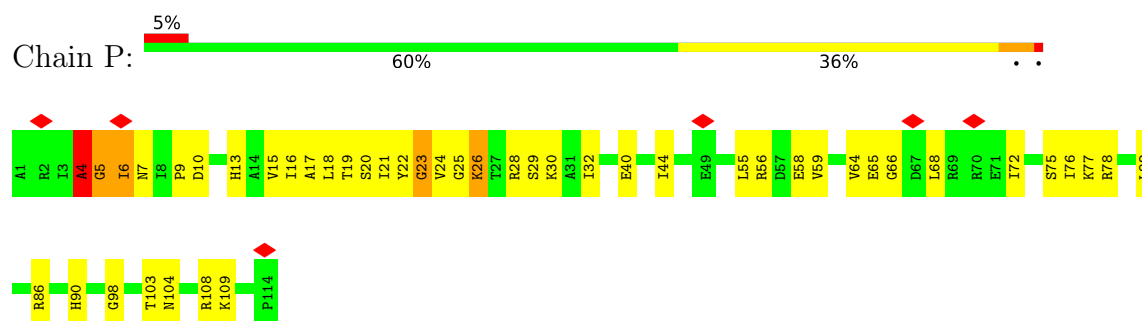
• Molecule 16: 30S ribosomal protein S11



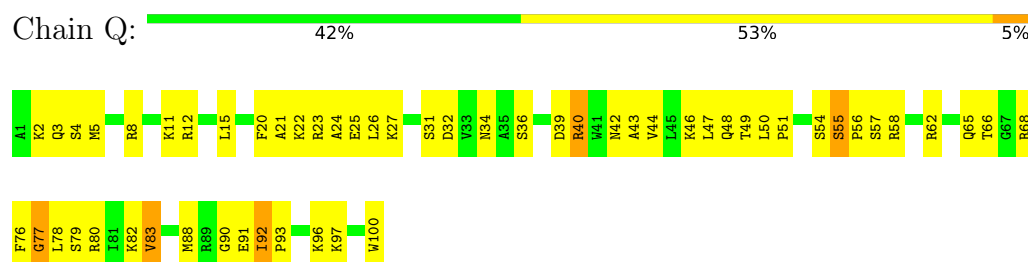
• Molecule 17: 30S ribosomal protein S12



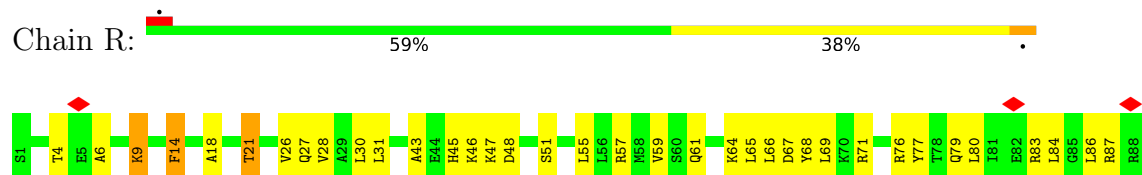
- Molecule 18: 30S ribosomal protein S13



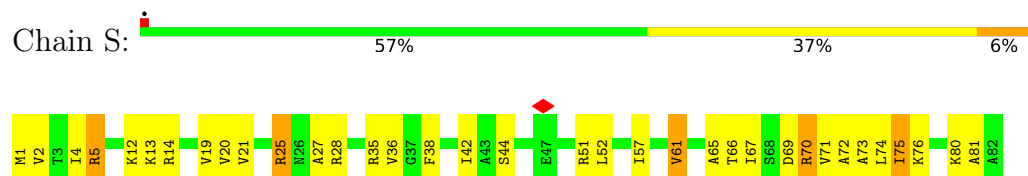
- Molecule 19: 30S ribosomal protein S14



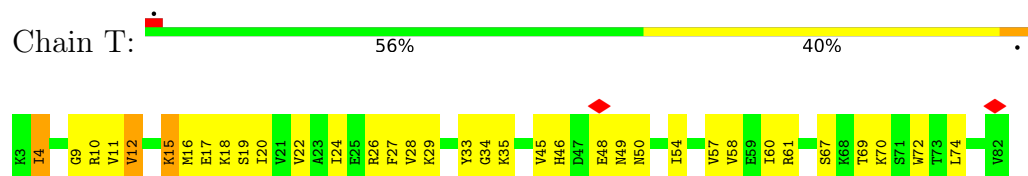
- Molecule 20: 30S ribosomal protein S15



- Molecule 21: 30S ribosomal protein S16

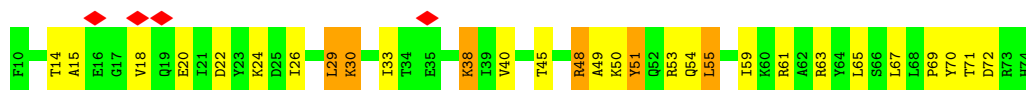


- Molecule 22: 30S ribosomal protein S17

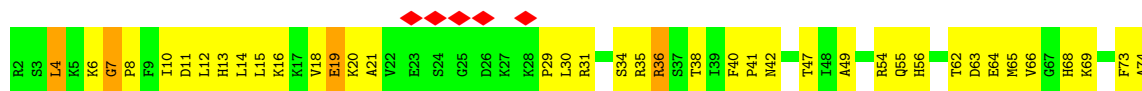


- Molecule 23: 30S ribosomal protein S18





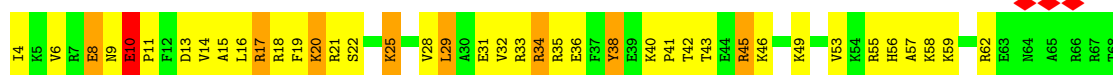
- Molecule 24: 30S ribosomal protein S19



- Molecule 25: 30S ribosomal protein S20



- Molecule 26: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	15012	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.0	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	25000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	10.060	Depositor
Minimum map value	-3.475	Depositor
Average map value	-0.013	Depositor
Map value standard deviation	0.657	Depositor
Recommended contour level	2	Depositor
Map size (Å)	459.98398, 459.98398, 459.98398	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.6428, 1.6428, 1.6428	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	0.42	0/34660	0.51	2/54067 (0.0%)
2	01	0.32	0/1774	1.00	17/2405 (0.7%)
2	02	0.37	0/1779	1.02	14/2411 (0.6%)
3	03	0.37	0/10433	1.09	84/14101 (0.6%)
4	04	0.36	0/10528	1.12	104/14224 (0.7%)
5	05	0.35	0/607	1.00	3/817 (0.4%)
6	B	0.55	0/65	0.96	0/86
7	E	0.42	0/1736	1.34	27/2338 (1.2%)
8	F	0.37	0/1652	1.01	11/2225 (0.5%)
9	G	0.35	0/1665	1.07	21/2227 (0.9%)
10	H	0.37	0/1170	1.10	16/1573 (1.0%)
11	I	0.36	0/836	0.91	1/1128 (0.1%)
12	J	0.34	0/1196	1.07	7/1602 (0.4%)
13	K	0.41	0/989	1.21	13/1326 (1.0%)
14	L	0.34	0/1034	1.03	10/1375 (0.7%)
15	M	0.43	0/797	0.99	0/1077
16	N	0.42	0/886	1.15	9/1195 (0.8%)
17	O	0.41	0/969	1.07	9/1300 (0.7%)
18	P	0.36	0/893	0.97	4/1193 (0.3%)
19	Q	0.36	0/817	1.10	10/1088 (0.9%)
20	R	0.35	0/722	1.12	7/964 (0.7%)
21	S	0.37	0/659	0.95	4/884 (0.5%)
22	T	0.37	0/658	0.93	3/881 (0.3%)
23	U	0.43	0/545	1.24	10/731 (1.4%)
24	V	0.41	0/653	0.98	3/877 (0.3%)
25	W	0.37	0/671	1.15	8/888 (0.9%)
26	X	0.47	0/551	1.19	10/728 (1.4%)
All	All	0.39	0/78945	0.87	407/113711 (0.4%)

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	2

There are no bond length outliers.

All (407) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	E	24	ASN	CA-C-N	16.25	140.15	119.84
7	E	24	ASN	C-N-CA	16.25	140.15	119.84
7	E	26	LYS	N-CA-C	-14.85	95.10	111.14
3	03	1034	ARG	N-CA-C	-10.58	99.71	111.14
4	04	1290	ARG	N-CA-C	-10.49	101.04	114.04
12	J	21	LEU	N-CA-C	-10.47	99.95	111.36
4	04	1298	VAL	N-CA-C	-10.10	103.63	113.53
23	U	22	ASP	N-CA-C	9.94	123.16	110.33
9	G	202	LEU	N-CA-C	-9.89	100.46	111.14
4	04	324	LEU	N-CA-C	9.79	124.63	110.24
19	Q	77	GLY	N-CA-C	-9.71	99.15	115.08
3	03	843	THR	N-CA-C	-9.71	93.96	109.59
19	Q	39	ASP	N-CA-C	-9.63	101.65	113.97
4	04	739	GLN	N-CA-C	-9.47	101.73	113.38
3	03	1143	GLU	N-CA-C	-9.44	100.96	111.07
4	04	774	ILE	N-CA-C	-9.39	101.59	110.42
4	04	50	LYS	CA-C-N	9.37	131.55	119.84
4	04	50	LYS	C-N-CA	9.37	131.55	119.84
4	04	205	LEU	N-CA-C	-9.34	101.31	112.89
4	04	1367	GLN	N-CA-C	-9.33	101.08	111.07
4	04	18	ASP	N-CA-C	9.29	122.31	110.33
16	N	117	HIS	N-CA-C	-9.27	102.55	112.93
4	04	803	VAL	N-CA-C	9.22	121.05	111.00
7	E	187	VAL	N-CA-C	8.92	121.63	108.96
3	03	1113	LEU	N-CA-C	-8.89	102.01	113.12
13	K	55	LYS	CA-C-N	8.82	130.87	119.84
13	K	55	LYS	C-N-CA	8.82	130.87	119.84
25	W	59	ARG	N-CA-C	-8.67	101.40	111.03
3	03	1322	SER	N-CA-C	-8.62	102.03	112.54
4	04	99	ARG	N-CA-C	-8.59	102.35	113.17
4	04	1170	LYS	N-CA-C	-8.37	100.67	113.89
13	K	9	MET	N-CA-C	-8.35	103.61	113.88
4	04	851	PRO	N-CA-C	-8.28	103.08	113.84
7	E	41	ILE	N-CA-C	8.26	120.86	108.23
3	03	1014	LEU	N-CA-C	8.24	123.11	112.89
3	03	900	LYS	N-CA-C	-8.16	102.92	113.12
20	R	4	THR	N-CA-C	8.13	121.17	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	02	135	ASP	N-CA-C	8.12	128.10	110.80
3	03	319	LEU	N-CA-C	8.08	121.00	111.71
4	04	1184	ASP	N-CA-C	8.06	127.63	109.81
26	X	9	ASN	N-CA-C	8.00	121.02	111.33
4	04	632	ALA	N-CA-C	-7.96	102.68	111.36
3	03	133	ASN	N-CA-C	-7.92	102.13	113.21
8	F	105	VAL	N-CA-C	-7.89	97.07	108.36
4	04	20	ILE	N-CA-C	7.83	120.78	108.87
4	04	294	ASN	N-CA-C	-7.69	103.36	112.89
14	L	57	VAL	N-CA-C	7.67	117.74	110.30
7	E	44	GLU	N-CA-C	7.67	120.37	111.02
3	03	408	SER	N-CA-C	-7.65	103.95	113.28
3	03	1310	ASP	N-CA-C	-7.65	104.56	114.04
3	03	1309	VAL	N-CA-C	-7.64	104.01	112.80
3	03	577	VAL	N-CA-C	7.60	118.14	110.23
4	04	196	GLN	N-CA-C	-7.51	103.02	111.14
4	04	804	ALA	N-CA-C	7.48	122.14	112.41
4	04	284	ASP	N-CA-C	-7.32	103.81	112.89
3	03	353	VAL	N-CA-C	-7.30	106.38	113.53
4	04	458	ASN	N-CA-C	-7.29	102.91	112.24
10	H	55	VAL	N-CA-C	7.28	121.09	112.35
7	E	73	LYS	N-CA-C	7.27	122.10	113.23
4	04	648	GLU	N-CA-C	-7.25	104.32	113.02
4	04	250	ARG	CA-C-N	7.23	127.16	119.85
4	04	250	ARG	C-N-CA	7.23	127.16	119.85
3	03	422	LYS	N-CA-C	7.22	119.83	111.02
13	K	28	SER	N-CA-C	7.21	121.32	110.14
10	H	152	VAL	N-CA-C	-7.19	106.48	113.53
4	04	108	ALA	N-CA-C	-7.19	103.06	112.41
26	X	45	ARG	N-CA-C	-7.15	104.03	112.89
3	03	279	LYS	N-CA-C	-7.14	104.69	113.41
10	H	17	VAL	N-CA-C	-7.14	97.90	108.97
16	N	75	GLU	N-CA-C	-7.13	105.11	114.31
4	04	649	LYS	N-CA-C	-7.13	104.58	113.28
17	O	56	LEU	N-CA-C	7.11	119.51	110.33
3	03	690	VAL	N-CA-C	7.08	116.74	108.96
4	04	1236	GLU	N-CA-C	-7.07	103.51	111.14
24	V	7	GLY	CA-C-N	7.07	128.67	119.84
24	V	7	GLY	C-N-CA	7.07	128.67	119.84
19	Q	40	ARG	N-CA-C	-7.05	103.64	111.82
22	T	12	VAL	N-CA-C	7.05	117.61	111.90
4	04	1311	LYS	N-CA-C	-7.05	105.21	113.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	E	40	ILE	N-CA-C	7.02	123.95	109.34
4	04	1193	TRP	N-CA-C	-7.02	104.74	113.38
4	04	835	LEU	N-CA-C	-7.02	103.06	111.69
23	U	51	TYR	N-CA-C	7.01	118.57	111.07
3	03	1162	SER	N-CA-C	-6.99	104.64	113.72
5	05	29	GLN	N-CA-C	-6.96	104.26	112.89
3	03	1323	PHE	N-CA-C	-6.96	103.75	111.82
4	04	870	ASP	N-CA-C	-6.92	103.51	112.23
3	03	143	ARG	N-CA-C	-6.91	98.96	109.95
3	03	1112	ILE	N-CA-C	-6.91	106.49	113.47
25	W	83	ASN	N-CA-C	-6.84	105.06	113.41
7	E	166	ALA	N-CA-C	-6.84	105.56	114.04
7	E	107	VAL	N-CA-C	-6.83	103.01	112.50
9	G	110	ARG	N-CA-C	-6.81	104.94	113.18
17	O	115	LYS	N-CA-C	-6.79	101.11	110.35
19	Q	21	ALA	N-CA-C	-6.78	103.44	113.61
12	J	124	SER	N-CA-C	-6.74	103.74	112.23
4	04	331	ILE	N-CA-C	-6.73	106.23	112.96
4	04	1296	GLY	N-CA-C	-6.73	97.22	113.18
4	04	92	VAL	N-CA-C	6.72	117.12	108.12
4	04	274	ASN	N-CA-C	-6.72	103.65	110.97
4	04	801	VAL	N-CA-C	-6.71	103.94	110.72
4	04	149	GLY	N-CA-C	-6.70	104.11	110.21
3	03	304	GLU	N-CA-C	6.69	121.18	112.89
4	04	215	LYS	N-CA-C	-6.69	103.68	110.97
3	03	1274	GLU	N-CA-C	-6.66	104.63	112.89
3	03	891	GLY	N-CA-C	6.61	128.84	113.18
9	G	38	GLY	N-CA-C	-6.56	103.33	112.13
3	03	1280	ALA	N-CA-C	-6.55	105.28	113.28
19	Q	36	SER	N-CA-C	6.55	118.33	107.20
3	03	742	TYR	N-CA-C	6.55	117.13	109.60
9	G	93	LEU	N-CA-C	-6.55	104.55	112.54
4	04	806	ASP	N-CA-C	6.51	120.94	113.19
4	04	950	ILE	N-CA-C	6.50	116.83	108.12
4	04	297	ARG	N-CA-C	-6.49	104.28	111.36
16	N	43	TRP	N-CA-C	6.49	117.70	108.74
4	04	240	THR	N-CA-C	-6.49	105.67	113.97
2	02	136	GLU	N-CA-C	6.48	124.61	110.80
2	02	36	GLY	N-CA-C	-6.44	106.88	115.32
3	03	322	LEU	N-CA-C	-6.44	104.26	111.28
2	01	228	LEU	N-CA-C	-6.43	106.02	114.31
4	04	1180	VAL	N-CA-C	-6.43	105.90	113.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	W	8	LYS	N-CA-C	-6.43	104.70	112.54
23	U	14	THR	N-CA-C	-6.42	105.31	112.57
10	H	61	LYS	N-CA-C	-6.42	104.14	112.23
3	03	1199	LEU	N-CA-C	-6.42	104.94	112.89
2	02	198	LEU	N-CA-C	-6.41	101.29	110.59
2	01	161	SER	N-CA-C	-6.41	103.58	111.40
3	03	1262	LYS	N-CA-C	-6.40	104.78	112.59
7	E	31	ILE	N-CA-C	6.40	117.98	111.00
2	02	212	ASP	CA-C-N	6.40	127.84	119.84
2	02	212	ASP	C-N-CA	6.40	127.84	119.84
21	S	70	ARG	N-CA-C	-6.39	104.53	112.90
9	G	108	ALA	N-CA-C	-6.38	104.98	112.89
3	03	708	VAL	N-CA-C	-6.38	104.64	110.82
9	G	9	LYS	N-CA-C	-6.37	104.56	112.90
4	04	1291	GLU	N-CA-C	-6.37	104.21	112.23
3	03	351	LEU	N-CA-C	-6.36	104.44	111.82
11	I	68	GLN	N-CA-C	6.35	118.21	111.28
1	A	343	U	C2'-C3'-O3'	6.35	119.03	109.50
3	03	114	VAL	N-CA-C	-6.35	106.61	112.96
3	03	671	LEU	N-CA-C	-6.35	105.50	113.18
2	01	212	ASP	CA-C-N	6.35	125.84	119.24
2	01	212	ASP	C-N-CA	6.35	125.84	119.24
17	O	54	VAL	N-CA-C	6.33	117.25	108.89
4	04	347	VAL	N-CA-C	6.32	118.55	109.51
4	04	904	ALA	N-CA-C	-6.31	105.44	113.02
2	02	125	LYS	CA-C-N	6.30	125.99	119.56
2	02	125	LYS	C-N-CA	6.30	125.99	119.56
3	03	98	VAL	N-CA-C	6.30	117.20	108.89
10	H	111	ARG	N-CA-C	-6.29	104.66	112.90
18	P	7	ASN	N-CA-C	6.29	118.83	109.59
3	03	445	ILE	N-CA-C	6.28	117.78	110.62
3	03	1208	GLY	N-CA-C	-6.27	106.49	115.64
2	02	18	GLN	N-CA-C	6.27	119.62	109.40
3	03	193	ASN	N-CA-C	6.24	118.47	107.61
24	V	19	GLU	N-CA-C	-6.21	104.51	111.28
4	04	233	LYS	CA-C-N	6.21	127.60	119.84
4	04	233	LYS	C-N-CA	6.21	127.60	119.84
25	W	21	ALA	N-CA-C	-6.20	105.21	112.89
4	04	85	CYS	N-CA-C	-6.17	99.80	109.25
10	H	141	ASP	N-CA-C	-6.16	105.25	112.89
2	02	190	ALA	N-CA-C	-6.16	101.40	110.52
4	04	302	ALA	N-CA-C	-6.16	104.65	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	G	44	LYS	CA-C-N	6.16	127.53	119.84
9	G	44	LYS	C-N-CA	6.16	127.53	119.84
4	04	308	ASP	N-CA-C	-6.15	97.70	110.80
2	01	191	ARG	N-CA-C	6.15	118.80	108.23
7	E	213	TYR	N-CA-C	6.15	117.78	111.14
8	F	115	VAL	N-CA-C	-6.14	106.93	111.90
9	G	115	GLN	N-CA-C	-6.13	104.51	111.07
3	03	1103	VAL	N-CA-C	6.12	122.09	108.88
14	L	98	ARG	N-CA-C	-6.12	105.62	114.12
16	N	16	SER	N-CA-C	-6.11	106.46	114.04
4	04	396	ALA	N-CA-C	-6.11	104.53	112.23
3	03	1031	ALA	N-CA-C	-6.11	104.74	111.82
3	03	433	ILE	N-CA-C	-6.10	104.56	110.72
7	E	109	GLN	N-CA-C	-6.10	104.54	111.07
7	E	190	ASN	N-CA-C	-6.10	103.17	112.99
4	04	30	ILE	N-CA-C	-6.09	104.09	113.16
4	04	173	GLY	N-CA-C	-6.08	98.77	113.18
20	R	43	ALA	N-CA-C	-6.07	106.42	113.88
4	04	533	ALA	N-CA-C	-6.03	104.82	111.82
2	02	203	ILE	N-CA-C	6.02	116.28	107.37
10	H	117	ALA	N-CA-C	-6.02	104.84	111.82
3	03	212	ALA	N-CA-C	-6.02	104.65	112.23
17	O	43	LYS	N-CA-C	6.01	123.10	109.81
3	03	225	PHE	N-CA-C	6.01	119.46	109.96
4	04	265	LEU	N-CA-C	-6.01	104.64	111.07
20	R	6	ALA	N-CA-C	-6.00	105.20	113.18
13	K	67	GLY	N-CA-C	-5.97	103.66	114.46
4	04	31	ARG	N-CA-C	-5.96	105.96	113.18
14	L	95	SER	N-CA-C	-5.96	104.72	112.23
3	03	663	VAL	N-CA-C	5.95	116.13	110.42
3	03	224	PHE	N-CA-C	5.92	123.42	110.80
4	04	239	LEU	N-CA-C	5.92	118.92	110.10
7	E	143	LYS	N-CA-C	-5.91	105.56	112.89
4	04	608	CYS	N-CA-C	-5.91	105.56	112.89
14	L	87	MET	N-CA-C	-5.90	106.04	113.18
26	X	10	GLU	N-CA-C	5.88	122.81	109.81
20	R	46	LYS	N-CA-C	5.87	123.30	110.80
13	K	116	ARG	N-CA-C	-5.86	104.85	112.23
25	W	48	LYS	N-CA-C	-5.84	106.32	113.50
3	03	746	ALA	CB-CA-C	-5.84	109.83	116.54
7	E	189	THR	N-CA-C	5.83	120.21	111.81
7	E	14	VAL	N-CA-C	-5.83	108.17	113.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	03	165	HIS	N-CA-C	-5.83	106.30	113.41
14	L	48	ARG	N-CA-C	-5.83	106.33	113.50
2	01	86	LYS	N-CA-C	-5.82	106.13	113.18
3	03	1015	ALA	N-CA-C	-5.82	104.93	111.28
21	S	73	ALA	N-CA-C	-5.82	105.68	112.89
14	L	127	SER	N-CA-C	-5.82	100.23	109.59
4	04	1252	HIS	N-CA-C	-5.80	104.86	111.07
4	04	270	ARG	N-CA-C	-5.80	105.04	111.36
3	03	213	LEU	N-CA-C	-5.79	106.25	113.15
25	W	5	SER	N-CA-C	-5.79	105.32	112.38
7	E	200	ILE	CA-C-N	5.78	127.06	119.84
7	E	200	ILE	C-N-CA	5.78	127.06	119.84
17	O	79	ILE	N-CA-C	5.78	117.67	108.89
3	03	825	GLU	N-CA-C	-5.77	106.22	113.72
12	J	56	SER	N-CA-C	5.77	118.33	110.55
7	E	16	PHE	N-CA-C	5.76	123.08	110.80
16	N	61	ALA	N-CA-C	-5.76	104.97	112.23
4	04	1184	ASP	CA-C-N	5.75	127.03	119.84
4	04	1184	ASP	C-N-CA	5.75	127.03	119.84
7	E	47	VAL	CA-C-N	-5.75	113.89	119.87
7	E	47	VAL	C-N-CA	-5.75	113.89	119.87
3	03	317	LEU	N-CA-C	5.74	119.42	110.17
4	04	186	GLN	N-CA-C	-5.74	105.11	111.36
2	01	208	ASN	N-CA-C	-5.72	106.13	113.23
3	03	685	MET	N-CA-C	5.72	119.52	112.54
20	R	18	ALA	N-CA-C	-5.71	106.66	113.97
13	K	123	GLU	N-CA-C	5.69	117.50	108.67
3	03	1171	ARG	N-CA-C	-5.69	104.99	111.14
3	03	29	SER	N-CA-C	-5.69	105.84	112.89
12	J	122	GLU	N-CA-C	5.66	118.22	111.71
26	X	57	ALA	N-CA-C	-5.65	105.88	112.89
3	03	976	ARG	N-CA-C	-5.65	106.35	113.18
22	T	49	ASN	N-CA-C	-5.65	105.04	111.14
1	A	184	G	N9-C1'-C2'	5.64	120.47	112.00
10	H	101	GLY	N-CA-C	-5.63	105.93	115.34
18	P	4	ALA	N-CA-C	5.63	122.79	110.80
10	H	16	ALA	N-CA-C	5.62	117.85	107.73
23	U	29	LEU	N-CA-C	-5.62	105.92	112.89
3	03	198	ILE	N-CA-C	5.61	117.40	108.87
4	04	641	ILE	N-CA-C	5.60	116.24	110.36
9	G	68	GLU	N-CA-C	5.59	117.84	111.02
14	L	27	ILE	N-CA-C	5.59	115.71	107.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	03	574	SER	N-CA-C	5.59	118.36	110.14
4	04	667	GLN	N-CA-C	-5.59	105.34	111.82
3	03	51	ALA	N-CA-C	-5.58	105.59	112.90
4	04	655	SER	N-CA-C	-5.58	105.10	111.07
4	04	1232	TYR	N-CA-C	-5.57	105.12	111.14
2	01	224	LEU	N-CA-C	-5.57	105.21	112.23
4	04	1282	TYR	N-CA-C	-5.56	105.30	111.36
3	03	842	ASP	N-CA-C	5.56	122.64	110.80
19	Q	92	ILE	N-CA-C	5.54	114.38	108.95
5	05	9	ALA	N-CA-C	-5.53	105.26	112.23
9	G	21	LYS	N-CA-C	-5.53	105.15	113.89
4	04	838	ARG	N-CA-C	-5.53	105.33	112.68
4	04	1185	PRO	N-CA-C	5.52	123.83	112.47
2	01	215	GLU	N-CA-C	-5.51	104.50	111.11
4	04	874	GLU	N-CA-C	-5.51	105.68	112.90
10	H	146	MET	N-CA-C	5.51	117.94	109.07
3	03	26	TYR	N-CA-C	-5.51	101.90	110.10
3	03	31	GLN	N-CA-C	-5.50	106.24	113.12
7	E	68	LEU	N-CA-C	-5.50	101.23	109.15
10	H	116	VAL	N-CA-C	-5.50	105.59	113.07
8	F	160	GLU	N-CA-C	-5.50	106.61	113.38
23	U	71	THR	N-CA-C	-5.49	102.62	110.59
23	U	67	LEU	N-CA-C	-5.49	104.14	112.04
9	G	166	LYS	CA-C-N	5.48	126.69	119.84
9	G	166	LYS	C-N-CA	5.48	126.69	119.84
26	X	13	ASP	N-CA-C	-5.48	105.22	112.24
4	04	450	HIS	CA-C-N	5.48	126.69	119.84
4	04	450	HIS	C-N-CA	5.48	126.69	119.84
16	N	56	LYS	N-CA-C	-5.47	106.10	112.89
4	04	365	GLN	N-CA-C	5.47	117.39	109.07
26	X	29	LEU	N-CA-C	-5.47	105.23	111.14
5	05	56	GLU	N-CA-C	-5.46	105.40	111.36
8	F	30	ASP	N-CA-C	5.46	117.24	111.28
14	L	80	HIS	N-CA-C	-5.46	106.74	113.41
4	04	17	PHE	N-CA-C	-5.46	100.27	108.96
4	04	494	ALA	N-CA-C	-5.46	107.27	114.04
4	04	1340	LYS	N-CA-C	5.46	117.01	109.15
4	04	412	LEU	N-CA-C	-5.46	105.41	111.36
25	W	7	LYS	N-CA-C	5.45	122.42	110.80
3	03	325	LEU	N-CA-C	5.45	117.03	111.14
3	03	409	LEU	N-CA-C	-5.45	106.64	113.72
4	04	660	GLU	N-CA-C	5.45	117.64	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	03	1114	GLU	N-CA-C	-5.44	105.50	111.82
3	03	1155	VAL	N-CA-C	-5.44	100.54	108.97
9	G	94	GLU	N-CA-C	-5.44	106.15	112.89
23	U	55	LEU	N-CA-C	-5.42	105.27	111.07
8	F	86	LEU	N-CA-C	-5.42	105.53	111.82
23	U	18	VAL	N-CA-C	5.42	115.92	108.12
7	E	89	GLN	N-CA-C	5.40	117.66	110.53
14	L	123	ARG	N-CA-C	-5.39	102.87	110.31
9	G	23	GLY	N-CA-C	-5.39	100.41	113.18
4	04	227	PHE	N-CA-C	-5.38	105.58	111.82
26	X	20	LYS	N-CA-C	-5.38	105.33	111.14
4	04	32	SER	N-CA-C	-5.37	105.98	112.54
4	04	87	LYS	N-CA-C	-5.37	105.07	111.03
4	04	226	ALA	N-CA-C	-5.36	105.47	112.23
2	01	218	ARG	N-CA-C	-5.35	105.11	111.69
17	O	7	VAL	N-CA-C	-5.35	104.40	111.09
10	H	138	ALA	N-CA-C	-5.34	105.90	112.90
9	G	136	VAL	N-CA-C	5.34	115.89	108.84
3	03	377	THR	N-CA-C	-5.33	99.45	110.80
4	04	736	GLN	N-CA-C	-5.33	105.17	110.97
9	G	10	LEU	N-CA-C	-5.32	106.76	113.20
16	N	60	PHE	N-CA-C	-5.32	105.53	112.23
4	04	1017	VAL	N-CA-C	-5.32	105.24	113.16
17	O	32	VAL	N-CA-C	-5.31	105.12	112.50
4	04	336	GLY	N-CA-C	-5.31	106.79	111.67
9	G	176	LYS	N-CA-C	-5.30	106.66	113.02
16	N	68	ARG	N-CA-C	-5.30	106.08	112.54
3	03	1202	GLY	N-CA-C	-5.29	102.36	111.57
3	03	1163	THR	N-CA-C	-5.29	102.16	110.36
19	Q	47	LEU	N-CA-C	-5.29	106.66	113.01
25	W	52	GLU	N-CA-C	-5.29	106.33	114.16
4	04	285	LEU	N-CA-C	-5.29	106.33	112.89
4	04	817	HIS	N-CA-C	-5.29	103.74	111.30
20	R	14	PHE	N-CA-C	5.28	117.04	111.28
7	E	103	ASN	N-CA-C	-5.28	106.87	113.15
2	02	210	THR	N-CA-C	-5.28	106.87	113.15
12	J	73	GLU	N-CA-C	-5.28	98.67	107.80
3	03	191	LYS	N-CA-C	-5.27	106.82	113.20
4	04	754	ILE	N-CA-C	5.27	115.87	108.17
4	04	1341	ARG	N-CA-C	5.27	122.03	110.80
10	H	153	ALA	N-CA-C	-5.27	106.35	112.89
3	03	369	MET	N-CA-C	-5.27	106.35	112.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	03	498	ILE	N-CA-C	-5.27	107.63	111.90
8	F	73	GLY	N-CA-C	5.27	119.02	112.64
2	01	125	LYS	CA-C-N	5.26	126.42	119.84
2	01	125	LYS	C-N-CA	5.26	126.42	119.84
23	U	15	ALA	N-CA-C	-5.26	105.18	113.02
13	K	70	VAL	N-CA-C	-5.25	104.94	112.35
4	04	1060	VAL	N-CA-C	5.25	115.15	108.12
3	03	1147	ARG	N-CA-C	-5.24	105.26	110.97
14	L	96	GLU	N-CA-C	-5.24	105.74	111.82
2	01	232	VAL	N-CA-C	-5.23	105.70	113.39
4	04	203	GLU	N-CA-C	-5.23	105.47	111.07
17	O	26	CYS	CA-C-N	5.22	126.37	119.84
17	O	26	CYS	C-N-CA	5.22	126.37	119.84
13	K	4	ASP	CA-C-N	5.22	124.67	119.24
13	K	4	ASP	C-N-CA	5.22	124.67	119.24
2	02	117	HIS	N-CA-C	5.22	116.81	108.41
3	03	513	GLN	N-CA-C	5.21	117.80	110.14
4	04	1351	VAL	N-CA-C	-5.21	105.76	110.82
21	S	61	VAL	N-CA-C	-5.21	105.26	112.50
12	J	60	ALA	N-CA-C	-5.21	106.95	113.15
4	04	339	ARG	N-CA-C	-5.20	99.72	110.80
26	X	56	HIS	N-CA-C	-5.20	106.45	112.89
26	X	58	LYS	N-CA-C	-5.19	106.79	113.23
3	03	420	LEU	N-CA-C	5.19	117.75	109.96
9	G	46	ARG	N-CA-C	-5.18	107.98	114.56
18	P	10	ASP	N-CA-C	5.18	117.08	108.02
18	P	20	SER	N-CA-C	-5.17	106.12	112.90
2	01	65	LEU	N-CA-C	-5.17	107.14	113.50
3	03	3	TYR	N-CA-C	5.14	118.08	110.46
2	02	228	LEU	N-CA-C	-5.13	105.37	113.02
4	04	595	ALA	N-CA-C	-5.13	106.87	112.72
20	R	21	THR	N-CA-C	-5.13	104.29	110.44
13	K	126	CYS	N-CA-C	5.12	116.63	108.79
3	03	782	VAL	N-CA-C	5.12	117.05	109.17
3	03	465	ARG	N-CA-C	-5.12	105.89	111.82
19	Q	83	VAL	N-CA-C	-5.11	105.61	110.42
26	X	38	TYR	N-CA-C	5.11	121.69	110.80
4	04	539	SER	N-CA-C	-5.11	104.68	112.04
19	Q	42	ASN	N-CA-C	-5.11	105.79	111.36
8	F	15	LYS	N-CA-C	5.11	116.83	109.48
9	G	162	GLU	N-CA-C	-5.11	107.07	113.15
7	E	221	VAL	N-CA-C	-5.11	104.60	111.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	S	75	ILE	N-CA-C	-5.11	105.40	112.50
4	04	766	GLY	N-CA-C	5.10	119.07	112.54
19	Q	49	THR	N-CA-C	-5.10	106.32	112.54
3	03	428	VAL	N-CA-C	-5.10	104.72	111.09
13	K	115	ALA	N-CA-C	-5.10	106.91	113.23
3	03	738	GLU	N-CA-C	5.09	117.56	111.71
2	01	196	THR	N-CA-C	-5.09	105.65	111.14
13	K	90	GLU	N-CA-C	-5.08	106.77	113.17
3	03	972	PHE	N-CA-C	-5.08	105.83	112.23
3	03	672	GLU	N-CA-C	-5.07	107.12	113.15
3	03	526	HIS	N-CA-C	-5.07	106.19	112.93
10	H	54	GLU	CA-C-N	5.07	124.38	120.33
10	H	54	GLU	C-N-CA	5.07	124.38	120.33
4	04	1050	THR	N-CA-C	-5.06	100.53	108.63
7	E	62	SER	N-CA-C	-5.06	107.06	113.18
16	N	96	ILE	N-CA-C	-5.06	105.61	110.72
4	04	571	ASP	N-CA-C	-5.05	98.82	108.17
4	04	166	LEU	N-CA-C	-5.05	105.85	111.36
2	01	169	GLY	N-CA-C	-5.05	101.22	113.18
8	F	67	ILE	N-CA-C	5.05	115.31	107.28
4	04	852	GLY	N-CA-C	-5.04	102.28	111.15
9	G	39	GLN	N-CA-C	-5.04	106.82	113.12
10	H	110	MET	N-CA-C	-5.04	108.16	114.56
3	03	990	ASP	N-CA-C	-5.04	105.89	112.23
22	T	20	ILE	N-CA-C	5.03	116.20	108.71
8	F	71	ARG	CA-C-N	5.03	124.47	119.24
8	F	71	ARG	C-N-CA	5.03	124.47	119.24
3	03	492	MET	N-CA-C	-5.03	106.29	112.72
8	F	41	TYR	N-CA-C	-5.02	105.89	111.36
3	03	183	TRP	N-CA-C	5.02	116.80	110.33
4	04	843	VAL	N-CA-C	5.01	115.07	107.75
23	U	30	LYS	N-CA-C	-5.01	106.42	112.54
12	J	148	LYS	N-CA-C	5.01	117.14	109.62
2	01	183	ILE	N-CA-C	5.00	115.23	107.28

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	25	C	Sidechain
1	A	872	A	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	30955	0	15586	433	0
2	01	1753	0	1780	115	0
2	02	1757	0	1778	115	0
3	03	10272	0	10138	584	0
4	04	10372	0	10512	631	0
5	05	605	0	612	44	0
6	B	774	0	200	5	0
7	E	1705	0	1732	161	0
8	F	1625	0	1699	61	0
9	G	1643	0	1710	104	0
10	H	1157	0	1199	70	0
11	I	818	0	808	46	0
12	J	1182	0	1240	61	0
13	K	979	0	1034	36	0
14	L	1022	0	1070	66	0
15	M	787	0	828	45	0
16	N	870	0	878	63	0
17	O	955	0	1019	39	0
18	P	884	0	944	41	0
19	Q	805	0	847	49	0
20	R	714	0	737	29	0
21	S	649	0	666	25	0
22	T	649	0	691	30	0
23	U	536	0	552	22	0
24	V	638	0	665	51	0
25	W	665	0	714	55	0
26	X	545	0	579	37	0
All	All	75316	0	60218	2780	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 (2780) 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)
7:E:26:LYS:O	7:E:29:PRO:HD2	1.44	1.14
1:A:664:G:H5''	23:U:53:ARG:HH12	1.05	1.10
7:E:47:VAL:HB	7:E:48:PRO:HD3	1.37	1.05
7:E:19:GLN:H	7:E:40:ILE:HA	1.14	1.04
4:04:246:PRO:HD2	4:04:249:LEU:HD12	1.38	1.03
3:03:1082:ILE:H	3:03:1082:ILE:HD12	1.22	1.03
25:W:54:GLN:HA	25:W:57:VAL:HG12	1.36	1.02
4:04:744:ARG:HB3	4:04:759:ILE:HB	1.40	1.02
7:E:31:ILE:HG21	7:E:189:THR:HG21	1.36	1.02
9:G:121:ALA:HB1	9:G:148:ALA:HB2	1.43	1.01
3:03:194:LEU:HB2	3:03:346:TYR:HB3	1.43	1.00
4:04:120:LEU:HB3	4:04:121:PRO:HD3	1.45	0.98
4:04:661:VAL:HG11	4:04:686:TRP:HE1	1.29	0.96
3:03:241:LEU:HD21	3:03:277:LEU:HD13	1.42	0.96
3:03:886:LYS:HB3	3:03:917:SER:HA	1.47	0.96
4:04:290:ILE:H	4:04:290:ILE:HD12	1.32	0.94
7:E:120:GLN:HA	7:E:124:GLY:HA3	1.49	0.93
4:04:214:ARG:HA	4:04:217:LEU:HB2	1.49	0.92
18:P:22:TYR:HB3	18:P:65:GLU:HG2	1.51	0.92
15:M:57:VAL:HG22	15:M:58:ASN:H	1.35	0.91
14:L:105:ARG:HH11	14:L:107:ALA:HA	1.33	0.90
14:L:98:ARG:HH11	14:L:103:VAL:HB	1.37	0.90
4:04:1046:ILE:HD12	4:04:1059:LEU:HB3	1.53	0.90
5:05:27:ALA:HA	5:05:30:MET:HE3	1.54	0.90
21:S:4:ILE:HD12	21:S:67:ILE:HG12	1.52	0.89
10:H:35:LEU:HD22	10:H:133:ILE:HG12	1.54	0.89
3:03:1131:MET:HE1	3:03:1141:LEU:HB3	1.54	0.89
3:03:241:LEU:HD11	3:03:246:LEU:HD11	1.53	0.88
3:03:817:LEU:HD21	3:03:1080:ASN:HD22	1.38	0.88
2:02:100:LEU:HD21	2:02:121:VAL:HG11	1.54	0.87
1:A:1500:A:H4'	1:A:1508:A:H5''	1.55	0.86
4:04:363:LEU:HD21	4:04:618:VAL:HG12	1.56	0.86
7:E:87:CYS:HB2	7:E:89:GLN:HE22	1.38	0.86
15:M:12:ALA:HB2	15:M:96:VAL:HG22	1.57	0.86
15:M:32:THR:HG23	15:M:33:GLY:H	1.40	0.86
1:A:1014:A:H4'	24:V:13:HIS:HB2	1.56	0.86
9:G:13:ARG:HD2	9:G:37:PRO:HB2	1.58	0.86
15:M:70:HIS:HB3	15:M:72:ARG:HH12	1.38	0.85
1:A:1279:G:H5''	15:M:9:ARG:HH12	1.40	0.85
3:03:690:VAL:HG11	3:03:1234:LYS:HB3	1.59	0.85
4:04:614:LEU:HD23	5:05:7:GLN:HB2	1.59	0.85
4:04:909:ILE:HD11	4:04:913:GLU:HG2	1.58	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:831:A:H3'	1:A:832:G:H5''	1.58	0.85
7:E:21:ARG:H	7:E:38:VAL:HG12	1.42	0.85
4:04:1231:ARG:HA	4:04:1234:VAL:HG22	1.59	0.85
4:04:1138:LEU:HB3	4:04:1139:PRO:HD3	1.59	0.84
4:04:520:ALA:HB1	4:04:543:SER:HB3	1.60	0.84
3:03:409:LEU:HD21	3:03:428:VAL:HG22	1.60	0.84
4:04:19:ALA:HB3	4:04:1373:ARG:HG2	1.59	0.84
12:J:78:ARG:H	12:J:78:ARG:HD2	1.42	0.84
4:04:958:ILE:HG23	4:04:982:LEU:HD11	1.59	0.84
3:03:521:LEU:HG	3:03:686:GLN:HE21	1.41	0.83
14:L:24:ASN:ND2	14:L:25:GLY:H	1.75	0.83
3:03:588:GLU:HB3	3:03:605:TYR:HB3	1.59	0.83
14:L:24:ASN:HD22	14:L:25:GLY:H	1.24	0.83
3:03:459:MET:HA	3:03:462:ASN:HD22	1.41	0.83
1:A:131:A:H4'	25:W:69:ASN:HD21	1.43	0.83
4:04:747:MET:HB2	4:04:774:ILE:HG22	1.61	0.83
3:03:8:LYS:HG3	3:03:1168:GLU:HG3	1.59	0.83
13:K:28:SER:HB2	13:K:58:LEU:HB2	1.60	0.83
11:I:46:GLN:HA	11:I:56:LYS:HG2	1.60	0.83
2:01:45:ARG:HH21	3:03:1216:ARG:HA	1.42	0.82
3:03:808:ASN:HA	4:04:629:PHE:HB3	1.59	0.82
19:Q:40:ARG:HH11	24:V:6:LYS:HD2	1.43	0.82
2:01:13:LEU:HD23	2:01:13:LEU:H	1.45	0.82
7:E:31:ILE:HG21	7:E:189:THR:CG2	2.08	0.82
19:Q:72:PHE:HE1	19:Q:77:GLY:HA2	1.45	0.82
1:A:618:C:H42	1:A:622:A:H62	1.24	0.82
23:U:26:ILE:HA	23:U:29:LEU:HD23	1.60	0.82
1:A:179:A:H61	1:A:196:A:H62	1.29	0.81
1:A:664:G:H5''	23:U:53:ARG:NH1	1.91	0.81
3:03:1112:ILE:CG2	4:04:640:GLY:HA2	2.09	0.81
7:E:41:ILE:HG22	7:E:43:LEU:H	1.45	0.81
7:E:23:TRP:CE2	7:E:25:PRO:HG3	2.16	0.81
26:X:43:THR:O	26:X:46:LYS:HB2	1.81	0.81
16:N:93:GLU:HA	26:X:17:ARG:HH12	1.46	0.80
4:04:1290:ARG:HH11	4:04:1299:GLY:HA2	1.45	0.80
25:W:23:ARG:HB3	25:W:60:GLN:HE22	1.46	0.80
3:03:1258:PRO:HG2	4:04:346:ARG:HB2	1.62	0.80
3:03:802:VAL:HA	3:03:1096:ILE:HB	1.61	0.80
3:03:1211:ARG:HB2	3:03:1220:GLN:HG3	1.63	0.80
12:J:70:PRO:HG3	12:J:137:ARG:HG2	1.62	0.80
4:04:1286:LYS:O	4:04:1290:ARG:HG2	1.82	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:02:59:VAL:HG21	2:02:85:LEU:HD13	1.64	0.80
3:03:1012:GLU:HG2	3:03:1013:GLN:H	1.45	0.80
4:04:485:MET:HB3	4:04:488:ASN:HD22	1.47	0.80
4:04:425:ARG:HG2	4:04:427:PRO:HD2	1.64	0.80
9:G:123:MET:HG2	9:G:128:VAL:HA	1.63	0.80
1:A:1236:A:H4'	1:A:1304:G:H4'	1.64	0.80
3:03:796:LEU:H	3:03:796:LEU:HD12	1.47	0.80
22:T:16:MET:HG2	22:T:19:SER:HB2	1.62	0.79
3:03:463:GLN:HE21	3:03:505:PHE:HB2	1.46	0.79
3:03:1242:LYS:HD3	4:04:354:VAL:HG11	1.63	0.79
22:T:58:VAL:HG21	22:T:74:LEU:HD22	1.64	0.79
3:03:569:ILE:HG21	4:04:783:LEU:HD13	1.65	0.79
3:03:1164:PHE:O	3:03:1168:GLU:HB3	1.82	0.79
4:04:1172:LYS:HD3	4:04:1189:MET:HB3	1.64	0.79
19:Q:46:LYS:O	19:Q:50:LEU:HD13	1.83	0.79
1:A:981:U:H3'	1:A:982:U:H5''	1.65	0.78
1:A:1220:G:H4'	24:V:35:ARG:HB2	1.63	0.78
4:04:974:VAL:HG21	4:04:1118:GLY:HA3	1.66	0.78
3:03:557:ARG:HB2	3:03:587:LEU:HD13	1.66	0.78
4:04:288:PRO:HG2	4:04:291:ILE:HD12	1.65	0.78
7:E:38:VAL:O	7:E:39:HIS:HB2	1.82	0.78
4:04:587:LEU:HD12	4:04:588:PRO:HD2	1.66	0.78
24:V:62:THR:H	24:V:65:MET:HE3	1.48	0.78
1:A:427:U:H1'	1:A:541:G:H5''	1.64	0.78
4:04:502:PRO:HB2	4:04:507:VAL:HG22	1.66	0.78
7:E:30:PHE:HB3	7:E:45:LYS:HG3	1.66	0.78
9:G:103:ARG:HB3	9:G:167:PRO:HG2	1.65	0.78
2:02:35:PHE:HA	2:02:38:THR:HG22	1.64	0.77
1:A:92:U:H2'	1:A:93:U:H4'	1.66	0.77
3:03:519:ASN:ND2	3:03:521:LEU:HB3	1.99	0.77
16:N:109:ILE:HG22	26:X:20:LYS:NZ	2.00	0.77
9:G:101:VAL:O	9:G:104:MET:HB2	1.85	0.77
7:E:23:TRP:O	7:E:190:ASN:HB3	1.84	0.77
1:A:151:A:H62	1:A:170:U:H3	1.32	0.77
2:01:14:VAL:HG22	2:01:15:ASP:H	1.50	0.77
2:01:31:LEU:HB2	2:01:199:ASP:O	1.85	0.77
10:H:13:LYS:HG2	10:H:112:ALA:HB1	1.65	0.77
2:01:29:GLU:HB3	2:01:30:PRO:HD3	1.67	0.76
3:03:152:SER:HA	3:03:452:ARG:HB2	1.67	0.76
1:A:922:G:H4'	10:H:25:LYS:HB3	1.66	0.76
4:04:504:GLN:HA	4:04:730:ALA:HB1	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:98:ARG:NH1	14:L:103:VAL:HB	2.01	0.76
18:P:4:ALA:HB3	18:P:21:ILE:HD13	1.67	0.76
3:03:1211:ARG:H	3:03:1211:ARG:HD2	1.51	0.76
1:A:961:U:H3	1:A:1201:A:H61	1.34	0.75
3:03:478:ARG:HG2	3:03:492:MET:HG2	1.68	0.75
3:03:723:VAL:HG22	3:03:776:PRO:HG3	1.67	0.75
1:A:1259:C:H3'	1:A:1260:G:H5''	1.66	0.75
1:A:25:C:H41	1:A:558:G:N2	1.83	0.75
3:03:1333:LEU:HD21	4:04:307:LEU:HD21	1.66	0.75
3:03:204:LEU:HD13	3:03:208:ILE:HD13	1.68	0.75
4:04:845:ALA:HA	4:04:883:ARG:HG3	1.68	0.75
24:V:21:ALA:HB2	24:V:30:LEU:HD21	1.68	0.75
3:03:11:ILE:H	3:03:1172:LEU:HD11	1.51	0.75
7:E:39:HIS:O	7:E:40:ILE:HB	1.84	0.75
9:G:117:VAL:HG22	9:G:122:ILE:HD12	1.68	0.75
1:A:244:U:H4'	1:A:245:U:H5'	1.68	0.75
1:A:1252:A:H61	1:A:1285:A:H61	1.35	0.75
8:F:69:THR:HG21	8:F:75:VAL:HG21	1.67	0.74
3:03:807:TRP:H	3:03:811:ASN:HD21	1.35	0.74
3:03:1328:LYS:HE2	4:04:102:MET:HE2	1.66	0.74
3:03:557:ARG:HG3	3:03:558:VAL:HG23	1.70	0.74
5:05:63:ILE:H	5:05:63:ILE:HD12	1.51	0.74
1:A:782:A:H62	1:A:800:G:H21	1.35	0.74
4:04:279:LEU:HD13	4:04:299:LEU:HD22	1.70	0.74
2:01:46:ILE:HG13	2:01:224:LEU:HD21	1.68	0.74
9:G:94:GLU:HG2	9:G:185:PRO:HG3	1.69	0.74
12:J:72:VAL:HG21	12:J:144:ALA:HB2	1.70	0.74
2:01:211:ILE:HG21	2:01:219:ARG:HH22	1.52	0.74
3:03:295:LYS:O	3:03:316:GLU:HA	1.88	0.73
4:04:736:GLN:HA	4:04:739:GLN:NE2	2.02	0.73
7:E:31:ILE:HG22	7:E:42:ASN:ND2	2.03	0.73
16:N:30:ILE:HA	16:N:45:THR:HG22	1.70	0.73
3:03:671:LEU:HD12	3:03:674:ASP:HB2	1.71	0.73
4:04:204:GLU:HA	4:04:207:GLU:HB2	1.70	0.73
4:04:526:VAL:HG12	4:04:549:LYS:HB2	1.69	0.73
7:E:11:LYS:O	7:E:14:VAL:HG22	1.89	0.73
3:03:1320:PRO:HB2	3:03:1323:PHE:HB2	1.71	0.73
4:04:11:GLN:HG3	4:04:13:LYS:H	1.54	0.72
2:02:12:ARG:HG2	2:02:13:LEU:H	1.52	0.72
3:03:1024:GLU:O	3:03:1028:LYS:HG2	1.88	0.72
4:04:483:LEU:HD13	5:05:17:PHE:HE1	1.55	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:849:LEU:HD23	4:04:849:LEU:H	1.54	0.72
24:V:14:LEU:O	24:V:18:VAL:HG23	1.88	0.72
7:E:186:ILE:HG13	7:E:200:ILE:O	1.90	0.72
26:X:14:VAL:HG13	26:X:16:LEU:HG	1.71	0.72
2:01:51:MET:HE1	2:01:216:ALA:HB1	1.70	0.72
3:03:1285:TYR:HB2	4:04:1356:LEU:HD21	1.71	0.72
16:N:109:ILE:HG22	26:X:20:LYS:HZ1	1.53	0.72
21:S:61:VAL:HA	21:S:65:ALA:HB3	1.70	0.72
4:04:763:PHE:HA	4:04:767:LEU:HD11	1.70	0.72
18:P:32:ILE:HG23	18:P:58:GLU:HB3	1.70	0.72
3:03:213:LEU:HD13	3:03:422:LYS:HE3	1.70	0.72
4:04:220:ARG:NH1	4:04:224:LEU:HD11	2.05	0.72
7:E:47:VAL:HB	7:E:48:PRO:CD	2.18	0.72
4:04:268:LEU:O	4:04:272:VAL:HG23	1.90	0.72
8:F:57:GLU:HB2	8:F:64:ARG:HB3	1.70	0.71
2:02:194:GLN:HG3	4:04:406:ALA:HB2	1.71	0.71
3:03:667:LEU:HD23	3:03:702:THR:HG22	1.72	0.71
9:G:57:LYS:HD3	9:G:202:LEU:HD21	1.71	0.71
1:A:701:U:H5''	1:A:703:G:H1'	1.72	0.71
4:04:1249:ASN:ND2	4:04:1251:LYS:HB2	2.04	0.71
3:03:971:LEU:HD12	3:03:1021:LEU:HD11	1.71	0.71
4:04:418:GLU:HG3	5:05:44:ASP:HA	1.73	0.71
10:H:148:SER:H	10:H:151:MET:HB3	1.55	0.71
2:02:192:VAL:HB	2:02:195:ARG:HB2	1.70	0.71
3:03:591:TYR:HD2	3:03:606:LEU:HD13	1.54	0.71
3:03:1062:PRO:HG3	3:03:1079:ILE:HG22	1.71	0.71
9:G:190:LEU:HD23	9:G:190:LEU:H	1.53	0.71
3:03:30:ILE:H	3:03:30:ILE:HD12	1.56	0.71
21:S:4:ILE:HG12	21:S:21:VAL:HG22	1.73	0.71
3:03:26:TYR:HB3	3:03:29:SER:OG	1.90	0.71
3:03:91:THR:HG21	3:03:503:LYS:NZ	2.06	0.71
10:H:131:ASN:HB3	10:H:134:ASN:HB2	1.73	0.71
19:Q:92:ILE:H	19:Q:92:ILE:HD12	1.53	0.71
4:04:356:THR:HG23	4:04:448:GLN:HG2	1.73	0.70
4:04:1024:THR:HG22	4:04:1026:PRO:HD3	1.73	0.70
12:J:28:ILE:HG22	12:J:104:VAL:HG21	1.73	0.70
2:01:211:ILE:HG21	2:01:219:ARG:NH2	2.06	0.70
4:04:84:ILE:HG12	7:E:74:ARG:HG2	1.73	0.70
3:03:255:ILE:HB	3:03:263:VAL:HB	1.71	0.70
3:03:359:ARG:O	3:03:363:LEU:HG	1.89	0.70
3:03:842:ASP:HA	3:03:847:PRO:HA	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:1151:LEU:HB2	3:03:1198:LEU:HD21	1.73	0.70
7:E:47:VAL:CB	7:E:48:PRO:HD3	2.20	0.70
9:G:113:ALA:O	9:G:117:VAL:HG23	1.91	0.70
1:A:1502:A:H8	1:A:1505:G:H22	1.40	0.70
4:04:60:ARG:HG3	4:04:88:CYS:HB3	1.72	0.70
4:04:1046:ILE:HG22	4:04:1061:VAL:HA	1.73	0.70
1:A:770:C:H1'	1:A:900:A:H2	1.55	0.70
3:03:561:ILE:HG22	3:03:683:ALA:HB2	1.73	0.70
4:04:712:GLN:HG3	4:04:713:GLU:H	1.56	0.70
2:01:195:ARG:HG2	2:01:198:LEU:HG	1.73	0.70
2:02:133:LEU:HD11	2:02:138:ALA:HB1	1.73	0.70
3:03:176:ILE:HD12	3:03:184:LEU:HD23	1.73	0.70
10:H:85:LYS:HG2	10:H:94:PHE:HD1	1.57	0.70
21:S:20:VAL:HG12	21:S:35:ARG:HB3	1.74	0.70
2:01:185:TYR:HB2	2:01:201:LEU:HD11	1.74	0.70
15:M:70:HIS:HB3	15:M:72:ARG:NH1	2.07	0.69
1:A:668:G:H4'	20:R:47:LYS:HB2	1.73	0.69
8:F:113:LYS:HD3	8:F:184:ASN:HD22	1.58	0.69
1:A:78:A:H2'	1:A:79:G:H4'	1.73	0.69
1:A:889:A:H61	1:A:907:A:H3'	1.56	0.69
3:03:402:ARG:NH1	3:03:406:ASN:HD21	1.90	0.69
3:03:402:ARG:HH11	3:03:406:ASN:HD21	1.41	0.69
4:04:646:ILE:HG12	4:04:764:ARG:HH11	1.57	0.69
11:I:5:GLU:HA	11:I:63:ASN:HA	1.74	0.69
1:A:1108:G:H5'	8:F:175:HIS:HD2	1.56	0.69
3:03:1101:LEU:H	3:03:1101:LEU:HD12	1.56	0.69
4:04:552:ILE:HD12	4:04:552:ILE:O	1.93	0.69
1:A:1280:A:O2'	1:A:1281:C:H5'	1.92	0.69
2:02:172:LEU:HD23	2:02:172:LEU:H	1.57	0.69
8:F:18:ASN:HA	8:F:55:VAL:HG12	1.74	0.69
9:G:7:LYS:HE3	9:G:20:LEU:HD22	1.73	0.69
4:04:510:LEU:HD21	4:04:624:ILE:HG23	1.74	0.69
7:E:40:ILE:HG23	7:E:41:ILE:HG13	1.73	0.69
11:I:47:LEU:HG	11:I:57:ALA:H	1.56	0.69
1:A:410:G:H21	1:A:432:A:H62	1.40	0.69
2:02:23:HIS:HB3	2:02:206:GLU:HG2	1.73	0.69
4:04:187:ALA:HA	4:04:190:LYS:HZ2	1.58	0.69
16:N:51:PHE:O	16:N:56:LYS:HG3	1.93	0.69
18:P:16:ILE:HD12	18:P:16:ILE:H	1.57	0.69
26:X:40:LYS:HB3	26:X:41:PRO:HD3	1.74	0.69
1:A:414:A:H62	1:A:430:A:H61	1.41	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:35:ILE:HG12	13:K:109:VAL:HG11	1.74	0.69
3:03:10:ARG:HD3	3:03:1181:PRO:HG2	1.74	0.69
4:04:21:LYS:HB3	4:04:1373:ARG:HH21	1.58	0.69
4:04:381:ILE:HD11	4:04:412:LEU:HD13	1.75	0.69
4:04:798:ARG:O	4:04:801:VAL:HG22	1.93	0.69
5:05:58:LEU:HD23	5:05:58:LEU:H	1.57	0.69
4:04:1252:HIS:O	4:04:1255:VAL:HG22	1.92	0.68
1:A:688:G:H5'	16:N:48:GLY:HA2	1.76	0.68
4:04:1282:TYR:O	4:04:1285:VAL:HG12	1.93	0.68
11:I:47:LEU:HD21	11:I:57:ALA:HB3	1.75	0.68
18:P:5:GLY:O	18:P:6:ILE:HG23	1.93	0.68
22:T:16:MET:HG3	22:T:17:GLU:H	1.58	0.68
1:A:664:G:C5'	23:U:53:ARG:HH12	1.94	0.68
4:04:1040:MET:HE3	4:04:1076:PRO:HB2	1.75	0.68
4:04:615:LYS:HB2	4:04:616:PRO:HD3	1.75	0.68
18:P:4:ALA:HB3	18:P:21:ILE:HG21	1.75	0.68
2:01:50:SER:HB3	2:01:223:ILE:HD13	1.75	0.68
4:04:1344:LEU:HD11	4:04:1353:VAL:HG11	1.75	0.68
1:A:884:U:H4'	1:A:885:G:H5''	1.74	0.68
2:02:52:PRO:HG3	2:02:150:ARG:HG2	1.75	0.68
19:Q:40:ARG:NH1	24:V:6:LYS:HD2	2.09	0.68
3:03:1063:GLY:H	3:03:1076:ILE:HG23	1.57	0.68
2:02:208:ASN:HD21	2:02:210:THR:HG23	1.59	0.68
1:A:1205:U:O2'	8:F:193:GLY:HA2	1.93	0.68
2:02:12:ARG:HB3	2:02:13:LEU:HD23	1.75	0.68
3:03:846:GLY:HA3	3:03:889:PRO:HG2	1.76	0.68
4:04:102:MET:HE3	4:04:246:PRO:HG3	1.75	0.68
4:04:598:LYS:O	4:04:601:ILE:HG22	1.94	0.68
16:N:85:VAL:HG21	16:N:96:ILE:HD11	1.76	0.68
3:03:296:VAL:HG12	3:03:316:GLU:HG3	1.75	0.68
3:03:1326:LEU:HB2	4:04:331:ILE:HG21	1.76	0.68
4:04:426:ALA:HB3	4:04:427:PRO:HD3	1.76	0.67
4:04:799:ARG:HD2	4:04:1309:ILE:HD12	1.75	0.67
7:E:23:TRP:CH2	7:E:25:PRO:HB3	2.29	0.67
7:E:161:LEU:HD13	7:E:181:ILE:HD12	1.74	0.67
1:A:920:U:H2'	1:A:921:U:C6	2.29	0.67
3:03:1320:PRO:O	3:03:1322:SER:N	2.26	0.67
22:T:45:VAL:HG21	22:T:60:ILE:HD13	1.77	0.67
3:03:1246:ARG:C	3:03:1246:ARG:HD3	2.19	0.67
4:04:501:VAL:HG23	4:04:602:SER:HB2	1.76	0.67
7:E:21:ARG:C	7:E:23:TRP:H	2.01	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:76:ASN:HD22	10:H:79:THR:CG2	2.08	0.67
1:A:8:A:N3	10:H:107:GLY:HA2	2.08	0.67
1:A:577:G:H1'	1:A:816:A:H2'	1.75	0.67
2:02:166:ARG:HB2	2:02:167:PRO:HD3	1.77	0.67
4:04:736:GLN:O	4:04:739:GLN:HG2	1.95	0.67
4:04:1290:ARG:NH1	4:04:1299:GLY:HA2	2.09	0.67
1:A:9:G:N2	1:A:10:A:C4	2.62	0.67
7:E:19:GLN:N	7:E:40:ILE:HA	1.99	0.67
4:04:349:TYR:HB3	4:04:470:VAL:HB	1.77	0.67
15:M:32:THR:HG23	15:M:33:GLY:N	2.08	0.67
1:A:245:U:H3	1:A:283:U:H3	1.41	0.67
1:A:632:U:H3'	1:A:633:G:H5'	1.76	0.67
2:01:66:HIS:HA	2:01:171:LEU:HD11	1.76	0.67
2:02:14:VAL:HG23	2:02:26:VAL:HG13	1.77	0.67
2:02:107:ILE:HG12	2:02:135:ASP:HA	1.75	0.67
3:03:431:LYS:O	3:03:435:ILE:HG13	1.95	0.67
3:03:564:PRO:HD2	3:03:572:ILE:HG21	1.75	0.67
4:04:502:PRO:HB3	4:04:506:VAL:HG13	1.77	0.67
8:F:163:ARG:H	8:F:163:ARG:HD3	1.60	0.67
25:W:79:THR:HA	25:W:82:ILE:HG12	1.77	0.67
2:02:80:GLU:HG2	4:04:569:LEU:HD21	1.77	0.67
7:E:157:LEU:HD23	7:E:157:LEU:H	1.60	0.67
1:A:626:G:H2'	1:A:627:G:H8	1.60	0.66
4:04:20:ILE:O	4:04:1343:GLU:HA	1.95	0.66
22:T:67:SER:H	22:T:70:LYS:HB3	1.59	0.66
3:03:1138:VAL:O	3:03:1142:ARG:HG3	1.95	0.66
4:04:189:LEU:HD22	4:04:234:PRO:HB3	1.77	0.66
1:A:778:G:H21	16:N:121:ARG:HD3	1.59	0.66
3:03:103:VAL:HG12	3:03:116:ASP:HA	1.77	0.66
4:04:749:LYS:HD3	4:04:753:SER:HB2	1.76	0.66
4:04:1249:ASN:HD21	4:04:1251:LYS:HE2	1.59	0.66
13:K:29:SER:HB3	13:K:32:LYS:HZ3	1.60	0.66
19:Q:48:GLN:HB3	24:V:12:LEU:HD22	1.76	0.66
3:03:193:ASN:HB3	3:03:195:PHE:CE2	2.30	0.66
4:04:811:GLU:HA	4:04:911:LYS:HE2	1.76	0.66
10:H:82:HIS:CD2	13:K:98:LEU:HD22	2.30	0.66
1:A:107:G:H2'	1:A:108:G:H5'	1.77	0.66
4:04:64:PRO:HG2	4:04:93:THR:H	1.61	0.66
9:G:100:VAL:O	9:G:104:MET:HG2	1.96	0.66
9:G:116:LEU:O	9:G:121:ALA:HB3	1.94	0.66
1:A:767:A:H4'	1:A:1524:C:O2'	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:296:VAL:CG1	3:03:316:GLU:HG3	2.26	0.66
3:03:557:ARG:NH1	3:03:608:ALA:HB2	2.09	0.66
4:04:800:LEU:O	4:04:803:VAL:HG12	1.96	0.66
25:W:56:ILE:HD12	25:W:56:ILE:N	2.10	0.66
3:03:817:LEU:HD21	3:03:1080:ASN:ND2	2.09	0.66
4:04:347:VAL:HG23	4:04:350:SER:HB2	1.77	0.66
4:04:773:PHE:HA	4:04:776:THR:OG1	1.94	0.66
4:04:1028:ILE:HB	4:04:1118:GLY:HA2	1.77	0.66
4:04:363:LEU:HD21	4:04:618:VAL:CG1	2.24	0.66
4:04:694:SER:C	4:04:696:ALA:H	2.04	0.66
14:L:91:GLU:HA	14:L:94:ARG:HB2	1.76	0.66
26:X:10:GLU:H	26:X:11:PRO:HD2	1.60	0.66
1:A:516:U:H5	1:A:533:A:H62	1.42	0.66
1:A:1299:A:H2'	1:A:1300:G:H4'	1.77	0.66
3:03:1090:ASN:HD22	3:03:1092:THR:HG23	1.61	0.65
4:04:698:MET:O	4:04:702:GLN:HB2	1.96	0.65
17:O:118:VAL:HG12	17:O:119:LYS:H	1.61	0.65
22:T:15:LYS:HB2	22:T:15:LYS:NZ	2.11	0.65
1:A:65:A:H4'	1:A:66:A:H5'	1.78	0.65
4:04:706:VAL:HG12	4:04:715:LYS:HB3	1.77	0.65
14:L:24:ASN:ND2	14:L:25:GLY:N	2.43	0.65
19:Q:26:LEU:HD22	19:Q:43:ALA:HA	1.76	0.65
1:A:194:C:H4'	25:W:59:ARG:HD2	1.78	0.65
1:A:552:U:H2'	1:A:553:A:H8	1.61	0.65
3:03:139:ASN:H	3:03:143:ARG:NH1	1.93	0.65
4:04:1037:PHE:HB3	4:04:1040:MET:HB2	1.78	0.65
4:04:1368:ASP:HB3	4:04:1372:ARG:HH12	1.61	0.65
19:Q:23:ARG:HB3	19:Q:50:LEU:HD21	1.77	0.65
3:03:149:LEU:HD11	3:03:451:ARG:HB3	1.78	0.65
4:04:361:LEU:HD11	4:04:448:GLN:HB3	1.79	0.65
7:E:33:GLY:HA3	7:E:41:ILE:O	1.96	0.65
20:R:69:LEU:HD11	20:R:76:ARG:HD2	1.79	0.65
3:03:1271:GLY:O	3:03:1275:VAL:HG23	1.96	0.65
4:04:926:PRO:HG2	4:04:1248:ILE:HD11	1.77	0.65
7:E:130:THR:HG22	7:E:132:LYS:H	1.61	0.65
14:L:24:ASN:HD22	14:L:25:GLY:N	1.94	0.65
3:03:246:LEU:HD23	3:03:249:GLU:OE1	1.97	0.65
1:A:1158:C:H5''	7:E:132:LYS:HD3	1.79	0.65
5:05:23:ALA:HB1	5:05:50:ALA:HB1	1.78	0.65
1:A:502:A:OP1	17:O:112:ALA:HA	1.97	0.65
4:04:749:LYS:HB3	4:04:755:ILE:HG13	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:96:GLN:NE2	10:H:97:PRO:HD2	2.12	0.65
19:Q:68:ARG:HH22	19:Q:80:ARG:NH2	1.95	0.65
9:G:77:GLU:O	9:G:81:LEU:HG	1.97	0.64
1:A:363:A:H5'	17:O:30:ARG:HB2	1.77	0.64
7:E:151:ILE:HG13	7:E:154:MET:HE2	1.79	0.64
2:O1:102:LEU:O	2:O1:141:SER:HA	1.97	0.64
3:O3:420:LEU:HB3	3:O3:425:ILE:HD11	1.79	0.64
3:O3:471:VAL:HG21	3:O3:493:ILE:HD12	1.77	0.64
4:O4:591:ILE:HG13	4:O4:604:MET:HE2	1.78	0.64
7:E:26:LYS:O	7:E:29:PRO:CD	2.36	0.64
22:T:24:ILE:H	22:T:24:ILE:HD12	1.62	0.64
3:O3:471:VAL:O	3:O3:475:VAL:HG23	1.98	0.64
3:O3:1313:HIS:HD2	5:O5:31:GLN:HE22	1.45	0.64
8:F:13:ILE:HG22	8:F:14:VAL:HG23	1.78	0.64
14:L:105:ARG:O	14:L:105:ARG:HD3	1.97	0.64
1:A:1158:C:H2'	1:A:1159:U:H4'	1.79	0.64
4:O4:98:ARG:HA	4:O4:101:ARG:HG2	1.80	0.64
24:V:15:LEU:O	24:V:19:GLU:HG2	1.97	0.64
2:O1:100:LEU:HD21	2:O1:121:VAL:HG11	1.80	0.64
3:O3:232:ILE:HG12	3:O3:237:LEU:HD23	1.79	0.64
3:O3:704:MET:O	3:O3:708:VAL:HG23	1.98	0.64
3:O3:1123:GLY:HA3	3:O3:1204:LEU:HD11	1.80	0.64
7:E:80:VAL:HG12	7:E:91:PHE:HB2	1.79	0.64
7:E:23:TRP:HE3	7:E:189:THR:HG1	1.46	0.64
1:A:105:G:H22	1:A:379:C:H4'	1.63	0.64
3:O3:1305:TYR:O	3:O3:1309:VAL:HG13	1.98	0.64
7:E:76:ALA:O	7:E:80:VAL:HG23	1.96	0.64
17:O:83:GLY:HA2	17:O:94:TYR:HD1	1.63	0.64
3:O3:890:LYS:HG2	3:O3:891:GLY:N	2.13	0.63
22:T:35:LYS:NZ	22:T:35:LYS:HB3	2.12	0.63
2:O2:95:LYS:HD3	2:O2:98:VAL:HB	1.80	0.63
3:O3:137:VAL:HG22	3:O3:142:GLU:HG2	1.78	0.63
4:O4:800:LEU:HD23	4:O4:920:ALA:HA	1.80	0.63
21:S:35:ARG:O	21:S:35:ARG:HD3	1.98	0.63
2:O1:91:ARG:HB2	2:O1:122:GLU:HB3	1.79	0.63
3:O3:1132:LEU:HD11	3:O3:1174:GLU:HG2	1.80	0.63
18:P:18:LEU:HD12	18:P:29:SER:OG	1.98	0.63
2:O2:30:PRO:C	2:O2:31:LEU:HD22	2.23	0.63
3:O3:488:MET:O	3:O3:491:ASP:HB2	1.99	0.63
4:O4:120:LEU:HB3	4:O4:121:PRO:CD	2.26	0.63
4:O4:531:LYS:HG2	4:O4:581:MET:HE3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:1112:ILE:O	4:04:641:ILE:HG12	1.99	0.63
4:04:97:VAL:HB	4:04:101:ARG:HH12	1.64	0.63
1:A:244:U:C4'	1:A:245:U:H5'	2.29	0.63
2:01:11:PRO:HA	2:01:30:PRO:HB2	1.81	0.63
2:01:113:ALA:HB2	2:01:126:PRO:HB3	1.80	0.63
2:02:33:ARG:H	2:02:33:ARG:HD3	1.63	0.63
4:04:1159:ILE:HG21	4:04:1179:PRO:HG3	1.79	0.63
13:K:50:VAL:O	13:K:50:VAL:HG22	1.99	0.63
1:A:553:A:H1'	17:O:27:PRO:HA	1.79	0.63
1:A:1128:C:O2'	1:A:1129:C:H5'	1.99	0.63
4:04:304:ASP:HB3	4:04:309:ASN:C	2.24	0.63
4:04:797:THR:HG22	4:04:924:GLY:HA3	1.79	0.63
2:02:12:ARG:C	2:02:13:LEU:HD23	2.23	0.63
4:04:1159:ILE:HG13	4:04:1160:SER:N	2.14	0.63
4:04:1264:ALA:HB2	4:04:1280:VAL:HG22	1.81	0.63
5:05:44:ASP:HB3	5:05:48:VAL:HB	1.81	0.63
8:F:127:VAL:HG22	8:F:128:MET:H	1.64	0.63
4:04:405:GLU:O	4:04:408:VAL:HG22	1.97	0.62
10:H:82:HIS:HD2	13:K:98:LEU:HD22	1.64	0.62
13:K:113:ARG:HA	13:K:116:ARG:NH1	2.14	0.62
2:01:31:LEU:HD13	2:01:36:GLY:HA3	1.81	0.62
3:03:1247:SER:HB2	4:04:349:TYR:H	1.64	0.62
4:04:865:HIS:HE1	4:04:867:GLN:HB2	1.64	0.62
4:04:1140:ARG:O	4:04:1144:LEU:HG	1.99	0.62
4:04:1231:ARG:HG2	4:04:1231:ARG:HH11	1.64	0.62
10:H:80:LEU:HG	10:H:81:GLN:H	1.64	0.62
20:R:48:ASP:HB3	20:R:51:SER:HB2	1.81	0.62
24:V:14:LEU:HD13	24:V:34:SER:HB3	1.81	0.62
4:04:525:MET:HE2	4:04:527:LEU:HD11	1.82	0.62
10:H:51:LYS:HE2	10:H:61:LYS:NZ	2.14	0.62
10:H:131:ASN:HB3	10:H:134:ASN:HD22	1.65	0.62
21:S:14:ARG:HE	21:S:42:ILE:HD12	1.65	0.62
2:01:26:VAL:HG22	2:01:203:ILE:HB	1.80	0.62
4:04:736:GLN:HA	4:04:739:GLN:HE21	1.65	0.62
4:04:1302:TYR:HE2	4:04:1304:ARG:HE	1.47	0.62
7:E:125:THR:HB	7:E:128:LYS:HB2	1.80	0.62
23:U:30:LYS:NZ	23:U:30:LYS:HB3	2.13	0.62
2:02:31:LEU:HD12	2:02:35:PHE:HB3	1.81	0.62
3:03:81:ASP:OD2	3:03:83:GLN:HB2	2.00	0.62
4:04:744:ARG:HD3	4:04:759:ILE:HG13	1.82	0.62
4:04:923:ILE:HG12	4:04:1248:ILE:HG21	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:X:10:GLU:HG3	26:X:11:PRO:HD3	1.81	0.62
3:03:97:ARG:HB3	3:03:121:GLU:HA	1.81	0.62
3:03:452:ARG:HG3	3:03:585:GLY:HA3	1.80	0.62
3:03:463:GLN:NE2	3:03:505:PHE:HB2	2.14	0.62
4:04:472:LEU:HD23	4:04:472:LEU:H	1.65	0.62
1:A:625:U:H2'	1:A:626:G:H8	1.64	0.62
1:A:656:G:N2	20:R:27:GLN:HE22	1.98	0.62
4:04:693:VAL:HG21	4:04:743:MET:HE3	1.80	0.62
7:E:104:TRP:O	7:E:108:ARG:HG3	2.00	0.62
11:I:47:LEU:HD11	11:I:57:ALA:HB2	1.81	0.62
22:T:16:MET:HG3	22:T:17:GLU:N	2.14	0.62
2:01:16:ILE:HG12	2:01:26:VAL:HG12	1.82	0.62
3:03:230:PHE:HB2	3:03:333:ILE:HB	1.81	0.62
3:03:1108:ASN:O	3:03:1111:GLN:HG2	2.00	0.62
4:04:187:ALA:HA	4:04:190:LYS:NZ	2.14	0.62
4:04:485:MET:CB	4:04:488:ASN:HD22	2.12	0.62
4:04:1240:VAL:O	4:04:1244:GLN:HG2	2.00	0.62
14:L:18:VAL:HG12	14:L:20:ILE:HG13	1.82	0.62
14:L:20:ILE:HG21	14:L:60:LEU:HD22	1.82	0.62
18:P:16:ILE:HD12	18:P:16:ILE:N	2.15	0.62
3:03:798:GLN:HB3	3:03:827:ARG:HH21	1.65	0.62
3:03:842:ASP:H	3:03:848:GLU:H	1.46	0.62
4:04:430:HIS:CD2	4:04:432:LEU:HB2	2.34	0.62
4:04:473:THR:HG23	4:04:476:ALA:H	1.64	0.62
4:04:600:ALA:HA	4:04:603:LYS:HE2	1.80	0.62
4:04:925:GLU:HB3	4:04:926:PRO:HD3	1.80	0.62
17:O:73:LEU:HD21	17:O:79:ILE:HG21	1.81	0.62
2:01:168:ILE:HD12	3:03:875:ALA:HA	1.80	0.61
2:02:190:ALA:HB2	2:02:200:LYS:HB2	1.82	0.61
3:03:102:LEU:HD22	3:03:489:PRO:HD3	1.82	0.61
3:03:668:ILE:HD13	3:03:1069:ARG:HB3	1.81	0.61
7:E:11:LYS:HG2	7:E:212:LEU:CD2	2.29	0.61
3:03:767:GLN:HB3	3:03:784:ALA:HB1	1.80	0.61
26:X:19:PHE:HA	26:X:22:SER:HB2	1.82	0.61
4:04:114:ILE:HG12	4:04:300:GLN:HG2	1.82	0.61
13:K:91:LEU:HD12	13:K:92:PRO:HD2	1.81	0.61
1:A:39:G:H2'	1:A:40:C:H5''	1.83	0.61
1:A:1379:G:O2'	1:A:1380:U:H5'	2.00	0.61
3:03:810:TYR:HB3	3:03:817:LEU:HD23	1.83	0.61
4:04:536:LEU:HD11	4:04:542:ALA:HB3	1.81	0.61
4:04:588:PRO:O	4:04:591:ILE:HG22	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:87:CYS:HB2	7:E:89:GLN:NE2	2.12	0.61
9:G:12:ARG:HG2	9:G:33:ILE:HD12	1.81	0.61
9:G:98:ASP:HB3	9:G:132:ALA:HB1	1.80	0.61
11:I:29:ILE:HG22	11:I:34:GLY:HA3	1.82	0.61
4:04:799:ARG:HD2	4:04:1309:ILE:CD1	2.30	0.61
4:04:850:LYS:HB3	4:04:851:PRO:HD2	1.82	0.61
9:G:201:GLU:HA	9:G:204:SER:HB3	1.82	0.61
3:03:402:ARG:HG3	3:03:406:ASN:HD22	1.64	0.61
10:H:22:LYS:HD3	10:H:24:VAL:HG12	1.83	0.61
25:W:23:ARG:HB3	25:W:60:GLN:NE2	2.16	0.61
1:A:454:G:H2'	1:A:455:G:C8	2.36	0.61
2:02:102:LEU:HB3	2:02:142:MET:HG2	1.82	0.61
20:R:27:GLN:O	20:R:31:LEU:HG	2.01	0.61
3:03:525:THR:HG21	3:03:687:ARG:HG2	1.81	0.61
3:03:724:VAL:HG12	3:03:734:ILE:CD1	2.31	0.61
4:04:21:LYS:HD2	4:04:21:LYS:C	2.26	0.61
14:L:114:LYS:HB2	14:L:117:LEU:HD12	1.83	0.61
1:A:1175:G:H2'	1:A:1176:A:H8	1.66	0.60
2:01:102:LEU:HD23	2:01:115:ILE:HG12	1.83	0.60
2:02:78:ILE:HA	2:02:81:ILE:HD12	1.83	0.60
3:03:530:ILE:HB	3:03:574:SER:HA	1.82	0.60
3:03:1028:LYS:O	3:03:1032:LYS:HD3	2.00	0.60
3:03:1319:MET:C	3:03:1321:GLU:H	2.08	0.60
4:04:393:THR:HG23	4:04:396:ALA:H	1.66	0.60
4:04:1249:ASN:HB3	4:04:1252:HIS:CD2	2.36	0.60
8:F:112:ALA:HB1	8:F:199:VAL:HG13	1.83	0.60
20:R:61:GLN:O	20:R:65:LEU:HD13	2.01	0.60
3:03:1141:LEU:O	3:03:1145:ILE:HG12	2.01	0.60
3:03:1261:GLY:HA2	4:04:346:ARG:HH22	1.65	0.60
14:L:18:VAL:HG21	14:L:81:GLY:HA3	1.83	0.60
3:03:1112:ILE:HG22	4:04:640:GLY:HA2	1.83	0.60
4:04:356:THR:CG2	4:04:448:GLN:HG2	2.31	0.60
11:I:75:GLU:HA	11:I:78:PHE:HD2	1.66	0.60
1:A:627:G:H5'	21:S:51:ARG:HH22	1.66	0.60
3:03:74:ARG:HD2	3:03:75:LEU:N	2.17	0.60
3:03:709:ALA:HB2	3:03:792:GLY:O	2.02	0.60
1:A:626:G:H2'	1:A:627:G:C8	2.37	0.60
2:02:56:VAL:CG2	2:02:144:ILE:HD11	2.30	0.60
1:A:59:A:H3'	1:A:60:A:H5'	1.82	0.60
2:01:61:ILE:HB	2:01:64:VAL:HB	1.83	0.60
4:04:119:SER:O	4:04:120:LEU:C	2.43	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:416:ILE:HG23	4:04:439:PRO:HB2	1.82	0.60
12:J:94:ARG:O	12:J:98:LEU:HD23	2.01	0.60
18:P:72:ILE:O	18:P:76:ILE:HG13	2.02	0.60
26:X:18:ARG:HD2	26:X:18:ARG:N	2.15	0.60
1:A:1103:C:H5''	7:E:97:LEU:HD23	1.83	0.60
1:A:1285:A:H4'	1:A:1286:U:H5''	1.83	0.60
2:01:83:LEU:HD23	3:03:694:ARG:NH2	2.16	0.60
4:04:1149:ARG:NH1	4:04:1153:PRO:HG2	2.16	0.60
4:04:1273:ASP:HB3	4:04:1276:GLU:HB2	1.83	0.60
2:01:166:ARG:N	2:01:167:PRO:HD2	2.17	0.60
3:03:91:THR:HA	3:03:138:ILE:HA	1.83	0.60
3:03:349:GLU:O	3:03:353:VAL:HG23	2.02	0.60
7:E:213:TYR:O	7:E:217:VAL:HG23	2.00	0.60
25:W:59:ARG:HG3	25:W:63:LYS:HE2	1.84	0.60
3:03:1082:ILE:H	3:03:1082:ILE:CD1	2.00	0.60
4:04:1221:LEU:HD22	4:04:1226:VAL:HA	1.84	0.60
4:04:1341:ARG:NH2	4:04:1343:GLU:HG3	2.17	0.60
11:I:7:VAL:HG13	11:I:61:LEU:HG	1.83	0.60
24:V:8:PRO:C	24:V:38:THR:HG21	2.27	0.60
1:A:1129:C:H5''	14:L:17:ARG:HH22	1.66	0.60
2:02:27:THR:CG2	2:02:200:LYS:HD3	2.32	0.60
3:03:660:VAL:HG13	3:03:661:VAL:HG13	1.83	0.60
4:04:678:ARG:O	4:04:682:VAL:HG23	2.02	0.60
4:04:1269:ALA:HB2	4:04:1274:PHE:HD1	1.67	0.60
10:H:80:LEU:HB3	10:H:97:PRO:HB3	1.84	0.60
1:A:8:A:HO2'	1:A:9:G:H8	1.48	0.59
7:E:21:ARG:NH1	7:E:38:VAL:HA	2.17	0.59
11:I:5:GLU:HB2	11:I:90:MET:HG3	1.83	0.59
26:X:28:VAL:O	26:X:32:VAL:HG22	2.02	0.59
1:A:35:G:H4'	17:O:117:GLY:HA2	1.84	0.59
1:A:119:A:H4'	1:A:120:A:O4'	2.02	0.59
1:A:150:U:H3	1:A:171:A:H62	1.50	0.59
1:A:410:G:H2'	1:A:429:U:C5	2.37	0.59
3:03:233:ARG:O	3:03:236:LYS:HG2	2.02	0.59
3:03:1109:ILE:HG12	4:04:644:MET:HE1	1.84	0.59
4:04:661:VAL:CG1	4:04:686:TRP:HE1	2.10	0.59
1:A:21:G:H21	1:A:914:A:H62	1.50	0.59
3:03:189:ASP:C	3:03:191:LYS:H	2.09	0.59
3:03:767:GLN:HA	3:03:785:ASP:O	2.02	0.59
4:04:923:ILE:HA	4:04:1248:ILE:HD13	1.83	0.59
11:I:38:ARG:HG3	11:I:40:GLU:HG3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:52:LEU:HD21	15:M:59:LYS:HZ2	1.67	0.59
1:A:376:G:H2'	1:A:377:G:H5'	1.85	0.59
3:03:1079:ILE:HG23	3:03:1079:ILE:O	2.02	0.59
4:04:419:HIS:HB2	5:05:45:LYS:HZ1	1.67	0.59
15:M:57:VAL:HG22	15:M:58:ASN:N	2.14	0.59
25:W:34:VAL:O	25:W:38:ILE:HG13	2.01	0.59
3:03:592:ARG:HD3	3:03:653:MET:HE2	1.85	0.59
14:L:48:ARG:O	14:L:52:GLU:HG3	2.02	0.59
1:A:108:G:N2	25:W:6:ALA:HB1	2.17	0.59
3:03:582:ASN:HA	3:03:588:GLU:OE2	2.02	0.59
3:03:1112:ILE:HG21	4:04:640:GLY:HA2	1.85	0.59
7:E:33:GLY:CA	7:E:41:ILE:HB	2.33	0.59
12:J:106:ALA:HB1	12:J:122:GLU:HG3	1.84	0.59
3:03:195:PHE:HD1	3:03:205:PRO:HA	1.66	0.59
3:03:1129:ASN:O	3:03:1133:LYS:HG2	2.03	0.59
3:03:862:LEU:HA	3:03:865:LEU:HB2	1.83	0.59
4:04:838:ARG:NH2	4:04:1235:ASN:HD21	1.99	0.59
7:E:23:TRP:CE3	7:E:189:THR:HB	2.38	0.59
16:N:118:ASN:HD22	26:X:32:VAL:HG12	1.68	0.59
1:A:570:G:H2'	1:A:571:U:C6	2.38	0.59
3:03:974:ARG:O	3:03:978:VAL:HG23	2.03	0.59
4:04:203:GLU:O	4:04:207:GLU:HG2	2.03	0.59
9:G:78:ALA:O	9:G:85:THR:HB	2.03	0.59
17:O:17:LYS:HB2	17:O:17:LYS:NZ	2.17	0.59
1:A:252:U:O2	1:A:252:U:H2'	2.01	0.59
3:03:1294:LYS:HG2	4:04:348:ASP:H	1.67	0.59
4:04:689:ALA:O	4:04:693:VAL:HG23	2.03	0.59
16:N:73:VAL:HA	16:N:76:TYR:HD2	1.67	0.59
18:P:28:ARG:O	18:P:32:ILE:HG12	2.02	0.59
1:A:440:C:H2'	1:A:441:A:H5''	1.83	0.58
3:03:98:VAL:O	3:03:122:VAL:HG12	2.02	0.58
3:03:389:PHE:HB3	3:03:420:LEU:HD12	1.85	0.58
3:03:1142:ARG:HD3	3:03:1165:SER:O	2.03	0.58
4:04:1252:HIS:O	4:04:1256:ILE:HG12	2.02	0.58
7:E:125:THR:HG22	7:E:128:LYS:HD2	1.84	0.58
17:O:98:ARG:NH1	17:O:106:VAL:HG12	2.18	0.58
1:A:1047:G:H5''	19:Q:3:GLN:HG3	1.83	0.58
1:A:1238:A:C2'	1:A:1239:A:H5'	2.33	0.58
2:01:75:GLN:HE21	3:03:772:SER:HA	1.68	0.58
3:03:178:PRO:HG3	3:03:182:SER:C	2.29	0.58
3:03:812:PHE:H	3:03:815:SER:HB3	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:132:PRO:HA	10:H:135:VAL:HG22	1.86	0.58
1:A:1060:U:H2'	1:A:1061:G:C8	2.38	0.58
3:03:104:ILE:HD12	3:03:104:ILE:N	2.19	0.58
4:04:1227:HIS:HA	4:04:1230:THR:HG22	1.85	0.58
19:Q:88:MET:HE2	19:Q:88:MET:HA	1.84	0.58
3:03:807:TRP:N	3:03:811:ASN:HD21	2.01	0.58
3:03:1082:ILE:HD12	3:03:1082:ILE:N	2.07	0.58
4:04:583:VAL:HG13	4:04:587:LEU:HD23	1.84	0.58
4:04:903:LEU:HG	4:04:904:ALA:H	1.68	0.58
10:H:73:VAL:HG21	10:H:143:LEU:HD22	1.84	0.58
16:N:115:ILE:HD13	26:X:28:VAL:HG21	1.86	0.58
26:X:55:ARG:O	26:X:59:LYS:HG2	2.04	0.58
2:02:56:VAL:HG21	2:02:144:ILE:HD11	1.83	0.58
2:02:61:ILE:O	2:02:62:ASP:HB2	2.02	0.58
4:04:431:ARG:HD2	4:04:493:PRO:HG3	1.86	0.58
4:04:523:GLU:HA	4:04:546:ALA:HB1	1.86	0.58
4:04:1342:ASP:C	4:04:1344:LEU:H	2.11	0.58
10:H:76:ASN:HB3	10:H:79:THR:HG23	1.85	0.58
1:A:59:A:H1'	1:A:354:G:C2	2.39	0.58
1:A:105:G:OP2	25:W:8:LYS:HG2	2.04	0.58
3:03:179:TYR:H	3:03:397:LEU:HD23	1.68	0.58
3:03:778:GLU:HB3	3:03:781:ASP:OD2	2.03	0.58
11:I:18:VAL:N	11:I:19:PRO:CD	2.67	0.58
25:W:81:GLN:HA	25:W:84:LYS:HZ2	1.69	0.58
2:02:51:MET:HE1	2:02:220:ALA:HB2	1.85	0.58
3:03:426:ILE:O	3:03:430:LYS:HG3	2.03	0.58
3:03:1272:GLU:O	3:03:1275:VAL:HB	2.04	0.58
9:G:8:LEU:O	9:G:12:ARG:HG3	2.03	0.58
11:I:93:LYS:HB3	11:I:93:LYS:NZ	2.19	0.58
1:A:516:U:H5	1:A:533:A:N6	2.00	0.58
1:A:1060:U:H2'	1:A:1061:G:H8	1.69	0.58
7:E:89:GLN:NE2	7:E:89:GLN:H	2.02	0.58
3:03:12:ARG:NH2	3:03:705:GLU:HG3	2.18	0.58
4:04:161:THR:HG23	4:04:164:GLN:H	1.68	0.58
4:04:799:ARG:O	4:04:802:ASP:HB2	2.04	0.58
5:05:3:ARG:HH21	5:05:52:ARG:HD2	1.66	0.58
10:H:44:ARG:HA	10:H:71:ILE:O	2.04	0.58
20:R:87:ARG:HA	20:R:87:ARG:HE	1.67	0.58
3:03:402:ARG:HG3	3:03:406:ASN:ND2	2.18	0.58
21:S:35:ARG:HD3	21:S:35:ARG:C	2.29	0.58
1:A:39:G:C3'	1:A:40:C:H5''	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:661:VAL:HG13	4:04:685:ILE:HD11	1.85	0.57
7:E:97:LEU:H	7:E:97:LEU:HD12	1.69	0.57
2:02:58:GLU:CB	2:02:170:ARG:HH21	2.17	0.57
2:02:133:LEU:CD1	2:02:138:ALA:HB1	2.33	0.57
3:03:28:LEU:HD13	3:03:133:ASN:O	2.04	0.57
4:04:123:ARG:NH2	4:04:1334:GLU:HA	2.20	0.57
4:04:215:LYS:O	4:04:218:THR:HG22	2.04	0.57
5:05:63:ILE:HD12	5:05:63:ILE:N	2.17	0.57
15:M:52:LEU:HD22	19:Q:80:ARG:HD2	1.86	0.57
21:S:71:VAL:O	21:S:75:ILE:HG12	2.03	0.57
1:A:244:U:H3	1:A:893:C:H42	1.50	0.57
1:A:1259:C:H3'	1:A:1260:G:C5'	2.35	0.57
3:03:1032:LYS:O	3:03:1036:ILE:HG13	2.04	0.57
7:E:21:ARG:CA	7:E:23:TRP:HD1	2.18	0.57
7:E:186:ILE:HG12	7:E:204:ASP:HB3	1.87	0.57
13:K:7:ALA:HB2	13:K:76:ARG:HD2	1.87	0.57
15:M:21:ALA:O	15:M:25:ILE:HG12	2.05	0.57
7:E:154:MET:HG3	7:E:156:GLY:O	2.04	0.57
1:A:1108:G:H5'	8:F:175:HIS:CD2	2.38	0.57
3:03:384:LEU:O	3:03:388:LEU:HG	2.05	0.57
3:03:670:PHE:HB3	3:03:673:HIS:HD2	1.69	0.57
4:04:430:HIS:HD2	4:04:432:LEU:HB2	1.70	0.57
9:G:18:LEU:HD21	9:G:63:ILE:HG12	1.85	0.57
14:L:115:VAL:CG1	15:M:62:ARG:HB3	2.34	0.57
3:03:708:VAL:HG11	3:03:794:LEU:HD13	1.85	0.57
4:04:1151:LYS:O	4:04:1153:PRO:HD3	2.04	0.57
19:Q:40:ARG:O	19:Q:44:VAL:HG22	2.05	0.57
3:03:7:GLU:OE1	3:03:11:ILE:HD12	2.04	0.57
3:03:1214:ASP:HB3	3:03:1217:THR:HB	1.87	0.57
4:04:478:LEU:HD12	5:05:24:ALA:HB2	1.86	0.57
4:04:579:LEU:O	4:04:583:VAL:HG23	2.03	0.57
12:J:96:ASN:HB3	12:J:100:MET:HE3	1.86	0.57
24:V:35:ARG:NH2	24:V:76:THR:HG21	2.20	0.57
1:A:824:G:H2'	1:A:825:A:H8	1.69	0.57
1:A:1393:U:H2'	1:A:1395:C:C5	2.40	0.57
3:03:1109:ILE:HD12	3:03:1112:ILE:HG13	1.87	0.57
4:04:154:LEU:HD22	4:04:160:LEU:CD2	2.34	0.57
4:04:1105:ALA:HB1	4:04:1122:ALA:HB1	1.86	0.57
9:G:109:THR:HG22	9:G:111:ALA:H	1.69	0.57
10:H:132:PRO:O	10:H:136:VAL:HG23	2.05	0.57
14:L:94:ARG:HH11	14:L:94:ARG:HA	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:P:77:LYS:NZ	18:P:77:LYS:HB3	2.20	0.57
2:01:18:GLN:NE2	2:01:24:ALA:HB2	2.20	0.57
2:02:158:ARG:HA	2:02:158:ARG:HE	1.68	0.57
3:03:144:VAL:HG21	3:03:527:LYS:HG2	1.85	0.57
3:03:179:TYR:HB3	3:03:397:LEU:HA	1.86	0.57
3:03:634:VAL:HG13	3:03:636:CYS:SG	2.45	0.57
3:03:1086:PRO:HB3	3:03:1221:PHE:HE2	1.69	0.57
3:03:1313:HIS:HB3	4:04:473:THR:HA	1.85	0.57
4:04:518:VAL:HG12	4:04:716:GLN:HB3	1.86	0.57
4:04:1227:HIS:O	4:04:1230:THR:HG22	2.05	0.57
14:L:49:GLN:C	14:L:51:LEU:H	2.12	0.57
4:04:332:LYS:HG2	4:04:336:GLY:O	2.04	0.57
4:04:378:LYS:HB3	4:04:382:TYR:CE2	2.40	0.57
14:L:20:ILE:HG12	14:L:62:LEU:HD23	1.87	0.57
3:03:725:GLN:CD	3:03:735:LYS:HB2	2.30	0.56
4:04:859:PRO:HG2	4:04:862:THR:OG1	2.05	0.56
4:04:980:THR:HG21	4:04:997:VAL:HB	1.87	0.56
7:E:217:VAL:O	7:E:221:VAL:HG23	2.05	0.56
12:J:55:LYS:HD2	12:J:59:GLU:OE2	2.04	0.56
3:03:765:ILE:HG13	3:03:787:PRO:HD3	1.87	0.56
4:04:41:PRO:HA	4:04:56:LEU:HD13	1.87	0.56
4:04:181:GLY:O	4:04:185:ILE:HG12	2.06	0.56
4:04:1000:GLY:HA3	4:04:1026:PRO:HG2	1.86	0.56
4:04:1040:MET:HE2	4:04:1046:ILE:HG21	1.87	0.56
14:L:115:VAL:HG11	15:M:62:ARG:HB3	1.86	0.56
20:R:55:LEU:O	20:R:59:VAL:HG23	2.04	0.56
1:A:454:G:H2'	1:A:455:G:H8	1.68	0.56
1:A:544:G:OP1	9:G:58:GLN:HG3	2.04	0.56
1:A:751:U:H2'	1:A:752:G:H5'	1.86	0.56
2:02:34:GLY:HA2	2:02:37:HIS:HD2	1.70	0.56
3:03:130:MET:HE3	3:03:456:VAL:HG11	1.87	0.56
3:03:616:ILE:HG13	3:03:652:TYR:HB2	1.87	0.56
3:03:720:ARG:HD2	3:03:736:VAL:HG11	1.87	0.56
3:03:724:VAL:HG12	3:03:734:ILE:HD12	1.88	0.56
3:03:979:LEU:HD21	3:03:989:LEU:HD22	1.87	0.56
4:04:485:MET:HE3	4:04:486:SER:H	1.70	0.56
4:04:870:ASP:O	4:04:874:GLU:HG2	2.05	0.56
4:04:1141:VAL:HA	4:04:1144:LEU:HD12	1.86	0.56
7:E:20:THR:O	7:E:23:TRP:N	2.37	0.56
2:02:86:LYS:HE3	4:04:526:VAL:O	2.06	0.56
3:03:590:PRO:HB2	3:03:655:VAL:HG21	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:796:LEU:HD12	3:03:796:LEU:N	2.20	0.56
3:03:890:LYS:HG2	3:03:891:GLY:H	1.69	0.56
4:04:1041:ILE:HD12	4:04:1041:ILE:N	2.20	0.56
9:G:61:ARG:HG2	9:G:66:VAL:O	2.06	0.56
15:M:29:ALA:HB1	15:M:83:THR:HG23	1.87	0.56
16:N:44:ALA:HB1	16:N:68:ARG:HB3	1.86	0.56
1:A:288:A:H2'	1:A:289:G:H5'	1.88	0.56
3:03:727:VAL:HG13	3:03:732:ILE:HG12	1.87	0.56
7:E:42:ASN:ND2	7:E:42:ASN:O	2.39	0.56
12:J:99:ALA:O	12:J:103:ILE:HG13	2.06	0.56
5:05:32:VAL:C	5:05:34:GLY:H	2.13	0.56
1:A:109:A:H62	1:A:324:G:H21	1.53	0.56
1:A:750:C:H2'	1:A:751:U:C6	2.41	0.56
2:01:118:ASP:HB3	2:01:121:VAL:HG23	1.88	0.56
3:03:556:GLY:HA2	3:03:660:VAL:HA	1.87	0.56
3:03:616:ILE:HD12	3:03:616:ILE:N	2.21	0.56
4:04:413:ASP:O	4:04:417:ARG:HG3	2.05	0.56
4:04:1370:MET:HE3	4:04:1373:ARG:HB3	1.86	0.56
15:M:32:THR:HG21	15:M:82:LYS:HB3	1.88	0.56
21:S:20:VAL:HA	21:S:35:ARG:HA	1.88	0.56
1:A:1175:G:H2'	1:A:1176:A:C8	2.40	0.56
3:03:1012:GLU:HG2	3:03:1013:GLN:N	2.16	0.56
4:04:210:SER:HB2	4:04:213:LYS:HD2	1.87	0.56
9:G:116:LEU:HD21	9:G:153:ARG:HB2	1.87	0.56
1:A:599:C:OP1	13:K:87:ARG:HG2	2.05	0.56
3:03:54:ARG:HB2	3:03:54:ARG:HH11	1.71	0.56
3:03:1141:LEU:HD12	3:03:1142:ARG:N	2.21	0.56
3:03:1145:ILE:O	3:03:1149:TYR:HB2	2.06	0.56
4:04:1266:ILE:HG21	4:04:1300:ALA:HB1	1.88	0.56
1:A:1384:C:H2'	1:A:1385:G:C8	2.41	0.56
3:03:983:GLY:O	3:03:985:GLU:HG3	2.04	0.56
3:03:1058:ARG:CZ	3:03:1240:ASP:HB3	2.36	0.56
8:F:58:ARG:H	15:M:94:ALA:HB1	1.70	0.56
18:P:64:VAL:HG23	18:P:66:GLY:H	1.71	0.56
1:A:676:A:H2	16:N:120:CYS:HB3	1.71	0.55
1:A:818:G:H3'	1:A:819:A:H5'	1.88	0.55
2:01:150:ARG:HD2	2:01:150:ARG:O	2.07	0.55
3:03:17:LYS:HB2	3:03:1155:VAL:HG12	1.88	0.55
3:03:732:ILE:HG21	3:03:783:LEU:HD12	1.88	0.55
7:E:186:ILE:HA	7:E:200:ILE:O	2.06	0.55
16:N:88:PRO:HG2	26:X:29:LEU:HD22	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:414:A:H2'	1:A:414:A:N3	2.21	0.55
1:A:1354:U:H2'	1:A:1355:G:C8	2.42	0.55
2:01:82:LEU:HD23	2:01:85:LEU:HD12	1.88	0.55
2:01:166:ARG:O	2:01:168:ILE:N	2.39	0.55
3:03:150:HIS:HD2	3:03:454:ARG:HH11	1.54	0.55
3:03:812:PHE:N	3:03:815:SER:HB3	2.22	0.55
3:03:1191:LYS:O	3:03:1195:ILE:HG13	2.05	0.55
4:04:746:LEU:N	4:04:746:LEU:HD12	2.22	0.55
5:05:12:LYS:HE2	5:05:57:GLY:HA3	1.88	0.55
16:N:74:LYS:HD3	16:N:74:LYS:H	1.71	0.55
24:V:16:LYS:O	24:V:16:LYS:HD3	2.05	0.55
1:A:8:A:O2'	1:A:9:G:H8	1.90	0.55
2:01:28:LEU:O	2:01:200:LYS:HA	2.06	0.55
2:01:227:GLN:NE2	2:02:11:PRO:HD3	2.21	0.55
3:03:839:VAL:HG23	3:03:1046:VAL:HG13	1.89	0.55
4:04:205:LEU:HD13	4:04:205:LEU:O	2.06	0.55
4:04:842:ARG:HG2	4:04:1251:LYS:HD3	1.87	0.55
3:03:242:VAL:HB	3:03:245:ARG:HD2	1.88	0.55
3:03:693:LEU:HG	3:03:829:THR:O	2.06	0.55
3:03:1113:LEU:HA	4:04:641:ILE:HG13	1.87	0.55
3:03:1176:LEU:HD13	3:03:1180:MET:HE2	1.87	0.55
4:04:628:GLY:O	4:04:632:ALA:HB2	2.06	0.55
4:04:1342:ASP:O	4:04:1344:LEU:N	2.38	0.55
16:N:29:THR:OG1	16:N:46:ALA:HB2	2.07	0.55
22:T:22:VAL:HG11	22:T:60:ILE:CD1	2.37	0.55
25:W:24:ARG:HB3	25:W:28:ARG:NH1	2.22	0.55
1:A:545:C:H5''	9:G:61:ARG:HH12	1.72	0.55
1:A:932:C:H5''	12:J:3:ARG:NH2	2.21	0.55
2:02:125:LYS:HE2	2:02:128:HIS:HB2	1.89	0.55
3:03:633:LEU:HD12	3:03:633:LEU:O	2.07	0.55
3:03:1335:ILE:HG22	3:03:1336:ASN:H	1.71	0.55
14:L:118:ARG:HE	14:L:122:ARG:HD3	1.71	0.55
16:N:109:ILE:HD12	16:N:109:ILE:N	2.21	0.55
24:V:4:LEU:HD23	24:V:4:LEU:N	2.22	0.55
1:A:242:G:H2'	1:A:243:A:H5'	1.89	0.55
1:A:501:C:H2'	1:A:502:A:C8	2.41	0.55
2:02:10:LYS:N	2:02:10:LYS:HD2	2.21	0.55
2:02:102:LEU:C	2:02:102:LEU:HD13	2.32	0.55
3:03:1328:LYS:HD2	3:03:1331:ARG:NH1	2.22	0.55
4:04:1047:THR:HB	4:04:1062:LEU:HD21	1.88	0.55
25:W:4:LYS:NZ	25:W:4:LYS:HB3	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:G:H5''	1:A:83:C:H4'	1.88	0.55
2:01:32:GLU:HB2	2:01:35:PHE:HD2	1.71	0.55
3:03:854:ILE:O	3:03:854:ILE:HG23	2.07	0.55
3:03:870:ILE:HG23	3:03:884:VAL:HG12	1.89	0.55
4:04:1042:ASP:HA	4:04:1046:ILE:O	2.07	0.55
8:F:63:ILE:O	8:F:98:ALA:HA	2.06	0.55
20:R:57:ARG:C	20:R:57:ARG:HD3	2.32	0.55
1:A:50:A:H4'	1:A:51:A:H5'	1.88	0.55
3:03:28:LEU:O	3:03:32:LEU:HD13	2.07	0.55
3:03:800:MET:HB2	3:03:1096:ILE:HD11	1.87	0.55
4:04:1231:ARG:HA	4:04:1234:VAL:CG2	2.35	0.55
7:E:33:GLY:HA3	7:E:41:ILE:HB	1.89	0.55
8:F:32:LEU:O	8:F:32:LEU:HD23	2.07	0.55
18:P:55:LEU:HD12	18:P:56:ARG:N	2.22	0.55
24:V:29:PRO:HA	24:V:47:THR:O	2.07	0.55
1:A:768:A:H4'	1:A:1523:G:N2	2.21	0.55
2:01:155:ALA:HA	2:01:158:ARG:HE	1.72	0.55
2:02:54:CYS:SG	2:02:92:VAL:HG22	2.47	0.55
3:03:18:ARG:HA	3:03:18:ARG:HE	1.70	0.55
3:03:424:ASP:O	3:03:428:VAL:HG23	2.07	0.55
3:03:1151:LEU:HG	3:03:1152:GLY:H	1.71	0.55
3:03:1211:ARG:O	3:03:1211:ARG:HG2	2.07	0.55
7:E:11:LYS:HG2	7:E:212:LEU:HD22	1.87	0.55
11:I:76:THR:HG23	11:I:79:ARG:NH2	2.22	0.55
25:W:78:LEU:C	25:W:78:LEU:HD23	2.31	0.55
1:A:779:C:H2'	1:A:780:A:O4'	2.07	0.55
2:02:145:LYS:HE2	2:02:147:GLN:HB2	1.88	0.55
3:03:405:PHE:O	3:03:409:LEU:HG	2.07	0.55
4:04:442:ILE:HG21	4:04:448:GLN:HE21	1.71	0.55
4:04:514:THR:HG23	4:04:514:THR:O	2.07	0.55
7:E:140:GLU:O	7:E:144:LEU:HD23	2.06	0.55
16:N:34:THR:HA	16:N:40:ALA:HA	1.89	0.55
25:W:24:ARG:HD2	25:W:66:ILE:HD11	1.88	0.55
1:A:730:G:H2'	1:A:731:G:O4'	2.07	0.54
2:02:208:ASN:ND2	2:02:210:THR:HG23	2.21	0.54
3:03:241:LEU:O	3:03:283:LYS:HG2	2.07	0.54
3:03:1137:GLU:OE2	3:03:1139:ALA:HB3	2.07	0.54
4:04:768:ASN:OD1	4:04:770:LEU:HB3	2.07	0.54
4:04:1227:HIS:O	4:04:1231:ARG:HD3	2.06	0.54
9:G:71:PHE:HE1	9:G:93:LEU:HD11	1.71	0.54
13:K:29:SER:HB3	13:K:32:LYS:NZ	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:U:30:LYS:HB3	23:U:30:LYS:HZ3	1.71	0.54
25:W:30:PHE:HB3	25:W:53:MET:HA	1.89	0.54
2:02:33:ARG:HD3	2:02:33:ARG:N	2.22	0.54
3:03:1113:LEU:HG	4:04:641:ILE:HG13	1.89	0.54
3:03:1308:ILE:HG22	3:03:1308:ILE:O	2.07	0.54
4:04:378:LYS:HB2	4:04:379:PRO:HD3	1.88	0.54
4:04:761:ALA:HB1	4:04:766:GLY:O	2.08	0.54
4:04:833:GLU:HB2	4:04:1242:ARG:NH2	2.22	0.54
7:E:186:ILE:HD11	7:E:203:ASN:O	2.06	0.54
24:V:36:ARG:HG3	24:V:36:ARG:HH11	1.72	0.54
1:A:40:C:H41	1:A:547:A:H3'	1.72	0.54
1:A:1509:C:H2'	1:A:1510:C:H6	1.71	0.54
2:01:194:GLN:O	2:01:195:ARG:HB2	2.07	0.54
3:03:493:ILE:HD11	3:03:498:ILE:HD11	1.89	0.54
3:03:706:ARG:NH1	3:03:706:ARG:HB3	2.21	0.54
4:04:649:LYS:O	4:04:653:ILE:HG13	2.07	0.54
4:04:818:GLU:HG3	4:04:819:GLY:N	2.22	0.54
4:04:1169:THR:OG1	4:04:1192:LYS:HD3	2.06	0.54
12:J:90:VAL:HG21	12:J:94:ARG:HD3	1.90	0.54
1:A:1374:A:H4'	12:J:27:ASN:HB3	1.90	0.54
3:03:149:LEU:HD12	3:03:452:ARG:O	2.08	0.54
3:03:1146:GLN:OE1	3:03:1146:GLN:HA	2.06	0.54
7:E:21:ARG:HA	7:E:23:TRP:CD1	2.42	0.54
7:E:90:PHE:HB3	7:E:150:GLY:O	2.08	0.54
8:F:115:VAL:HG21	8:F:201:ILE:HD11	1.87	0.54
13:K:77:VAL:O	13:K:79:ARG:HD2	2.06	0.54
15:M:8:ILE:HD11	15:M:87:LEU:HD23	1.88	0.54
1:A:219:U:H2'	1:A:220:G:C4'	2.38	0.54
1:A:437:U:O2'	1:A:438:U:H5'	2.08	0.54
1:A:1103:C:H4'	7:E:97:LEU:HB3	1.90	0.54
2:02:58:GLU:HB2	2:02:170:ARG:HH21	1.71	0.54
3:03:1101:LEU:H	3:03:1101:LEU:CD1	2.19	0.54
4:04:1362:GLY:HA2	4:04:1365:TYR:HB3	1.89	0.54
7:E:39:HIS:O	7:E:40:ILE:CB	2.53	0.54
8:F:138:GLN:O	8:F:142:ARG:HG2	2.06	0.54
9:G:178:GLU:HG2	9:G:179:GLY:N	2.23	0.54
20:R:9:LYS:NZ	20:R:9:LYS:HB3	2.22	0.54
1:A:935:A:H2	1:A:1383:C:H42	1.55	0.54
3:03:617:ALA:HB2	3:03:650:VAL:HG11	1.90	0.54
4:04:56:LEU:H	4:04:56:LEU:HD12	1.73	0.54
4:04:586:GLY:HA3	4:04:612:LEU:HD13	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:1249:ASN:HD21	4:04:1251:LYS:HB2	1.71	0.54
23:U:50:LYS:O	23:U:54:GLN:HG3	2.07	0.54
24:V:62:THR:H	24:V:65:MET:CE	2.19	0.54
1:A:770:C:H1'	1:A:900:A:C2	2.40	0.54
2:01:219:ARG:O	2:01:223:ILE:HG13	2.08	0.54
3:03:690:VAL:CG1	3:03:1234:LYS:HB3	2.33	0.54
4:04:721:SER:HA	4:04:724:MET:HE3	1.88	0.54
4:04:746:LEU:HD12	4:04:746:LEU:H	1.73	0.54
4:04:1151:LYS:C	4:04:1153:PRO:HD3	2.33	0.54
8:F:127:VAL:HG22	8:F:128:MET:N	2.23	0.54
11:I:18:VAL:HA	11:I:21:MET:HE3	1.88	0.54
2:01:130:ILE:N	2:01:130:ILE:HD12	2.22	0.54
3:03:56:VAL:HB	3:03:465:ARG:HH12	1.73	0.54
3:03:591:TYR:CD2	3:03:606:LEU:HD13	2.41	0.54
5:05:13:ILE:HD11	5:05:60:ASN:HB2	1.90	0.54
14:L:50:PRO:HA	14:L:97:LEU:HD11	1.89	0.54
26:X:17:ARG:HD3	26:X:17:ARG:N	2.23	0.54
1:A:530:G:H3'	1:A:531:U:H5''	1.88	0.54
1:A:1527:U:O2'	1:A:1528:U:H5'	2.07	0.54
4:04:857:LEU:HD23	4:04:857:LEU:H	1.72	0.54
4:04:865:HIS:HA	4:04:901:ARG:HH21	1.73	0.54
4:04:1046:ILE:CD1	4:04:1059:LEU:HB3	2.33	0.54
9:G:121:ALA:O	9:G:144:ILE:HG23	2.08	0.54
23:U:40:VAL:CG1	23:U:45:THR:HG23	2.38	0.54
1:A:1053:G:H4'	1:A:1054:C:H3'	1.90	0.54
3:03:979:LEU:HD12	3:03:980:VAL:N	2.24	0.54
4:04:362:ARG:HB3	4:04:365:GLN:HG2	1.89	0.54
4:04:795:TYR:HD1	4:04:798:ARG:HE	1.56	0.54
4:04:863:LEU:HD22	4:04:908:ILE:HD11	1.88	0.54
11:I:11:HIS:NE2	11:I:85:ILE:HG21	2.23	0.54
18:P:19:THR:HG22	18:P:25:GLY:C	2.33	0.54
1:A:26:A:N3	9:G:205:LYS:HE2	2.23	0.53
1:A:92:U:H3'	1:A:93:U:H5''	1.88	0.53
1:A:932:C:H5''	12:J:3:ARG:HH21	1.73	0.53
1:A:1305:G:H22	1:A:1331:G:H2'	1.73	0.53
1:A:1509:C:H2'	1:A:1510:C:C6	2.43	0.53
2:01:48:LEU:HA	2:01:180:VAL:HG21	1.90	0.53
3:03:243:PRO:HA	3:03:246:LEU:HD12	1.90	0.53
4:04:53:ARG:HE	4:04:54:ASP:CG	2.16	0.53
4:04:517:CYS:SG	4:04:545:HIS:HB2	2.49	0.53
4:04:255:LEU:HD13	4:04:256:ASP:N	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:526:VAL:C	4:04:527:LEU:HD12	2.34	0.53
4:04:737:ILE:O	4:04:740:LEU:HB3	2.08	0.53
4:04:1063:ASP:O	4:04:1067:ARG:HG3	2.08	0.53
7:E:103:ASN:O	7:E:107:VAL:HG23	2.09	0.53
9:G:58:GLN:OE1	9:G:61:ARG:HD3	2.08	0.53
9:G:144:ILE:HD12	9:G:177:MET:HB2	1.90	0.53
11:I:29:ILE:CG2	11:I:34:GLY:HA3	2.37	0.53
1:A:105:G:N2	1:A:379:C:H4'	2.21	0.53
1:A:362:G:H21	1:A:365:U:H5	1.56	0.53
2:01:27:THR:C	2:01:28:LEU:HD12	2.33	0.53
3:03:838:CYS:HB2	3:03:918:LEU:HD22	1.91	0.53
4:04:865:HIS:CE1	4:04:867:GLN:HB2	2.43	0.53
8:F:18:ASN:HB2	19:Q:90:GLY:O	2.07	0.53
11:I:47:LEU:HG	11:I:57:ALA:N	2.21	0.53
22:T:60:ILE:HG22	22:T:72:TRP:HE3	1.74	0.53
24:V:16:LYS:O	24:V:20:LYS:HG3	2.07	0.53
1:A:66:A:H1'	1:A:173:U:H2'	1.91	0.53
2:01:14:VAL:HG22	2:01:15:ASP:N	2.21	0.53
2:02:101:THR:H	2:02:116:THR:HG22	1.73	0.53
3:03:198:ILE:HB	3:03:369:MET:HE2	1.91	0.53
3:03:401:GLY:O	3:03:405:PHE:HB2	2.08	0.53
3:03:429:MET:O	3:03:433:ILE:HG13	2.09	0.53
3:03:882:ILE:HD12	3:03:882:ILE:N	2.23	0.53
4:04:193:ASP:O	4:04:197:GLU:HG2	2.08	0.53
7:E:26:LYS:C	7:E:28:LYS:H	2.16	0.53
1:A:125:U:H3	1:A:236:A:H61	1.57	0.53
1:A:501:C:H2'	1:A:502:A:H8	1.73	0.53
1:A:552:U:H2'	1:A:553:A:C8	2.41	0.53
1:A:692:U:H2'	1:A:694:A:OP2	2.08	0.53
1:A:1348:U:H4'	14:L:121:ARG:HG3	1.91	0.53
2:02:67:GLU:HB2	2:02:79:LEU:HD23	1.89	0.53
8:F:118:SER:O	8:F:122:GLN:HG2	2.07	0.53
10:H:119:VAL:CG1	10:H:122:VAL:HG13	2.38	0.53
20:R:28:VAL:HA	20:R:31:LEU:HD12	1.89	0.53
23:U:38:LYS:NZ	23:U:38:LYS:HB3	2.23	0.53
1:A:645:G:H1'	22:T:27:PHE:CZ	2.43	0.53
1:A:837:U:H2'	1:A:838:G:C8	2.43	0.53
1:A:1245:C:H2'	1:A:1246:A:H8	1.74	0.53
2:02:12:ARG:HB3	2:02:12:ARG:HH11	1.74	0.53
2:02:172:LEU:HD23	2:02:172:LEU:N	2.23	0.53
3:03:564:PRO:CD	3:03:572:ILE:HG21	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:697:LYS:H	3:03:697:LYS:HD3	1.73	0.53
4:04:383:GLY:O	4:04:387:LEU:HB2	2.08	0.53
4:04:740:LEU:HD12	4:04:763:PHE:HB2	1.90	0.53
4:04:1165:PHE:CZ	4:04:1198:VAL:HG11	2.44	0.53
5:05:63:ILE:H	5:05:63:ILE:CD1	2.21	0.53
7:E:25:PRO:O	7:E:28:LYS:HB2	2.09	0.53
8:F:21:TRP:CZ3	8:F:23:ALA:HB2	2.44	0.53
9:G:64:TYR:HA	9:G:110:ARG:HD2	1.91	0.53
12:J:90:VAL:CG2	12:J:94:ARG:HD3	2.38	0.53
13:K:28:SER:HB2	13:K:58:LEU:CB	2.38	0.53
1:A:511:C:O2'	1:A:512:U:H5'	2.09	0.53
1:A:831:A:C3'	1:A:832:G:H5''	2.35	0.53
2:01:56:VAL:HG13	2:01:173:VAL:HG21	1.88	0.53
2:02:209:GLY:C	2:02:211:ILE:H	2.16	0.53
3:03:75:LEU:HD11	3:03:127:ILE:HD11	1.89	0.53
3:03:971:LEU:O	3:03:975:ILE:HG13	2.07	0.53
4:04:1227:HIS:HA	4:04:1230:THR:CG2	2.39	0.53
9:G:159:GLU:OE1	9:G:159:GLU:HA	2.08	0.53
16:N:84:MET:HE2	16:N:112:VAL:HG11	1.90	0.53
25:W:78:LEU:HD23	25:W:79:THR:N	2.24	0.53
1:A:701:U:H5''	1:A:703:G:C1'	2.38	0.53
4:04:1227:HIS:C	4:04:1230:THR:HG22	2.34	0.53
7:E:25:PRO:CB	7:E:28:LYS:HB2	2.39	0.53
8:F:69:THR:CG2	8:F:75:VAL:HG21	2.39	0.53
14:L:104:THR:HG22	14:L:106:ASP:H	1.74	0.53
25:W:30:PHE:CD2	25:W:56:ILE:HG12	2.43	0.53
1:A:8:A:O2'	1:A:9:G:C8	2.61	0.53
2:01:28:LEU:HD12	2:01:28:LEU:N	2.24	0.53
2:01:228:LEU:O	2:01:232:VAL:HG23	2.09	0.53
2:02:111:THR:HA	2:02:129:VAL:HA	1.91	0.53
4:04:426:ALA:C	4:04:428:THR:H	2.17	0.53
7:E:13:GLY:O	7:E:16:PHE:HE1	1.92	0.53
7:E:31:ILE:HB	7:E:42:ASN:HA	1.91	0.53
7:E:142:GLU:HA	7:E:145:GLU:HG3	1.91	0.53
7:E:143:LYS:HA	7:E:146:ASN:HD21	1.73	0.53
9:G:22:SER:HA	9:G:26:ALA:HA	1.90	0.53
12:J:91:ARG:O	12:J:95:ARG:HG3	2.09	0.53
14:L:7:GLY:HA3	14:L:18:VAL:HB	1.91	0.53
20:R:14:PHE:HB3	20:R:26:VAL:HG22	1.91	0.53
1:A:273:U:H2'	1:A:274:A:H5'	1.90	0.53
1:A:1150:A:H2'	1:A:1151:A:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1354:U:H2'	1:A:1355:G:H8	1.73	0.53
14:L:29:ILE:HA	14:L:64:ILE:O	2.09	0.53
18:P:4:ALA:CB	18:P:21:ILE:HG21	2.39	0.53
19:Q:20:PHE:HD1	19:Q:24:ALA:HB2	1.73	0.53
3:03:10:ARG:HG3	3:03:10:ARG:HH11	1.74	0.52
3:03:929:ILE:HG13	3:03:930:ASP:N	2.25	0.52
4:04:66:LYS:HG2	4:04:67:ASP:H	1.74	0.52
4:04:317:THR:HG23	4:04:320:ASN:HB3	1.90	0.52
4:04:720:ASN:HB3	4:04:722:ILE:HG22	1.92	0.52
7:E:10:LEU:C	7:E:11:LYS:HD2	2.33	0.52
12:J:115:MET:HA	12:J:118:ARG:HG2	1.91	0.52
21:S:20:VAL:HG12	21:S:35:ARG:CB	2.39	0.52
1:A:545:C:O2'	1:A:549:C:H5''	2.09	0.52
2:01:45:ARG:NH2	3:03:1216:ARG:HA	2.18	0.52
3:03:748:ILE:HD12	3:03:748:ILE:N	2.24	0.52
3:03:1067:ALA:HB2	3:03:1073:LYS:HA	1.92	0.52
3:03:1246:ARG:HG3	3:03:1265:PHE:HB3	1.91	0.52
7:E:21:ARG:C	7:E:23:TRP:HD1	2.17	0.52
12:J:49:LEU:HD12	12:J:50:ALA:N	2.24	0.52
13:K:49:LYS:O	13:K:58:LEU:HD12	2.08	0.52
14:L:46:VAL:HA	14:L:49:GLN:HE21	1.73	0.52
17:O:73:LEU:N	17:O:73:LEU:HD12	2.25	0.52
20:R:26:VAL:O	20:R:30:LEU:HD13	2.09	0.52
23:U:61:ARG:O	23:U:65:LEU:HD13	2.08	0.52
1:A:440:C:C3'	1:A:441:A:H5''	2.39	0.52
1:A:625:U:H2'	1:A:626:G:C8	2.43	0.52
1:A:668:G:H21	20:R:45:HIS:CE1	2.27	0.52
3:03:151:ARG:HE	3:03:450:ASN:HB3	1.75	0.52
4:04:527:LEU:HD23	4:04:532:GLU:HG3	1.92	0.52
10:H:39:GLY:HA3	10:H:45:VAL:HG12	1.92	0.52
16:N:122:PRO:HB2	16:N:123:PRO:HD2	1.90	0.52
18:P:13:HIS:HB2	18:P:16:ILE:HD13	1.90	0.52
20:R:79:GLN:O	20:R:83:ARG:HB2	2.10	0.52
2:01:102:LEU:HD13	2:01:102:LEU:C	2.34	0.52
3:03:6:THR:HG21	3:03:706:ARG:HH21	1.74	0.52
3:03:145:ILE:HD12	3:03:456:VAL:HG13	1.91	0.52
3:03:174:ALA:HB2	3:03:432:LEU:HD13	1.91	0.52
4:04:631:TYR:HA	4:04:634:ARG:HG2	1.91	0.52
1:A:39:G:H3'	1:A:40:C:H5''	1.90	0.52
1:A:107:G:C2'	1:A:108:G:H5'	2.38	0.52
1:A:142:G:H1'	1:A:195:A:H61	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:716:A:N3	16:N:119:GLY:HA2	2.24	0.52
2:01:43:LEU:HD23	2:01:224:LEU:HD11	1.92	0.52
2:01:91:ARG:HD2	2:01:210:THR:HA	1.91	0.52
6:B:208:UNK:HA	6:B:216:UNK:O	2.09	0.52
10:H:50:GLY:HA3	10:H:58:ALA:O	2.09	0.52
19:Q:40:ARG:O	19:Q:40:ARG:HD2	2.10	0.52
1:A:106:C:H2'	1:A:107:G:C8	2.45	0.52
1:A:1393:U:H2'	1:A:1395:C:H5	1.72	0.52
2:02:12:ARG:CB	2:02:12:ARG:NH1	2.72	0.52
2:02:115:ILE:HD11	2:02:130:ILE:HD11	1.91	0.52
3:03:496:LYS:HB3	3:03:497:PRO:HD3	1.91	0.52
3:03:516:ASP:H	3:03:526:HIS:CD2	2.27	0.52
3:03:519:ASN:HD21	3:03:521:LEU:HB3	1.73	0.52
3:03:1132:LEU:HD23	3:03:1132:LEU:O	2.09	0.52
3:03:1160:ASP:CG	3:03:1161:LEU:H	2.18	0.52
3:03:1226:THR:H	4:04:638:SER:HB3	1.74	0.52
4:04:591:ILE:HG23	4:04:592:VAL:HG13	1.90	0.52
4:04:858:VAL:HG13	4:04:858:VAL:O	2.09	0.52
7:E:21:ARG:N	7:E:38:VAL:HG12	2.17	0.52
9:G:61:ARG:O	9:G:65:GLY:HA2	2.10	0.52
23:U:29:LEU:O	23:U:33:ILE:HG12	2.10	0.52
26:X:34:ARG:HD3	26:X:34:ARG:H	1.73	0.52
1:A:404:G:H1	1:A:499:A:H62	1.56	0.52
1:A:865:A:H2'	1:A:866:C:C6	2.45	0.52
2:02:28:LEU:HD23	2:02:28:LEU:C	2.34	0.52
3:03:195:PHE:HE1	3:03:353:VAL:HG11	1.75	0.52
3:03:502:VAL:HG13	3:03:503:LYS:N	2.24	0.52
3:03:1336:ASN:HB3	4:04:25:ALA:HB3	1.92	0.52
4:04:101:ARG:HG2	4:04:101:ARG:HH11	1.74	0.52
4:04:831:VAL:O	4:04:831:VAL:HG13	2.09	0.52
7:E:206:ALA:O	7:E:210:VAL:HG23	2.09	0.52
8:F:12:GLY:HA3	19:Q:96:LYS:HE2	1.91	0.52
12:J:36:SER:HA	14:L:42:THR:HB	1.92	0.52
16:N:36:ARG:NH1	16:N:36:ARG:HB2	2.25	0.52
1:A:1369:C:H2'	1:A:1370:G:H8	1.74	0.52
3:03:833:ILE:HG23	3:03:1054:LEU:O	2.10	0.52
3:03:1258:PRO:HD2	4:04:346:ARG:HD3	1.91	0.52
3:03:1321:GLU:HG2	4:04:99:ARG:NE	2.25	0.52
4:04:650:LYS:O	4:04:654:ILE:HG13	2.10	0.52
5:05:42:GLU:O	5:05:43:ASN:HB2	2.07	0.52
7:E:23:TRP:HE3	7:E:189:THR:CB	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:105:ARG:NH1	14:L:107:ALA:HA	2.14	0.52
15:M:32:THR:CG2	15:M:33:GLY:H	2.19	0.52
23:U:59:ILE:O	23:U:63:ARG:HG3	2.09	0.52
1:A:131:A:H4'	25:W:69:ASN:ND2	2.20	0.52
1:A:974:A:H4'	1:A:976:G:H4'	1.91	0.52
1:A:1129:C:H5'	14:L:17:ARG:HH12	1.75	0.52
2:01:224:LEU:O	2:01:228:LEU:HG	2.09	0.52
3:03:189:ASP:C	3:03:191:LYS:N	2.66	0.52
3:03:663:VAL:HG23	3:03:664:GLY:N	2.25	0.52
3:03:931:VAL:HG12	3:03:933:VAL:HG13	1.92	0.52
4:04:154:LEU:HD22	4:04:160:LEU:HD21	1.90	0.52
7:E:11:LYS:NZ	7:E:212:LEU:HD11	2.25	0.52
7:E:19:GLN:HG2	7:E:189:THR:OG1	2.10	0.52
7:E:87:CYS:SG	7:E:222:ARG:HD2	2.49	0.52
15:M:15:HIS:HA	15:M:18:ILE:HG22	1.92	0.52
22:T:15:LYS:HB2	22:T:15:LYS:HZ2	1.74	0.52
22:T:35:LYS:HB3	22:T:35:LYS:HZ2	1.75	0.52
3:03:1062:PRO:CG	3:03:1079:ILE:HG22	2.40	0.52
3:03:1214:ASP:OD2	3:03:1216:ARG:HB2	2.10	0.52
7:E:44:GLU:O	7:E:48:PRO:HD2	2.10	0.52
9:G:27:ILE:O	9:G:28:ASP:HB2	2.09	0.52
16:N:95:THR:HG23	16:N:96:ILE:N	2.25	0.52
17:O:3:VAL:O	17:O:7:VAL:HG23	2.09	0.52
18:P:68:LEU:O	18:P:72:ILE:HG12	2.10	0.52
1:A:1190:G:H5''	8:F:175:HIS:CE1	2.44	0.51
3:03:1058:ARG:NH1	3:03:1240:ASP:HB3	2.24	0.51
4:04:217:LEU:O	4:04:221:ILE:HG22	2.10	0.51
4:04:514:THR:HG21	4:04:596:LEU:HD23	1.92	0.51
4:04:719:PHE:O	4:04:724:MET:HE2	2.10	0.51
7:E:11:LYS:HD2	7:E:11:LYS:N	2.25	0.51
13:K:116:ARG:NH1	13:K:116:ARG:HB2	2.25	0.51
1:A:1238:A:H2'	1:A:1239:A:H5'	1.91	0.51
1:A:1384:C:H2'	1:A:1385:G:H8	1.75	0.51
4:04:1262:ARG:O	4:04:1280:VAL:HG23	2.10	0.51
4:04:1356:LEU:HB3	4:04:1362:GLY:HA3	1.92	0.51
5:05:58:LEU:HG	5:05:59:ILE:HG12	1.92	0.51
7:E:23:TRP:CE3	7:E:189:THR:OG1	2.61	0.51
8:F:113:LYS:HD3	8:F:184:ASN:ND2	2.23	0.51
1:A:35:G:H4'	17:O:117:GLY:CA	2.40	0.51
3:03:138:ILE:HG22	3:03:139:ASN:OD1	2.09	0.51
3:03:251:ALA:HB2	3:03:263:VAL:HG11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:646:SER:HB3	3:03:649:GLN:HE21	1.74	0.51
3:03:835:GLU:HA	3:03:1052:VAL:O	2.10	0.51
3:03:1065:LYS:HD2	4:04:462:ASP:O	2.11	0.51
3:03:1286:THR:O	3:03:1290:MET:HB2	2.10	0.51
3:03:30:ILE:HG23	3:03:581:THR:H	1.76	0.51
3:03:605:TYR:C	3:03:606:LEU:HD12	2.35	0.51
3:03:1246:ARG:NH1	3:03:1258:PRO:HB3	2.25	0.51
4:04:615:LYS:HG2	5:05:5:THR:OG1	2.11	0.51
4:04:1249:ASN:HB3	4:04:1252:HIS:HD2	1.73	0.51
13:K:104:SER:HB2	13:K:125:ILE:HD11	1.92	0.51
25:W:23:ARG:CZ	25:W:59:ARG:HH22	2.23	0.51
25:W:79:THR:HG23	25:W:82:ILE:HD11	1.92	0.51
1:A:348:G:H2'	1:A:349:A:H8	1.75	0.51
1:A:1271:A:H5'	1:A:1314:C:H5''	1.92	0.51
1:A:1350:A:H2	12:J:33:GLY:HA3	1.75	0.51
3:03:569:ILE:HD13	4:04:780:ARG:HE	1.76	0.51
3:03:905:ILE:HG21	23:U:45:THR:HG22	1.93	0.51
4:04:292:VAL:O	4:04:295:GLU:HB3	2.10	0.51
4:04:1188:GLU:O	4:04:1189:MET:HE2	2.11	0.51
7:E:23:TRP:HE3	7:E:189:THR:HB	1.74	0.51
9:G:129:VAL:HG12	9:G:131:ILE:H	1.76	0.51
17:O:49:ARG:HH11	17:O:49:ARG:HG3	1.74	0.51
19:Q:40:ARG:HH11	19:Q:40:ARG:HG3	1.73	0.51
19:Q:92:ILE:HD12	19:Q:92:ILE:N	2.23	0.51
22:T:28:VAL:HG22	22:T:29:LYS:O	2.11	0.51
26:X:18:ARG:HD2	26:X:18:ARG:H	1.75	0.51
1:A:39:G:C2'	1:A:40:C:H5''	2.40	0.51
1:A:980:C:H4'	19:Q:58:ARG:HH21	1.75	0.51
1:A:1066:C:C2'	1:A:1067:A:H5'	2.41	0.51
3:03:119:GLU:HB2	3:03:489:PRO:HG2	1.93	0.51
3:03:367:TYR:CD2	3:03:376:PRO:HB3	2.45	0.51
3:03:835:GLU:C	3:03:836:LEU:HD12	2.35	0.51
3:03:1257:GLN:HE21	4:04:346:ARG:CD	2.24	0.51
4:04:21:LYS:HD2	4:04:22:ILE:N	2.26	0.51
4:04:507:VAL:HB	4:04:730:ALA:HB2	1.92	0.51
4:04:596:LEU:HD13	4:04:597:GLY:N	2.25	0.51
4:04:923:ILE:HD11	4:04:1252:HIS:HB3	1.93	0.51
5:05:62:GLN:O	5:05:66:VAL:HG23	2.10	0.51
7:E:18:HIS:HA	7:E:40:ILE:O	2.10	0.51
8:F:120:THR:HG23	8:F:188:ALA:HA	1.92	0.51
10:H:40:ASP:OD1	10:H:44:ARG:HB3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:72:PHE:CE1	19:Q:77:GLY:HA2	2.36	0.51
24:V:38:THR:HA	24:V:69:LYS:HA	1.92	0.51
1:A:314:C:H2'	1:A:315:A:C8	2.46	0.51
3:03:691:PRO:HG2	3:03:763:THR:HG21	1.91	0.51
4:04:536:LEU:C	4:04:536:LEU:HD13	2.36	0.51
7:E:23:TRP:CE3	7:E:189:THR:CB	2.94	0.51
15:M:11:LYS:NZ	15:M:11:LYS:HB2	2.24	0.51
21:S:5:ARG:HH11	21:S:5:ARG:HG2	1.76	0.51
1:A:751:U:C2'	1:A:752:G:H5'	2.41	0.51
2:01:100:LEU:O	2:01:143:ARG:HA	2.10	0.51
2:01:233:ASP:C	2:01:234:LEU:HD22	2.35	0.51
3:03:1242:LYS:HD3	4:04:354:VAL:CG1	2.39	0.51
7:E:20:THR:HB	7:E:22:TYR:CE1	2.46	0.51
8:F:206:ILE:OXT	8:F:206:ILE:HG12	2.10	0.51
14:L:97:LEU:O	14:L:102:PHE:HB2	2.11	0.51
15:M:40:ILE:HG22	15:M:42:LEU:HG	1.92	0.51
24:V:12:LEU:HD23	24:V:13:HIS:H	1.76	0.51
1:A:161:A:N6	1:A:347:G:H21	2.09	0.51
1:A:273:U:C2'	1:A:274:A:H5'	2.41	0.51
1:A:323:U:H4'	25:W:13:SER:HA	1.93	0.51
1:A:1290:G:O2'	14:L:41:GLU:HG3	2.11	0.51
3:03:196:VAL:HG13	3:03:196:VAL:O	2.11	0.51
3:03:209:ILE:HG23	3:03:210:LEU:N	2.26	0.51
3:03:725:GLN:O	3:03:773:LEU:HD11	2.11	0.51
4:04:768:ASN:OD1	4:04:771:GLN:HG3	2.11	0.51
4:04:850:LYS:C	4:04:852:GLY:N	2.66	0.51
4:04:1004:ALA:HB3	4:04:1017:VAL:HG12	1.93	0.51
25:W:4:LYS:C	25:W:6:ALA:N	2.68	0.51
1:A:358:U:H2'	1:A:359:G:C8	2.45	0.51
1:A:912:C:H5''	17:O:42:LYS:NZ	2.26	0.51
1:A:1071:C:H2'	1:A:1072:G:H8	1.75	0.51
1:A:1502:A:H5'	1:A:1504:G:N7	2.26	0.51
2:01:115:ILE:HG22	2:01:116:THR:N	2.26	0.51
3:03:540:ARG:HD3	3:03:568:ASN:HB3	1.92	0.51
3:03:812:PHE:HZ	4:04:503:SER:HB2	1.76	0.51
3:03:1151:LEU:HD12	3:03:1198:LEU:HD21	1.93	0.51
6:B:171:UNK:O	6:B:172:UNK:C	2.57	0.51
7:E:18:HIS:HA	7:E:40:ILE:HG13	1.91	0.51
7:E:21:ARG:O	7:E:23:TRP:CD1	2.64	0.51
10:H:24:VAL:HG13	10:H:29:ILE:HG22	1.93	0.51
16:N:110:THR:HG22	16:N:112:VAL:HG13	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:87:ARG:HA	20:R:87:ARG:NE	2.26	0.51
24:V:68:HIS:HB2	24:V:73:PHE:HE2	1.74	0.51
1:A:1345:U:H4'	1:A:1346:A:C8	2.46	0.50
3:03:20:GLN:HE21	3:03:1156:ARG:HH22	1.59	0.50
3:03:199:ASP:OD2	3:03:369:MET:HE1	2.11	0.50
3:03:468:LEU:O	3:03:472:GLU:HB2	2.10	0.50
4:04:108:ALA:HB3	4:04:280:LYS:HG2	1.93	0.50
7:E:28:LYS:O	7:E:31:ILE:HG13	2.10	0.50
9:G:117:VAL:CG2	9:G:122:ILE:HD12	2.38	0.50
14:L:64:ILE:HD13	14:L:78:ILE:HG23	1.92	0.50
23:U:38:LYS:HB3	23:U:38:LYS:HZ3	1.76	0.50
1:A:44:A:H2'	1:A:45:G:H5'	1.92	0.50
1:A:184:G:H2'	1:A:184:G:N3	2.26	0.50
1:A:409:U:H2'	1:A:410:G:C8	2.46	0.50
1:A:754:C:H5'	20:R:71:ARG:HH22	1.77	0.50
1:A:837:U:H2'	1:A:838:G:H8	1.74	0.50
3:03:241:LEU:HD13	3:03:285:ILE:HD13	1.92	0.50
7:E:16:PHE:HE2	7:E:40:ILE:HD11	1.75	0.50
7:E:45:LYS:O	7:E:45:LYS:HD3	2.11	0.50
9:G:56:GLU:O	9:G:60:VAL:HG23	2.11	0.50
1:A:156:C:O2'	1:A:157:U:H5'	2.12	0.50
4:04:497:GLU:O	4:04:499:ILE:N	2.44	0.50
7:E:17:GLY:CA	7:E:203:ASN:HB3	2.41	0.50
11:I:14:GLN:HB3	11:I:21:MET:HE1	1.93	0.50
13:K:10:LEU:HA	13:K:13:ILE:HD12	1.94	0.50
24:V:19:GLU:C	24:V:21:ALA:H	2.20	0.50
1:A:61:G:N7	25:W:4:LYS:HA	2.27	0.50
1:A:942:G:H21	14:L:125:GLN:CD	2.19	0.50
1:A:1273:C:H2'	1:A:1274:A:H5'	1.92	0.50
1:A:1375:A:H2'	1:A:1376:U:C6	2.46	0.50
2:01:150:ARG:HD2	2:01:150:ARG:C	2.36	0.50
3:03:698:PRO:HG3	3:03:1231:TYR:CE2	2.46	0.50
3:03:1141:LEU:HD12	3:03:1141:LEU:C	2.36	0.50
3:03:1331:ARG:HH22	4:04:245:LEU:HA	1.76	0.50
4:04:1145:PHE:HB3	4:04:1309:ILE:HD13	1.94	0.50
12:J:67:ASN:O	12:J:134:VAL:HG23	2.11	0.50
2:02:208:ASN:HD21	2:02:210:THR:CG2	2.23	0.50
3:03:515:MET:HA	3:03:526:HIS:CE1	2.47	0.50
3:03:1101:LEU:HD23	4:04:504:GLN:HB2	1.93	0.50
4:04:843:VAL:HG11	4:04:897:HIS:C	2.37	0.50
10:H:35:LEU:HD13	10:H:49:TYR:HD1	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:22:ILE:O	11:I:26:THR:HG22	2.11	0.50
12:J:125:ASP:HB3	12:J:130:LYS:O	2.11	0.50
13:K:120:LEU:HD12	13:K:120:LEU:O	2.11	0.50
15:M:84:VAL:HA	15:M:87:LEU:HG	1.93	0.50
1:A:319:G:O2'	1:A:320:A:H5'	2.11	0.50
3:03:150:HIS:CD2	3:03:454:ARG:HH11	2.30	0.50
3:03:1261:GLY:HA2	4:04:346:ARG:NH2	2.27	0.50
4:04:93:THR:HG22	4:04:94:GLN:H	1.77	0.50
4:04:1026:PRO:HB3	4:04:1120:THR:HG22	1.92	0.50
16:N:125:LYS:NZ	26:X:33:ARG:HD2	2.27	0.50
1:A:975:A:N6	15:M:50:THR:HG21	2.27	0.50
1:A:1500:A:H4'	1:A:1508:A:C5'	2.35	0.50
2:02:180:VAL:HA	2:02:207:THR:HA	1.92	0.50
3:03:839:VAL:HG13	3:03:886:LYS:NZ	2.27	0.50
3:03:940:GLU:HB3	3:03:946:LEU:HD21	1.93	0.50
3:03:1152:GLY:HA3	3:03:1197:GLU:HG2	1.93	0.50
4:04:130:MET:HE2	4:04:135:ILE:HG12	1.92	0.50
4:04:527:LEU:HB2	4:04:550:VAL:HG12	1.93	0.50
9:G:94:GLU:HA	9:G:99:ASN:OD1	2.11	0.50
11:I:21:MET:O	11:I:24:ARG:HB3	2.12	0.50
16:N:33:ILE:HG13	16:N:41:LEU:HB2	1.94	0.50
20:R:28:VAL:HG11	20:R:66:LEU:HD21	1.94	0.50
1:A:618:C:H5'	1:A:619:U:H5''	1.94	0.50
3:03:1214:ASP:HB2	3:03:1221:PHE:CZ	2.47	0.50
4:04:437:PHE:HA	4:04:485:MET:HE1	1.94	0.50
10:H:104:ILE:HD11	10:H:114:LEU:HB2	1.93	0.50
16:N:125:LYS:HZ1	26:X:33:ARG:HD2	1.76	0.50
19:Q:8:ARG:O	19:Q:12:ARG:NH1	2.45	0.50
1:A:867:G:H2'	1:A:868:C:C6	2.47	0.50
3:03:130:MET:CE	3:03:456:VAL:HG11	2.41	0.50
3:03:582:ASN:HB3	3:03:586:PHE:HB2	1.94	0.50
3:03:964:LEU:HD22	3:03:1025:PHE:CG	2.47	0.50
4:04:759:ILE:HD12	4:04:771:GLN:HB3	1.94	0.50
4:04:812:ASP:O	4:04:895:CYS:HB2	2.11	0.50
4:04:1362:GLY:HA2	4:04:1365:TYR:CB	2.42	0.50
7:E:135:LEU:HD12	7:E:138:THR:HB	1.93	0.50
9:G:149:LYS:HB3	9:G:149:LYS:NZ	2.27	0.50
14:L:29:ILE:HD12	14:L:64:ILE:O	2.12	0.50
14:L:43:ALA:HB1	14:L:46:VAL:HG11	1.93	0.50
24:V:54:ARG:HG3	24:V:55:GLN:H	1.77	0.50
1:A:1056:U:H4'	8:F:162:ALA:CB	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1240:U:H5'	12:J:41:ILE:HD11	1.93	0.49
7:E:44:GLU:OE2	7:E:48:PRO:HG2	2.12	0.49
1:A:376:G:H2'	1:A:377:G:C5'	2.42	0.49
1:A:418:C:H2'	1:A:419:C:C6	2.48	0.49
1:A:631:C:H3'	1:A:632:U:H5'	1.93	0.49
1:A:880:C:H2'	1:A:881:G:H8	1.77	0.49
2:02:35:PHE:HA	2:02:38:THR:CG2	2.37	0.49
3:03:475:VAL:O	3:03:479:LEU:HG	2.11	0.49
3:03:528:ARG:HD3	3:03:575:LEU:HD23	1.94	0.49
3:03:698:PRO:HD2	3:03:705:GLU:OE1	2.12	0.49
3:03:1321:GLU:O	3:03:1324:ASN:HB3	2.12	0.49
4:04:485:MET:HB3	4:04:488:ASN:ND2	2.23	0.49
4:04:799:ARG:HA	4:04:802:ASP:OD2	2.11	0.49
4:04:952:VAL:HG12	4:04:1015:GLU:O	2.13	0.49
17:O:79:ILE:HG22	17:O:103:CYS:HB2	1.94	0.49
1:A:137:U:H6	1:A:137:U:H5'	1.76	0.49
1:A:1202:U:O2'	19:Q:68:ARG:HB2	2.12	0.49
1:A:1218:C:H2'	1:A:1219:A:C8	2.47	0.49
2:01:124:VAL:HG13	2:01:125:LYS:HG2	1.92	0.49
3:03:176:ILE:HB	3:03:184:LEU:HB3	1.93	0.49
3:03:205:PRO:O	3:03:208:ILE:HG22	2.11	0.49
3:03:488:MET:HB2	3:03:491:ASP:OD2	2.13	0.49
4:04:22:ILE:H	4:04:1341:ARG:HG2	1.77	0.49
4:04:38:VAL:HG21	4:04:244:VAL:HG11	1.94	0.49
4:04:41:PRO:HA	4:04:56:LEU:CD1	2.42	0.49
4:04:422:LEU:HD13	4:04:471:PRO:HG3	1.95	0.49
4:04:1173:ARG:NH2	4:04:1196:LEU:HG	2.27	0.49
11:I:92:THR:O	11:I:93:LYS:HB2	2.12	0.49
12:J:144:ALA:O	12:J:148:LYS:HG3	2.12	0.49
16:N:22:ILE:HG12	16:N:31:VAL:HG13	1.94	0.49
24:V:20:LYS:NZ	24:V:20:LYS:HB3	2.27	0.49
1:A:828:U:O2	7:E:26:LYS:HG2	2.13	0.49
1:A:1279:G:H5''	15:M:9:ARG:NH1	2.18	0.49
2:01:184:ALA:HB2	3:03:1091:GLY:CA	2.42	0.49
2:01:232:VAL:HG22	2:02:221:ALA:HB1	1.93	0.49
4:04:53:ARG:HH22	4:04:88:CYS:CB	2.24	0.49
4:04:357:VAL:HG12	4:04:358:GLY:N	2.28	0.49
4:04:885:VAL:HA	4:04:888:CYS:HB2	1.93	0.49
7:E:36:ASN:C	7:E:38:VAL:H	2.20	0.49
9:G:33:ILE:HG13	9:G:34:GLU:HG3	1.95	0.49
12:J:24:LYS:HB3	12:J:24:LYS:HZ3	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:22:LYS:C	19:Q:22:LYS:HD3	2.38	0.49
1:A:405:U:C5	9:G:4:LEU:HG	2.48	0.49
1:A:864:A:H5''	10:H:89:THR:HG22	1.94	0.49
1:A:1377:A:N6	12:J:9:ARG:HH22	2.11	0.49
2:01:31:LEU:HD11	2:01:201:LEU:HB2	1.95	0.49
3:03:731:ARG:HH22	3:03:958:LYS:HB2	1.77	0.49
4:04:478:LEU:O	4:04:482:ALA:HB2	2.12	0.49
5:05:32:VAL:O	5:05:34:GLY:N	2.43	0.49
7:E:16:PHE:O	7:E:17:GLY:C	2.54	0.49
7:E:31:ILE:HD12	7:E:32:PHE:O	2.12	0.49
8:F:179:ALA:HB1	8:F:202:PHE:HE1	1.78	0.49
10:H:119:VAL:HG12	10:H:122:VAL:HG13	1.93	0.49
18:P:22:TYR:CB	18:P:65:GLU:HG2	2.32	0.49
1:A:348:G:H2'	1:A:349:A:C8	2.48	0.49
2:01:184:ALA:HB2	3:03:1091:GLY:HA3	1.93	0.49
2:02:100:LEU:N	2:02:100:LEU:HD12	2.27	0.49
3:03:61:SER:OG	3:03:476:LYS:HB3	2.13	0.49
3:03:139:ASN:H	3:03:143:ARG:HH11	1.61	0.49
3:03:207:THR:HG21	3:03:351:LEU:HD23	1.95	0.49
3:03:1082:ILE:HA	3:03:1085:MET:HG2	1.95	0.49
4:04:620:PHE:CE2	4:04:624:ILE:HD11	2.48	0.49
5:05:26:ARG:HD3	5:05:64:LEU:HD13	1.93	0.49
7:E:23:TRP:CZ2	7:E:25:PRO:HG3	2.46	0.49
14:L:34:LEU:C	14:L:34:LEU:HD23	2.38	0.49
23:U:40:VAL:HG11	23:U:45:THR:HG23	1.94	0.49
1:A:392:C:H2'	1:A:393:A:C8	2.48	0.49
1:A:865:A:H5'	1:A:1078:U:O4	2.12	0.49
2:01:26:VAL:CG2	2:01:203:ILE:HB	2.42	0.49
2:02:28:LEU:HD23	2:02:29:GLU:N	2.27	0.49
3:03:723:VAL:HA	3:03:776:PRO:HA	1.94	0.49
3:03:1285:TYR:O	3:03:1288:GLN:HB3	2.12	0.49
3:03:1293:VAL:HG11	3:03:1304:MET:HE2	1.94	0.49
4:04:81:ARG:HB2	7:E:206:ALA:HA	1.95	0.49
9:G:2:ARG:HD3	9:G:2:ARG:N	2.26	0.49
11:I:36:ILE:HA	11:I:64:VAL:HG23	1.94	0.49
13:K:95:MET:HB3	13:K:98:LEU:HB2	1.95	0.49
14:L:49:GLN:N	14:L:50:PRO:HD2	2.28	0.49
18:P:55:LEU:O	18:P:59:VAL:HG22	2.12	0.49
1:A:993:G:H21	1:A:996:A:H61	1.60	0.49
1:A:1014:A:C4'	24:V:13:HIS:HB2	2.36	0.49
1:A:1245:C:H2'	1:A:1246:A:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:363:LEU:HD11	3:03:382:GLU:HG2	1.95	0.49
4:04:554:GLU:HG3	4:04:566:LYS:HG3	1.94	0.49
7:E:24:ASN:N	7:E:25:PRO:HD3	2.24	0.49
15:M:59:LYS:HE3	15:M:62:ARG:HH12	1.77	0.49
23:U:49:ALA:O	23:U:50:LYS:C	2.53	0.49
1:A:440:C:C2'	1:A:441:A:H5''	2.42	0.49
1:A:952:U:H4'	1:A:964:A:H61	1.78	0.49
2:02:40:GLY:HA3	2:02:185:TYR:CD2	2.48	0.49
3:03:149:LEU:HD21	3:03:451:ARG:HD2	1.94	0.49
3:03:550:VAL:HG11	4:04:776:THR:HB	1.94	0.49
3:03:616:ILE:HG22	3:03:617:ALA:O	2.12	0.49
3:03:753:LEU:HB3	3:03:767:GLN:HB2	1.94	0.49
3:03:1107:MET:HG2	4:04:740:LEU:HD13	1.94	0.49
4:04:233:LYS:O	4:04:235:GLU:N	2.46	0.49
4:04:582:ILE:HD13	4:04:627:THR:HG21	1.94	0.49
4:04:722:ILE:HG23	4:04:723:TYR:N	2.27	0.49
4:04:1028:ILE:HG22	4:04:1119:ASP:C	2.38	0.49
7:E:41:ILE:HG22	7:E:43:LEU:N	2.23	0.49
22:T:24:ILE:HD12	22:T:24:ILE:N	2.27	0.49
1:A:686:U:O2'	1:A:687:A:H5'	2.13	0.49
1:A:815:A:H2'	1:A:1510:C:H1'	1.95	0.49
2:02:111:THR:HG22	2:02:129:VAL:HG22	1.94	0.49
3:03:15:PHE:HB3	3:03:1183:ALA:O	2.13	0.49
3:03:796:LEU:H	3:03:796:LEU:CD1	2.23	0.49
3:03:1331:ARG:HH22	4:04:245:LEU:CA	2.26	0.49
4:04:110:PRO:O	4:04:182:ALA:HB3	2.13	0.49
4:04:1282:TYR:O	4:04:1286:LYS:HG2	2.12	0.49
6:B:139:UNK:O	6:B:141:UNK:N	2.46	0.49
11:I:10:VAL:HA	11:I:83:ALA:O	2.13	0.49
14:L:80:HIS:O	14:L:83:THR:HB	2.13	0.49
17:O:98:ARG:HB2	17:O:116:TYR:HA	1.95	0.49
1:A:938:A:H4'	12:J:94:ARG:HH22	1.77	0.48
2:02:112:ALA:HB3	2:02:126:PRO:HA	1.95	0.48
3:03:387:ASN:HA	3:03:391:SER:HB2	1.93	0.48
3:03:448:LEU:HD11	3:03:557:ARG:HH11	1.78	0.48
4:04:64:PRO:HG2	4:04:92:VAL:HA	1.95	0.48
4:04:265:LEU:HD23	4:04:325:LYS:HG2	1.94	0.48
4:04:825:VAL:HG22	4:04:833:GLU:HB3	1.94	0.48
10:H:131:ASN:HD21	10:H:133:ILE:HB	1.78	0.48
13:K:113:ARG:HA	13:K:116:ARG:HH12	1.78	0.48
19:Q:54:SER:HB2	19:Q:57:SER:OG	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:X:42:THR:O	26:X:46:LYS:HG2	2.13	0.48
1:A:29:U:O2'	1:A:30:U:H5'	2.13	0.48
1:A:959:A:H2'	1:A:960:U:H4'	1.94	0.48
2:01:194:GLN:OE1	2:01:194:GLN:HA	2.13	0.48
2:02:95:LYS:CD	2:02:98:VAL:HB	2.43	0.48
3:03:180:ARG:HD2	3:03:180:ARG:C	2.38	0.48
3:03:1168:GLU:O	3:03:1172:LEU:HD23	2.13	0.48
4:04:83:VAL:HG23	7:E:73:LYS:O	2.13	0.48
4:04:372:MET:O	4:04:376:LEU:HD13	2.13	0.48
4:04:646:ILE:HG12	4:04:764:ARG:NH1	2.27	0.48
9:G:131:ILE:HG22	9:G:133:SER:H	1.77	0.48
10:H:15:ILE:HG23	10:H:109:ALA:HB1	1.95	0.48
16:N:27:ASN:O	16:N:56:LYS:HE2	2.12	0.48
16:N:59:PRO:HA	16:N:62:ALA:HB3	1.95	0.48
16:N:80:ASN:HA	16:N:105:ARG:O	2.13	0.48
17:O:88:ASP:HB2	17:O:89:LEU:HD12	1.95	0.48
19:Q:23:ARG:CB	19:Q:50:LEU:HD21	2.43	0.48
1:A:1170:A:H2'	1:A:1171:A:O4'	2.13	0.48
2:02:52:PRO:HA	2:02:149:GLY:O	2.13	0.48
3:03:204:LEU:HD13	3:03:208:ILE:CD1	2.42	0.48
4:04:22:ILE:HG23	4:04:22:ILE:O	2.12	0.48
4:04:680:ASN:HA	4:04:683:ILE:HD12	1.94	0.48
4:04:725:MET:C	4:04:732:GLY:HA3	2.38	0.48
4:04:1257:VAL:HA	4:04:1260:MET:HE3	1.95	0.48
12:J:96:ASN:C	12:J:98:LEU:H	2.20	0.48
19:Q:65:GLN:NE2	19:Q:82:LYS:HD2	2.28	0.48
23:U:55:LEU:O	23:U:59:ILE:HG13	2.12	0.48
2:01:25:LYS:HG2	2:01:204:GLU:HA	1.93	0.48
3:03:496:LYS:HA	3:03:499:SER:HB2	1.95	0.48
3:03:948:ILE:O	3:03:952:GLN:HG3	2.13	0.48
3:03:1164:PHE:HB2	3:03:1168:GLU:HB2	1.94	0.48
4:04:350:SER:HA	4:04:468:VAL:O	2.14	0.48
4:04:479:GLU:HG3	5:05:20:VAL:HG11	1.96	0.48
4:04:579:LEU:HD23	4:04:592:VAL:HB	1.95	0.48
4:04:960:LEU:HB3	4:04:963:VAL:CG1	2.43	0.48
5:05:50:ALA:O	5:05:54:ILE:HG12	2.13	0.48
7:E:118:GLU:OE1	7:E:152:LYS:HD3	2.13	0.48
11:I:85:ILE:HG13	11:I:86:ARG:N	2.29	0.48
14:L:83:THR:HG23	14:L:97:LEU:HD23	1.95	0.48
16:N:29:THR:HG21	16:N:62:ALA:HB2	1.95	0.48
18:P:86:ARG:O	18:P:90:HIS:HB2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:404:G:H1	1:A:499:A:N6	2.12	0.48
1:A:539:A:H2'	1:A:540:G:C8	2.49	0.48
1:A:684:U:O2	16:N:40:ALA:HB3	2.13	0.48
1:A:1258:G:H2'	1:A:1259:C:C6	2.48	0.48
3:03:193:ASN:HB3	3:03:195:PHE:CD2	2.48	0.48
3:03:453:ILE:HD12	3:03:586:PHE:O	2.12	0.48
4:04:435:GLN:OE1	4:04:453:VAL:HG11	2.13	0.48
7:E:21:ARG:O	7:E:23:TRP:N	2.46	0.48
7:E:117:LEU:HD23	7:E:141:LEU:HD13	1.96	0.48
13:K:107:LYS:NZ	13:K:107:LYS:HB3	2.28	0.48
16:N:29:THR:HG22	16:N:90:PRO:HG2	1.95	0.48
1:A:35:G:H2'	1:A:36:C:C6	2.49	0.48
1:A:1329:A:H5''	18:P:25:GLY:N	2.29	0.48
2:01:123:ILE:HG22	2:01:125:LYS:H	1.78	0.48
3:03:589:THR:HG22	3:03:606:LEU:C	2.38	0.48
4:04:60:ARG:HA	4:04:89:GLY:O	2.13	0.48
4:04:612:LEU:HD23	4:04:616:PRO:HB3	1.96	0.48
4:04:1289:ASN:HA	4:04:1292:LEU:HB2	1.95	0.48
4:04:1368:ASP:HA	4:04:1371:ARG:NH2	2.29	0.48
5:05:37:PRO:C	5:05:38:LEU:HD12	2.38	0.48
1:A:244:U:H5'	1:A:894:G:N2	2.28	0.48
1:A:987:G:H2'	1:A:988:G:C8	2.48	0.48
2:01:52:PRO:HD2	2:01:219:ARG:CZ	2.44	0.48
3:03:431:LYS:HA	3:03:434:ASP:OD2	2.13	0.48
3:03:448:LEU:HD11	3:03:557:ARG:NH1	2.28	0.48
3:03:579:ALA:HB1	3:03:587:LEU:HD21	1.94	0.48
3:03:603:ILE:O	3:03:603:ILE:HG13	2.13	0.48
4:04:450:HIS:HE1	4:04:452:LEU:HB2	1.79	0.48
4:04:537:TYR:CZ	4:04:544:LEU:HB2	2.48	0.48
4:04:818:GLU:HG3	4:04:819:GLY:H	1.78	0.48
4:04:848:VAL:HB	4:04:858:VAL:CG1	2.44	0.48
4:04:1307:LEU:HD12	4:04:1307:LEU:N	2.28	0.48
7:E:26:LYS:C	7:E:28:LYS:N	2.69	0.48
10:H:100:GLU:C	10:H:102:THR:H	2.20	0.48
11:I:18:VAL:HG12	11:I:19:PRO:HD3	1.96	0.48
12:J:28:ILE:CG2	12:J:104:VAL:HG21	2.43	0.48
25:W:80:ALA:O	25:W:84:LYS:HG3	2.14	0.48
1:A:358:U:H2'	1:A:359:G:H8	1.78	0.48
2:01:71:LYS:O	2:01:74:VAL:HG12	2.14	0.48
3:03:462:ASN:O	3:03:466:VAL:HG23	2.13	0.48
3:03:1101:LEU:HD12	3:03:1101:LEU:N	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:200:GLN:HA	4:04:203:GLU:OE1	2.14	0.48
4:04:221:ILE:HG23	4:04:222:LYS:N	2.29	0.48
4:04:693:VAL:O	4:04:696:ALA:HB3	2.14	0.48
10:H:10:LEU:HD12	10:H:11:GLN:N	2.29	0.48
10:H:133:ILE:O	10:H:137:ARG:HG3	2.13	0.48
11:I:93:LYS:HB3	11:I:93:LYS:HZ2	1.78	0.48
13:K:10:LEU:HD23	13:K:13:ILE:HD12	1.96	0.48
16:N:81:LEU:HD23	16:N:81:LEU:H	1.79	0.48
1:A:402:G:H5''	9:G:70:GLN:NE2	2.29	0.48
1:A:443:C:H2'	1:A:444:G:C8	2.48	0.48
1:A:1238:A:H2	1:A:1241:G:H1'	1.78	0.48
2:01:47:LEU:O	2:01:180:VAL:HG11	2.14	0.48
3:03:42:ASP:N	3:03:43:PRO:HD3	2.28	0.48
3:03:798:GLN:OE1	3:03:827:ARG:HB2	2.12	0.48
4:04:278:ARG:O	4:04:282:LEU:HG	2.14	0.48
4:04:547:ARG:HH11	4:04:547:ARG:HG3	1.78	0.48
4:04:1166:GLY:O	4:04:1174:ARG:HB2	2.14	0.48
4:04:1227:HIS:CA	4:04:1230:THR:HG22	2.43	0.48
7:E:67:ILE:CD1	7:E:160:ALA:HB3	2.43	0.48
9:G:120:LYS:HG2	9:G:130:ASN:HD22	1.79	0.48
1:A:1317:C:OP2	19:Q:27:LYS:HD3	2.14	0.48
1:A:1369:C:H2'	1:A:1370:G:C8	2.48	0.48
2:01:56:VAL:O	2:01:173:VAL:HG23	2.14	0.48
2:01:78:ILE:HD13	2:01:81:ILE:HD12	1.96	0.48
3:03:431:LYS:O	3:03:434:ASP:HB2	2.13	0.48
3:03:1253:LEU:O	3:03:1253:LEU:HD13	2.14	0.48
9:G:170:LEU:HD23	9:G:181:PHE:HA	1.96	0.48
18:P:9:PRO:HG2	18:P:44:ILE:HG21	1.96	0.48
21:S:70:ARG:O	21:S:74:LEU:HG	2.14	0.48
25:W:55:PRO:C	25:W:56:ILE:HD12	2.39	0.48
1:A:359:G:C5	1:A:360:G:H1'	2.48	0.47
1:A:676:A:C2	16:N:120:CYS:HB3	2.49	0.47
2:02:12:ARG:HB2	2:02:12:ARG:CZ	2.44	0.47
3:03:615:VAL:C	3:03:616:ILE:HD12	2.39	0.47
3:03:689:ALA:HA	3:03:1233:LEU:HD11	1.96	0.47
4:04:399:LYS:O	4:04:402:GLU:HB3	2.14	0.47
4:04:442:ILE:CG2	4:04:448:GLN:HE21	2.27	0.47
9:G:48:SER:O	9:G:52:VAL:HG23	2.14	0.47
10:H:12:GLU:HA	10:H:38:VAL:HG12	1.96	0.47
10:H:131:ASN:CB	10:H:134:ASN:HD22	2.25	0.47
13:K:110:MET:HB2	13:K:114:ALA:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1306:A:H61	1:A:1331:G:H1'	1.78	0.47
3:03:97:ARG:HB3	3:03:121:GLU:CA	2.43	0.47
3:03:575:LEU:HD11	3:03:579:ALA:HB3	1.95	0.47
4:04:41:PRO:HB2	4:04:270:ARG:HG3	1.95	0.47
4:04:845:ALA:O	4:04:860:ARG:HG3	2.14	0.47
4:04:1011:VAL:HG12	4:04:1012:ALA:N	2.29	0.47
9:G:161:ALA:C	9:G:163:GLN:H	2.22	0.47
18:P:19:THR:HG21	18:P:26:LYS:HD2	1.96	0.47
26:X:49:LYS:O	26:X:53:VAL:HG23	2.14	0.47
1:A:454:G:H22	1:A:478:A:H2	1.62	0.47
1:A:620:C:H5'	9:G:127:ARG:HD3	1.97	0.47
2:01:32:GLU:HB2	2:01:35:PHE:CD2	2.49	0.47
3:03:56:VAL:HG22	3:03:59:ILE:HG12	1.96	0.47
3:03:1025:PHE:O	3:03:1028:LYS:HB2	2.14	0.47
3:03:1156:ARG:HH11	3:03:1156:ARG:HG3	1.79	0.47
4:04:662:ALA:O	4:04:666:GLU:HG3	2.14	0.47
4:04:1341:ARG:HH21	4:04:1343:GLU:HG3	1.79	0.47
15:M:102:LEU:N	15:M:102:LEU:HD23	2.29	0.47
24:V:10:ILE:HD12	24:V:10:ILE:O	2.13	0.47
24:V:54:ARG:HG3	24:V:55:GLN:N	2.28	0.47
1:A:17:U:O2'	1:A:18:C:H5'	2.14	0.47
1:A:370:C:H2'	1:A:371:A:C8	2.49	0.47
1:A:517:G:H4'	1:A:519:C:C2	2.49	0.47
1:A:735:C:O2'	1:A:736:C:H5'	2.15	0.47
3:03:237:LEU:HD13	3:03:292:ILE:HD12	1.95	0.47
3:03:757:THR:OG1	3:03:765:ILE:HG23	2.14	0.47
4:04:506:VAL:O	4:04:510:LEU:HD13	2.14	0.47
4:04:646:ILE:CG1	4:04:764:ARG:HD3	2.44	0.47
4:04:984:LEU:HB3	4:04:993:GLU:H	1.80	0.47
9:G:158:LEU:O	9:G:162:GLU:HG2	2.14	0.47
9:G:158:LEU:O	9:G:158:LEU:HD23	2.13	0.47
15:M:40:ILE:HB	15:M:73:LEU:HB2	1.96	0.47
16:N:60:PHE:O	16:N:64:VAL:HG23	2.14	0.47
1:A:229:U:H2'	1:A:230:G:C8	2.50	0.47
1:A:1129:C:C5'	14:L:17:ARG:HH22	2.26	0.47
2:02:14:VAL:CG2	2:02:26:VAL:HG13	2.42	0.47
2:02:181:GLU:HB3	4:04:531:LYS:HE3	1.96	0.47
3:03:228:VAL:HG23	3:03:337:PHE:HB2	1.96	0.47
4:04:247:PRO:HA	4:04:250:ARG:HE	1.79	0.47
4:04:449:LEU:HD21	4:04:457:TYR:CE2	2.49	0.47
4:04:490:ILE:HG13	4:04:491:LEU:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:691:ASP:O	4:04:694:SER:HB3	2.13	0.47
12:J:86:VAL:O	12:J:88:VAL:HG23	2.13	0.47
12:J:138:GLU:HB3	12:J:142:ARG:HH12	1.79	0.47
18:P:82:LEU:HD13	24:V:64:GLU:HB2	1.97	0.47
25:W:35:TYR:CE2	25:W:78:LEU:HD12	2.50	0.47
1:A:645:G:H1'	22:T:27:PHE:HZ	1.79	0.47
2:01:159:ILE:HG12	2:01:159:ILE:O	2.15	0.47
2:01:182:ARG:H	2:01:206:GLU:HB3	1.80	0.47
4:04:28:ASP:C	4:04:29:MET:HE2	2.39	0.47
4:04:697:MET:O	4:04:701:LEU:HD23	2.14	0.47
7:E:30:PHE:HB3	7:E:45:LYS:CG	2.42	0.47
10:H:21:SER:HA	10:H:31:SER:H	1.80	0.47
16:N:126:ARG:HA	16:N:126:ARG:HE	1.78	0.47
19:Q:91:GLU:HB3	19:Q:92:ILE:HD12	1.96	0.47
21:S:72:ALA:O	21:S:76:LYS:HG2	2.15	0.47
25:W:23:ARG:NH1	25:W:59:ARG:HH22	2.12	0.47
1:A:6:G:O2'	1:A:298:A:H1'	2.15	0.47
1:A:33:A:H61	1:A:551:U:H3	1.61	0.47
1:A:107:G:H2'	1:A:108:G:C5'	2.45	0.47
1:A:136:C:H2'	1:A:137:U:H5'	1.97	0.47
1:A:521:G:H21	1:A:536:C:H5'	1.79	0.47
2:01:70:THR:HG22	2:01:77:ASP:HA	1.96	0.47
2:02:15:ASP:HB3	2:02:27:THR:HB	1.96	0.47
2:02:99:ILE:C	2:02:100:LEU:HD12	2.40	0.47
3:03:455:SER:OG	3:03:458:GLU:HG3	2.14	0.47
3:03:893:THR:HG21	4:04:254:PRO:HB3	1.97	0.47
4:04:141:PHE:CE1	4:04:181:GLY:HA3	2.50	0.47
4:04:598:LYS:HB2	4:04:728:SER:O	2.14	0.47
4:04:957:SER:HB3	4:04:985:ILE:O	2.15	0.47
7:E:27:MET:HG3	7:E:189:THR:HA	1.96	0.47
8:F:71:ARG:HA	8:F:72:PRO:HD2	1.75	0.47
8:F:135:ARG:HH11	8:F:135:ARG:HG3	1.80	0.47
9:G:20:LEU:HD12	9:G:21:LYS:N	2.30	0.47
9:G:30:LYS:O	9:G:32:LYS:N	2.48	0.47
14:L:94:ARG:HH12	14:L:103:VAL:CG2	2.27	0.47
15:M:9:ARG:HG2	15:M:11:LYS:HG3	1.96	0.47
19:Q:25:GLU:C	19:Q:27:LYS:H	2.21	0.47
1:A:211:G:C2'	1:A:212:G:H5'	2.45	0.47
1:A:722:G:H3'	1:A:722:G:N3	2.30	0.47
2:01:81:ILE:HG23	2:01:130:ILE:HG22	1.97	0.47
2:02:193:GLU:HB3	4:04:406:ALA:HB1	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:39:ILE:HA	3:03:49:LEU:HD12	1.96	0.47
3:03:119:GLU:HG3	3:03:489:PRO:CD	2.45	0.47
3:03:964:LEU:HD22	3:03:1025:PHE:CD1	2.49	0.47
4:04:19:ALA:HB1	4:04:1343:GLU:O	2.15	0.47
7:E:9:MET:O	7:E:10:LEU:HB2	2.15	0.47
7:E:21:ARG:HA	7:E:23:TRP:HD1	1.78	0.47
8:F:42:LEU:HD21	8:F:67:ILE:HD11	1.97	0.47
14:L:128:LYS:HB2	14:L:128:LYS:NZ	2.30	0.47
16:N:81:LEU:CD2	16:N:104:PHE:HB3	2.45	0.47
19:Q:48:GLN:CB	24:V:12:LEU:HD22	2.42	0.47
3:03:119:GLU:HG3	3:03:489:PRO:HD2	1.97	0.47
3:03:521:LEU:O	3:03:525:THR:HG22	2.15	0.47
3:03:591:TYR:O	3:03:603:ILE:HA	2.12	0.47
3:03:1331:ARG:HH22	4:04:245:LEU:N	2.13	0.47
4:04:347:VAL:HG23	4:04:350:SER:CB	2.44	0.47
4:04:744:ARG:HB3	4:04:759:ILE:CB	2.29	0.47
4:04:1250:ASP:O	4:04:1254:GLU:HG3	2.15	0.47
7:E:20:THR:O	7:E:21:ARG:C	2.58	0.47
10:H:87:VAL:O	10:H:87:VAL:HG13	2.15	0.47
10:H:131:ASN:ND2	10:H:133:ILE:HB	2.30	0.47
11:I:75:GLU:HA	11:I:78:PHE:CD2	2.48	0.47
16:N:24:ALA:HB3	16:N:87:GLY:O	2.14	0.47
21:S:36:VAL:HG13	21:S:36:VAL:O	2.15	0.47
25:W:34:VAL:HG21	25:W:53:MET:SD	2.55	0.47
25:W:43:LYS:O	25:W:47:GLN:HG3	2.15	0.47
3:03:97:ARG:HD2	3:03:121:GLU:HB2	1.97	0.47
3:03:498:ILE:N	3:03:498:ILE:HD12	2.29	0.47
3:03:667:LEU:HD21	3:03:704:MET:HB2	1.97	0.47
3:03:724:VAL:HG11	3:03:771:VAL:HG11	1.97	0.47
3:03:862:LEU:HD23	3:03:865:LEU:HB2	1.97	0.47
3:03:934:PHE:HA	3:03:1040:ASP:HB3	1.96	0.47
3:03:1029:LEU:HA	3:03:1032:LYS:HB2	1.97	0.47
4:04:263:SER:O	4:04:265:LEU:N	2.48	0.47
4:04:811:GLU:O	4:04:895:CYS:HA	2.15	0.47
4:04:1221:LEU:HD13	4:04:1221:LEU:C	2.40	0.47
7:E:126:PHE:HD1	7:E:126:PHE:H	1.63	0.47
8:F:59:PRO:HG2	8:F:62:SER:OG	2.15	0.47
12:J:78:ARG:H	12:J:78:ARG:CD	2.21	0.47
16:N:81:LEU:HD21	16:N:104:PHE:HB3	1.97	0.47
25:W:13:SER:O	25:W:17:ARG:HB2	2.15	0.47
25:W:31:ILE:HG12	25:W:53:MET:HE3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:54:GLN:HA	25:W:57:VAL:CG1	2.26	0.47
1:A:59:A:H1'	1:A:354:G:N2	2.30	0.46
1:A:219:U:H2'	1:A:220:G:C5'	2.45	0.46
1:A:383:A:H5''	1:A:454:G:H4'	1.97	0.46
1:A:545:C:H5''	9:G:61:ARG:NH1	2.30	0.46
1:A:987:G:H2'	1:A:988:G:H8	1.80	0.46
1:A:1237:C:OP1	1:A:1238:A:H1'	2.14	0.46
3:03:753:LEU:HD23	3:03:767:GLN:O	2.14	0.46
3:03:1335:ILE:HD11	4:04:1336:ALA:HB2	1.98	0.46
4:04:174:ASP:O	4:04:175:GLU:C	2.57	0.46
4:04:197:GLU:O	4:04:201:LEU:HG	2.14	0.46
4:04:1344:LEU:HD11	4:04:1353:VAL:CG1	2.44	0.46
7:E:40:ILE:HG23	7:E:41:ILE:N	2.31	0.46
10:H:18:ASN:O	10:H:32:PHE:HD1	1.98	0.46
10:H:119:VAL:HG11	10:H:122:VAL:CG1	2.45	0.46
12:J:74:VAL:HG12	12:J:87:PRO:HA	1.97	0.46
12:J:138:GLU:O	12:J:142:ARG:HG3	2.14	0.46
21:S:12:LYS:O	21:S:13:LYS:HB2	2.15	0.46
1:A:219:U:H2'	1:A:220:G:H5''	1.96	0.46
1:A:228:A:H2	21:S:1:MET:HA	1.80	0.46
1:A:350:G:H2'	1:A:351:G:C8	2.50	0.46
1:A:1014:A:H4'	24:V:13:HIS:CB	2.38	0.46
1:A:1329:A:H4'	18:P:23:GLY:O	2.16	0.46
1:A:1343:G:H4'	14:L:123:ARG:HB3	1.97	0.46
1:A:1392:G:H2'	1:A:1393:U:C6	2.51	0.46
2:01:48:LEU:HG	2:01:183:ILE:HD12	1.98	0.46
2:02:155:ALA:HB1	2:02:172:LEU:HD12	1.97	0.46
3:03:153:PRO:CD	3:03:452:ARG:HD2	2.45	0.46
4:04:81:ARG:HB2	7:E:207:ILE:H	1.81	0.46
4:04:598:LYS:HA	4:04:601:ILE:HG22	1.98	0.46
5:05:3:ARG:NH2	5:05:52:ARG:HD2	2.29	0.46
5:05:27:ALA:CA	5:05:30:MET:HE3	2.35	0.46
7:E:80:VAL:HA	7:E:214:LEU:HD21	1.97	0.46
10:H:113:VAL:O	10:H:116:VAL:HG22	2.16	0.46
12:J:90:VAL:HG22	12:J:91:ARG:N	2.29	0.46
2:01:58:GLU:HG2	2:01:172:LEU:HG	1.97	0.46
3:03:934:PHE:O	3:03:1048:LYS:HA	2.15	0.46
3:03:1131:MET:HG2	3:03:1136:GLN:HB2	1.98	0.46
3:03:1235:LEU:HD12	3:03:1235:LEU:N	2.29	0.46
3:03:1280:ALA:HB3	4:04:431:ARG:HB3	1.97	0.46
4:04:29:MET:O	4:04:32:SER:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:55:GLY:H	4:04:58:CYS:HB2	1.79	0.46
4:04:214:ARG:CA	4:04:217:LEU:HB2	2.34	0.46
4:04:309:ASN:ND2	4:04:312:ARG:HB2	2.30	0.46
4:04:973:LEU:HB3	4:04:1003:LEU:HB2	1.96	0.46
4:04:1150:PRO:HG2	4:04:1153:PRO:HG3	1.97	0.46
4:04:1286:LYS:HD2	4:04:1290:ARG:NH2	2.29	0.46
7:E:27:MET:CB	7:E:189:THR:HG22	2.46	0.46
16:N:110:THR:CG2	16:N:112:VAL:HG13	2.45	0.46
16:N:116:PRO:C	16:N:118:ASN:H	2.23	0.46
17:O:20:VAL:HG23	17:O:20:VAL:O	2.15	0.46
1:A:18:C:H4'	1:A:1078:U:O2	2.16	0.46
1:A:440:C:H3'	1:A:441:A:H5''	1.96	0.46
1:A:1123:U:O2'	1:A:1124:G:H5'	2.16	0.46
1:A:1210:C:H2'	1:A:1211:U:H5'	1.98	0.46
1:A:1225:A:H5'	1:A:1226:C:OP2	2.15	0.46
2:02:26:VAL:O	2:02:202:VAL:HA	2.16	0.46
3:03:980:VAL:HA	3:03:984:VAL:HA	1.97	0.46
3:03:1011:LEU:O	3:03:1012:GLU:C	2.58	0.46
3:03:1313:HIS:CD2	5:05:31:GLN:HE22	2.30	0.46
4:04:796:LEU:O	4:04:800:LEU:HD13	2.15	0.46
5:05:53:GLU:O	5:05:58:LEU:HD23	2.15	0.46
7:E:20:THR:HA	7:E:38:VAL:CG1	2.45	0.46
7:E:20:THR:HA	7:E:38:VAL:HG12	1.97	0.46
17:O:43:LYS:HG3	17:O:44:PRO:HD3	1.97	0.46
20:R:64:LYS:HA	20:R:67:ASP:HB3	1.98	0.46
2:01:112:ALA:HB2	2:01:130:ILE:HD11	1.97	0.46
2:02:136:GLU:HB3	2:02:137:ASN:H	1.55	0.46
3:03:557:ARG:HH12	3:03:608:ALA:HB2	1.76	0.46
3:03:842:ASP:N	3:03:848:GLU:H	2.12	0.46
4:04:132:LEU:C	4:04:132:LEU:HD13	2.41	0.46
4:04:380:PHE:HB3	4:04:415:VAL:HG11	1.97	0.46
4:04:586:GLY:HA3	4:04:612:LEU:CD1	2.45	0.46
4:04:647:PRO:C	4:04:649:LYS:H	2.23	0.46
4:04:1156:LEU:HD13	4:04:1209:VAL:HA	1.98	0.46
5:05:42:GLU:C	5:05:44:ASP:H	2.23	0.46
12:J:41:ILE:HG23	12:J:116:ALA:HB2	1.97	0.46
14:L:57:VAL:HB	14:L:58:GLU:OE1	2.16	0.46
25:W:53:MET:HG3	25:W:54:GLN:N	2.31	0.46
25:W:54:GLN:N	25:W:55:PRO:CD	2.78	0.46
1:A:193:C:O2'	1:A:194:C:H5'	2.15	0.46
1:A:778:G:N2	16:N:121:ARG:HD3	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:02:75:GLN:N	2:02:134:THR:HG22	2.31	0.46
3:03:178:PRO:HD3	3:03:183:TRP:HA	1.98	0.46
3:03:436:ARG:HA	3:03:436:ARG:NE	2.31	0.46
3:03:753:LEU:HA	3:03:767:GLN:OE1	2.16	0.46
3:03:899:GLU:O	3:03:903:ARG:HB2	2.15	0.46
4:04:364:HIS:NE2	5:05:2:ALA:HB3	2.31	0.46
9:G:164:ARG:HG2	9:G:164:ARG:HH11	1.80	0.46
12:J:47:GLU:OE2	12:J:57:GLU:HG2	2.16	0.46
14:L:124:PRO:O	14:L:125:GLN:C	2.59	0.46
24:V:49:ALA:HB1	24:V:56:HIS:HB3	1.98	0.46
1:A:22:G:OP2	1:A:561:U:H1'	2.16	0.46
1:A:1123:U:H2'	1:A:1124:G:C8	2.50	0.46
1:A:1319:A:H4'	1:A:1320:C:C5	2.51	0.46
3:03:593:LYS:HB3	3:03:602:GLU:HB2	1.98	0.46
4:04:68:TYR:CE1	4:04:81:ARG:HG2	2.51	0.46
4:04:108:ALA:CB	4:04:280:LYS:HG2	2.46	0.46
4:04:423:LEU:HD22	4:04:437:PHE:CD2	2.51	0.46
4:04:436:ALA:O	4:04:485:MET:HE3	2.16	0.46
4:04:1322:ALA:O	4:04:1326:GLN:HB2	2.16	0.46
7:E:25:PRO:O	7:E:28:LYS:CB	2.64	0.46
11:I:9:MET:O	11:I:84:VAL:HA	2.15	0.46
15:M:93:ALA:HB3	15:M:96:VAL:HB	1.96	0.46
16:N:86:LYS:HE3	16:N:114:PRO:HD2	1.98	0.46
18:P:18:LEU:O	18:P:24:VAL:HG13	2.15	0.46
22:T:67:SER:N	22:T:70:LYS:HB3	2.30	0.46
1:A:557:G:H2'	1:A:558:G:O4'	2.15	0.46
1:A:981:U:H5''	19:Q:5:MET:SD	2.56	0.46
1:A:993:G:H2'	1:A:993:G:N3	2.31	0.46
2:02:12:ARG:HB3	2:02:12:ARG:NH1	2.31	0.46
3:03:698:PRO:HG3	3:03:1231:TYR:CZ	2.51	0.46
3:03:929:ILE:HG13	3:03:930:ASP:H	1.81	0.46
4:04:81:ARG:NE	7:E:206:ALA:HB1	2.31	0.46
4:04:121:PRO:O	4:04:123:ARG:N	2.49	0.46
4:04:421:VAL:HG11	4:04:439:PRO:HG3	1.97	0.46
4:04:1266:ILE:O	4:04:1275:LEU:HA	2.16	0.46
4:04:1321:SER:O	4:04:1324:SER:HB2	2.16	0.46
7:E:25:PRO:HB2	7:E:28:LYS:HB2	1.97	0.46
7:E:163:VAL:HB	7:E:185:ALA:HB2	1.98	0.46
13:K:6:ILE:O	13:K:10:LEU:HG	2.15	0.46
1:A:1056:U:H4'	8:F:162:ALA:HB2	1.97	0.46
2:01:218:ARG:HA	2:02:231:PHE:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:6:THR:HG21	3:03:706:ARG:NH2	2.31	0.46
3:03:86:GLN:HE22	3:03:754:THR:HG21	1.81	0.46
3:03:157:PHE:HA	3:03:174:ALA:HA	1.97	0.46
3:03:175:ARG:HA	3:03:185:ASP:HA	1.97	0.46
4:04:527:LEU:HD13	4:04:548:VAL:HG11	1.97	0.46
25:W:59:ARG:O	25:W:63:LYS:HG3	2.16	0.46
2:01:71:LYS:HG2	2:01:140:ILE:HG22	1.98	0.46
2:02:65:LEU:HG	2:02:169:GLY:HA2	1.98	0.46
3:03:257:ALA:HB1	3:03:282:VAL:HG11	1.97	0.46
3:03:829:THR:HG23	3:03:1059:ARG:HA	1.97	0.46
3:03:1132:LEU:CD1	3:03:1174:GLU:HG2	2.45	0.46
3:03:1223:ARG:O	3:03:1224:PRO:C	2.59	0.46
4:04:64:PRO:CG	4:04:92:VAL:HA	2.46	0.46
4:04:1089:LEU:N	4:04:1089:LEU:HD12	2.31	0.46
9:G:105:GLY:O	9:G:158:LEU:HA	2.15	0.46
11:I:5:GLU:HB2	11:I:90:MET:CG	2.45	0.46
11:I:76:THR:HG23	11:I:79:ARG:HH21	1.81	0.46
14:L:62:LEU:N	14:L:62:LEU:HD12	2.31	0.46
17:O:85:ARG:HH12	17:O:93:ARG:HG2	1.81	0.46
26:X:35:ARG:HH11	26:X:35:ARG:HB2	1.80	0.46
1:A:352:C:H4'	1:A:354:G:OP1	2.14	0.45
1:A:1167:A:H2'	1:A:1167:A:N3	2.31	0.45
1:A:1323:G:H2'	1:A:1324:A:C8	2.51	0.45
2:01:77:ASP:O	2:01:81:ILE:HG13	2.16	0.45
3:03:39:ILE:HG23	3:03:39:ILE:O	2.15	0.45
3:03:215:TYR:HD2	3:03:220:ILE:HG12	1.81	0.45
3:03:962:GLU:O	3:03:966:ILE:HG13	2.15	0.45
4:04:664:ILE:HG22	4:04:678:ARG:HG2	1.97	0.45
4:04:747:MET:O	4:04:754:ILE:HD12	2.16	0.45
4:04:863:LEU:HD21	4:04:901:ARG:HD3	1.98	0.45
4:04:1137:GLY:O	4:04:1141:VAL:HG23	2.15	0.45
7:E:27:MET:O	7:E:28:LYS:C	2.59	0.45
8:F:129:PHE:CE2	8:F:156:LEU:HD13	2.51	0.45
11:I:10:VAL:O	11:I:57:ALA:HB1	2.16	0.45
17:O:89:LEU:HD12	17:O:89:LEU:N	2.31	0.45
25:W:66:ILE:HG23	25:W:70:LYS:HD3	1.98	0.45
1:A:104:G:C8	25:W:8:LYS:HE3	2.51	0.45
3:03:532:ALA:HB3	3:03:571:LEU:HA	1.97	0.45
3:03:575:LEU:HG	3:03:576:SER:N	2.32	0.45
3:03:615:VAL:CG2	3:03:636:CYS:HB3	2.46	0.45
3:03:738:GLU:HA	3:03:741:MET:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:43:THR:HA	4:04:52:GLU:HB3	1.98	0.45
4:04:293:ARG:HA	4:04:296:LYS:HZ3	1.81	0.45
4:04:569:LEU:HD12	4:04:569:LEU:N	2.31	0.45
10:H:20:VAL:HG23	10:H:31:SER:HB3	1.97	0.45
12:J:59:GLU:C	12:J:61:PHE:H	2.24	0.45
12:J:113:LYS:HB2	12:J:117:LEU:HD23	1.98	0.45
1:A:367:U:O2'	1:A:368:U:H4'	2.17	0.45
1:A:666:G:H2'	1:A:667:G:H8	1.81	0.45
1:A:1237:C:H4'	1:A:1334:G:N2	2.32	0.45
3:03:139:ASN:HB2	3:03:143:ARG:HH12	1.81	0.45
3:03:833:ILE:HA	3:03:1054:LEU:O	2.16	0.45
3:03:926:GLY:HA3	3:03:1056:VAL:HG22	1.98	0.45
4:04:336:GLY:HA2	4:04:1324:SER:HB3	1.98	0.45
4:04:1235:ASN:HA	4:04:1238:GLN:CB	2.46	0.45
8:F:129:PHE:CD2	8:F:156:LEU:HD13	2.52	0.45
9:G:102:TYR:C	9:G:104:MET:H	2.24	0.45
9:G:170:LEU:HD21	9:G:181:PHE:HD1	1.81	0.45
9:G:186:GLU:HB3	9:G:189:ASP:OD2	2.16	0.45
17:O:73:LEU:CD2	17:O:79:ILE:HG21	2.45	0.45
1:A:1230:C:H41	18:P:103:THR:HG21	1.81	0.45
2:01:68:TYR:OH	3:03:1057:LYS:HG3	2.17	0.45
2:02:115:ILE:HG22	2:02:116:THR:N	2.30	0.45
2:02:145:LYS:C	2:02:145:LYS:HD3	2.42	0.45
2:02:215:GLU:O	2:02:218:ARG:HG2	2.16	0.45
3:03:1246:ARG:HD3	3:03:1246:ARG:O	2.16	0.45
4:04:976:THR:HG22	4:04:1028:ILE:HG13	1.99	0.45
8:F:126:ARG:HG2	8:F:126:ARG:HH11	1.82	0.45
10:H:82:HIS:HB2	10:H:83:PRO:HD2	1.99	0.45
17:O:31:GLY:HA3	17:O:54:VAL:HG13	1.98	0.45
22:T:11:VAL:HA	22:T:22:VAL:HA	1.97	0.45
2:01:145:LYS:HD3	2:01:145:LYS:C	2.41	0.45
2:02:158:ARG:HA	2:02:158:ARG:NE	2.30	0.45
3:03:841:ARG:CB	3:03:1047:LEU:HB2	2.47	0.45
3:03:842:ASP:H	3:03:848:GLU:N	2.12	0.45
9:G:158:LEU:HD23	9:G:158:LEU:C	2.41	0.45
9:G:171:GLU:HB2	9:G:180:THR:HB	1.97	0.45
10:H:111:ARG:O	10:H:115:GLU:HG3	2.17	0.45
12:J:36:SER:HB3	14:L:42:THR:HG22	1.98	0.45
2:01:102:LEU:HD13	2:01:103:ASN:N	2.31	0.45
2:02:98:VAL:HG11	2:02:121:VAL:HG22	1.99	0.45
3:03:29:SER:HA	3:03:32:LEU:HB2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:97:ARG:HB3	3:03:121:GLU:CB	2.46	0.45
3:03:520:PRO:O	3:03:524:ILE:HG13	2.16	0.45
4:04:1230:THR:HG23	4:04:1231:ARG:N	2.32	0.45
5:05:24:ALA:O	5:05:28:ARG:HG3	2.17	0.45
7:E:163:VAL:HB	7:E:185:ALA:CB	2.47	0.45
8:F:7:ASN:O	8:F:11:LEU:HG	2.17	0.45
8:F:163:ARG:HD3	8:F:163:ARG:N	2.30	0.45
10:H:29:ILE:HG23	10:H:29:ILE:O	2.17	0.45
17:O:85:ARG:NH1	17:O:93:ARG:HG2	2.32	0.45
1:A:44:A:C2'	1:A:45:G:H5'	2.46	0.45
2:01:76:GLU:OE2	2:01:131:CYS:HA	2.16	0.45
2:01:79:LEU:HD13	2:01:79:LEU:C	2.42	0.45
2:01:144:ILE:HG22	2:01:146:VAL:HG23	1.98	0.45
3:03:300:ASP:OD1	3:03:313:ALA:HB2	2.17	0.45
3:03:1170:MET:O	3:03:1173:ALA:HB3	2.16	0.45
4:04:1005:LYS:HG3	4:04:1011:VAL:CG2	2.46	0.45
4:04:1047:THR:HG23	4:04:1049:GLN:HG3	1.99	0.45
4:04:1238:GLN:O	4:04:1242:ARG:HB2	2.17	0.45
7:E:21:ARG:C	7:E:23:TRP:N	2.66	0.45
7:E:25:PRO:C	7:E:28:LYS:H	2.24	0.45
8:F:134:LYS:O	8:F:134:LYS:HD3	2.17	0.45
9:G:104:MET:SD	9:G:179:GLY:HA3	2.56	0.45
10:H:63:MET:HA	10:H:63:MET:HE2	1.98	0.45
11:I:9:MET:HE1	23:U:65:LEU:CA	2.46	0.45
11:I:48:ALA:HB1	23:U:69:PRO:HB3	1.97	0.45
15:M:78:GLU:HG3	15:M:78:GLU:O	2.17	0.45
1:A:1526:G:H2'	1:A:1527:U:C6	2.52	0.45
2:01:156:SER:O	2:01:159:ILE:HG22	2.17	0.45
3:03:470:ARG:HD3	3:03:470:ARG:C	2.41	0.45
3:03:1011:LEU:O	3:03:1015:ALA:HB3	2.17	0.45
3:03:1119:MET:HG3	3:03:1204:LEU:HD13	1.99	0.45
3:03:1176:LEU:HD22	3:03:1180:MET:HG3	1.99	0.45
3:03:1319:MET:SD	3:03:1324:ASN:HB2	2.57	0.45
4:04:97:VAL:HG12	4:04:97:VAL:O	2.17	0.45
4:04:129:ASP:HB2	4:04:220:ARG:NE	2.31	0.45
4:04:492:SER:C	4:04:494:ALA:H	2.24	0.45
4:04:734:ALA:HB1	4:04:738:ARG:HH21	1.82	0.45
4:04:844:THR:HB	4:04:860:ARG:O	2.17	0.45
4:04:1048:ARG:HH11	4:04:1059:LEU:HD21	1.82	0.45
5:05:29:GLN:O	5:05:32:VAL:O	2.34	0.45
13:K:88:LYS:HD2	13:K:119:GLY:HA2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:35:GLU:O	14:L:40:ARG:HD3	2.17	0.45
24:V:4:LEU:HD23	24:V:4:LEU:H	1.81	0.45
3:03:619:ALA:HA	3:03:653:MET:HE3	1.99	0.45
3:03:974:ARG:HB3	3:03:1014:LEU:HD22	1.98	0.45
3:03:1061:GLN:HE22	4:04:445:LYS:NZ	2.14	0.45
3:03:1246:ARG:HG3	3:03:1246:ARG:HH11	1.82	0.45
4:04:81:ARG:HE	7:E:206:ALA:HB1	1.82	0.45
4:04:81:ARG:HB3	7:E:207:ILE:HG22	1.98	0.45
4:04:1068:THR:O	4:04:1072:LYS:HG3	2.16	0.45
9:G:96:ARG:HB3	9:G:98:ASP:OD1	2.17	0.45
12:J:61:PHE:O	12:J:65:LEU:HB2	2.17	0.45
17:O:110:LYS:N	17:O:110:LYS:HD2	2.31	0.45
18:P:9:PRO:HG3	18:P:17:ALA:HB1	1.99	0.45
25:W:35:TYR:O	25:W:39:GLU:HG3	2.16	0.45
1:A:419:C:H2'	1:A:420:U:O4'	2.16	0.45
1:A:548:G:H2'	1:A:549:C:C6	2.52	0.45
1:A:791:G:H2'	1:A:792:A:H8	1.82	0.45
1:A:1255:G:H2'	1:A:1279:G:N2	2.32	0.45
2:01:31:LEU:CB	2:01:199:ASP:HB2	2.47	0.45
2:01:110:VAL:O	2:01:129:VAL:HA	2.16	0.45
3:03:152:SER:HB2	3:03:451:ARG:C	2.42	0.45
9:G:169:TRP:CD1	9:G:170:LEU:HG	2.52	0.45
10:H:14:LEU:C	10:H:15:ILE:HD12	2.41	0.45
14:L:49:GLN:C	14:L:51:LEU:N	2.75	0.45
1:A:754:C:H5'	20:R:71:ARG:NH2	2.31	0.44
1:A:921:U:H5'	1:A:1082:A:H5'	2.00	0.44
3:03:91:THR:HG21	3:03:503:LYS:HZ2	1.79	0.44
3:03:505:PHE:O	3:03:512:SER:HB3	2.17	0.44
3:03:706:ARG:HB3	3:03:706:ARG:CZ	2.46	0.44
4:04:559:ALA:HB3	4:04:562:GLU:HB2	1.99	0.44
7:E:68:LEU:HB3	7:E:161:LEU:HG	1.98	0.44
8:F:49:ALA:HB2	8:F:74:ILE:CG2	2.47	0.44
9:G:62:ARG:HG2	9:G:62:ARG:HH11	1.82	0.44
17:O:50:LYS:HD3	17:O:71:HIS:CD2	2.52	0.44
22:T:22:VAL:HG11	22:T:60:ILE:HD11	1.98	0.44
1:A:754:C:H6	20:R:68:TYR:CD2	2.35	0.44
1:A:820:U:H4'	1:A:821:G:OP2	2.17	0.44
1:A:952:U:H2'	1:A:953:G:C8	2.52	0.44
1:A:1071:C:H2'	1:A:1072:G:C8	2.52	0.44
1:A:1330:U:H2'	1:A:1331:G:O4'	2.17	0.44
3:03:459:MET:HA	3:03:462:ASN:ND2	2.20	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:522:SER:HA	3:03:525:THR:HG22	1.98	0.44
3:03:839:VAL:HG13	3:03:886:LYS:HZ1	1.82	0.44
4:04:131:PRO:O	4:04:135:ILE:HG13	2.17	0.44
4:04:368:LEU:HA	4:04:369:PRO:HD3	1.87	0.44
4:04:485:MET:HB3	4:04:488:ASN:HB2	1.99	0.44
4:04:523:GLU:CA	4:04:546:ALA:HB1	2.47	0.44
4:04:572:THR:OG1	4:04:576:ARG:HD2	2.17	0.44
4:04:1024:THR:HG21	4:04:1123:ARG:NH1	2.32	0.44
4:04:1048:ARG:HH11	4:04:1059:LEU:CD2	2.31	0.44
4:04:1342:ASP:C	4:04:1344:LEU:N	2.75	0.44
10:H:95:MET:HE1	10:H:142:GLY:HA3	1.99	0.44
21:S:25:ARG:HD3	21:S:25:ARG:N	2.33	0.44
24:V:21:ALA:CB	24:V:30:LEU:HD21	2.43	0.44
25:W:4:LYS:C	25:W:6:ALA:H	2.25	0.44
1:A:407:U:H2'	1:A:408:A:H8	1.81	0.44
2:01:91:ARG:NH2	2:01:122:GLU:HG2	2.32	0.44
2:02:147:GLN:O	2:02:177:TYR:HE1	2.00	0.44
3:03:317:LEU:CD2	3:03:325:LEU:HD13	2.48	0.44
4:04:33:TRP:HB3	4:04:102:MET:HB3	1.99	0.44
4:04:311:ARG:HH11	4:04:311:ARG:HG3	1.82	0.44
4:04:535:ARG:NH1	4:04:535:ARG:HB2	2.32	0.44
4:04:740:LEU:HA	4:04:763:PHE:HD2	1.82	0.44
8:F:24:ASN:ND2	8:F:25:THR:H	2.15	0.44
9:G:22:SER:O	9:G:160:LEU:HD11	2.17	0.44
12:J:49:LEU:HD22	12:J:123:LEU:HD23	1.98	0.44
18:P:108:ARG:NE	18:P:108:ARG:HA	2.32	0.44
25:W:27:MET:HG3	25:W:57:VAL:HA	1.97	0.44
1:A:248:C:O2'	1:A:249:U:H5'	2.17	0.44
1:A:760:G:H2'	1:A:761:G:H5'	1.99	0.44
1:A:1240:U:H4'	12:J:37:THR:HG22	1.99	0.44
2:02:44:ARG:HG2	2:02:44:ARG:HH11	1.83	0.44
2:02:79:LEU:HD13	2:02:79:LEU:C	2.42	0.44
3:03:463:GLN:HE21	3:03:505:PHE:CB	2.25	0.44
3:03:472:GLU:HG2	3:03:476:LYS:HG3	1.99	0.44
4:04:885:VAL:O	4:04:1258:ARG:HD2	2.18	0.44
4:04:1188:GLU:C	4:04:1189:MET:HE2	2.42	0.44
4:04:1234:VAL:HA	4:04:1237:VAL:HG12	1.99	0.44
9:G:75:TYR:CE1	9:G:200:VAL:HG23	2.53	0.44
10:H:136:VAL:O	10:H:140:ILE:HG12	2.17	0.44
15:M:72:ARG:HG2	15:M:72:ARG:HH11	1.80	0.44
16:N:22:ILE:HG23	16:N:31:VAL:HG22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:62:ALA:O	16:N:65:ALA:HB3	2.18	0.44
1:A:288:A:C2'	1:A:289:G:H5'	2.47	0.44
1:A:459:A:H61	1:A:473:U:H3	1.66	0.44
1:A:563:A:H61	1:A:884:U:H3	1.66	0.44
1:A:575:G:H21	1:A:576:C:H5	1.64	0.44
3:03:119:GLU:CB	3:03:489:PRO:HG2	2.47	0.44
3:03:671:LEU:C	3:03:673:HIS:H	2.24	0.44
3:03:814:ASP:HB2	4:04:461:PHE:HB2	1.99	0.44
3:03:823:VAL:HB	3:03:1060:ILE:HG23	1.99	0.44
4:04:83:VAL:HG13	4:04:83:VAL:O	2.18	0.44
4:04:331:ILE:HD12	4:04:331:ILE:N	2.33	0.44
4:04:475:GLU:O	4:04:479:GLU:HG3	2.17	0.44
4:04:554:GLU:HA	4:04:580:TRP:CZ2	2.52	0.44
4:04:863:LEU:HD22	4:04:908:ILE:CD1	2.47	0.44
6:B:218:UNK:HA	6:B:257:UNK:O	2.18	0.44
8:F:3:LYS:HD3	8:F:174:LEU:HD22	1.99	0.44
13:K:9:MET:SD	13:K:32:LYS:HD2	2.57	0.44
13:K:10:LEU:HD22	13:K:74:ILE:CD1	2.48	0.44
16:N:43:TRP:CE3	16:N:45:THR:HG23	2.52	0.44
16:N:83:VAL:HG12	16:N:85:VAL:HG23	2.00	0.44
16:N:125:LYS:HG2	26:X:34:ARG:HB3	1.99	0.44
19:Q:11:LYS:O	19:Q:15:LEU:HD13	2.17	0.44
20:R:57:ARG:HH11	20:R:57:ARG:HG3	1.81	0.44
22:T:4:ILE:O	22:T:61:ARG:HG3	2.17	0.44
25:W:4:LYS:HB3	25:W:4:LYS:HZ3	1.81	0.44
1:A:670:G:H2'	1:A:671:G:H8	1.83	0.44
1:A:769:G:OP2	1:A:803:G:H4'	2.17	0.44
1:A:1106:G:O2'	1:A:1107:C:H5'	2.18	0.44
1:A:1216:A:H5''	19:Q:4:SER:HB3	1.99	0.44
2:01:89:ALA:HB3	2:01:124:VAL:CG1	2.47	0.44
3:03:1174:GLU:HA	3:03:1177:ARG:HD2	2.00	0.44
3:03:1304:MET:O	3:03:1308:ILE:HG12	2.17	0.44
4:04:442:ILE:HD12	4:04:448:GLN:NE2	2.32	0.44
4:04:501:VAL:O	4:04:502:PRO:C	2.60	0.44
4:04:838:ARG:HH12	4:04:1238:GLN:HE21	1.66	0.44
4:04:1242:ARG:HG2	4:04:1242:ARG:HH11	1.82	0.44
7:E:31:ILE:HD12	7:E:32:PHE:N	2.33	0.44
7:E:45:LYS:O	7:E:49:MET:HB2	2.18	0.44
9:G:154:VAL:O	9:G:158:LEU:HB2	2.18	0.44
10:H:10:LEU:HD22	10:H:67:ARG:HH21	1.83	0.44
10:H:148:SER:O	10:H:152:VAL:HG23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:36:ILE:HD13	11:I:39:LEU:HB2	2.00	0.44
12:J:22:LEU:O	12:J:26:VAL:HG23	2.18	0.44
18:P:16:ILE:H	18:P:16:ILE:CD1	2.29	0.44
22:T:9:GLY:O	22:T:57:VAL:HA	2.18	0.44
1:A:427:U:H1'	1:A:541:G:C5'	2.41	0.44
1:A:585:G:H2'	1:A:586:C:C6	2.52	0.44
1:A:1349:A:OP1	14:L:119:LYS:HB2	2.17	0.44
2:01:129:VAL:O	2:01:129:VAL:HG13	2.17	0.44
2:01:231:PHE:CE1	2:02:217:ILE:HG23	2.52	0.44
2:02:12:ARG:HG2	2:02:13:LEU:N	2.28	0.44
3:03:421:SER:OG	3:03:424:ASP:HB2	2.17	0.44
3:03:524:ILE:HA	3:03:527:LYS:HE3	1.99	0.44
3:03:811:ASN:HA	3:03:815:SER:O	2.17	0.44
3:03:1192:GLU:O	3:03:1196:LYS:HD3	2.16	0.44
4:04:279:LEU:HD12	4:04:295:GLU:HG3	2.00	0.44
4:04:354:VAL:HA	4:04:465:GLN:HA	1.99	0.44
4:04:639:VAL:HG13	4:04:639:VAL:O	2.17	0.44
4:04:1268:ASN:HB3	4:04:1301:THR:H	1.83	0.44
4:04:1293:GLU:C	4:04:1295:ASN:H	2.25	0.44
7:E:77:SER:O	7:E:93:ASN:HB2	2.17	0.44
9:G:44:LYS:HA	9:G:45:PRO:HD3	1.69	0.44
9:G:101:VAL:HG21	9:G:122:ILE:HD13	2.00	0.44
11:I:25:TYR:HD1	11:I:74:LEU:HD11	1.83	0.44
12:J:26:VAL:HG22	12:J:42:VAL:HG21	2.00	0.44
17:O:120:ARG:HD3	17:O:120:ARG:C	2.43	0.44
18:P:18:LEU:HD21	18:P:55:LEU:HD13	1.99	0.44
24:V:18:VAL:O	24:V:21:ALA:HB3	2.17	0.44
24:V:30:LEU:HD12	24:V:30:LEU:N	2.33	0.44
3:03:18:ARG:HA	3:03:18:ARG:NE	2.33	0.44
3:03:57:PHE:CD1	3:03:59:ILE:HG13	2.53	0.44
3:03:297:VAL:HG22	3:03:298:ALA:N	2.32	0.44
3:03:530:ILE:HG12	3:03:575:LEU:H	1.83	0.44
3:03:587:LEU:HD23	3:03:587:LEU:C	2.43	0.44
3:03:727:VAL:HG22	3:03:732:ILE:HG23	2.00	0.44
3:03:1059:ARG:HH11	3:03:1059:ARG:HG3	1.83	0.44
4:04:1040:MET:CE	4:04:1061:VAL:HG22	2.48	0.44
7:E:16:PHE:H	7:E:16:PHE:HD1	1.66	0.44
7:E:27:MET:HB3	7:E:189:THR:HG22	1.99	0.44
10:H:104:ILE:HG23	10:H:104:ILE:O	2.17	0.44
10:H:148:SER:O	10:H:151:MET:N	2.50	0.44
16:N:124:LYS:HB3	26:X:35:ARG:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:U:H2'	1:A:57:G:H8	1.82	0.44
1:A:545:C:H2'	1:A:546:A:O4'	2.17	0.44
1:A:1002:G:H2'	1:A:1003:G:C8	2.53	0.44
2:01:179:PRO:HB3	2:01:210:THR:OG1	2.18	0.44
2:02:99:ILE:HG13	2:02:144:ILE:O	2.17	0.44
3:03:732:ILE:HG22	3:03:734:ILE:HD11	1.99	0.44
3:03:760:ASN:C	3:03:762:ASN:H	2.25	0.44
3:03:764:CYS:HB3	3:03:831:ILE:HB	2.00	0.44
4:04:422:LEU:C	4:04:423:LEU:HD12	2.43	0.44
7:E:10:LEU:HB3	7:E:15:HIS:CD2	2.53	0.44
8:F:21:TRP:HZ3	8:F:23:ALA:HB2	1.82	0.44
12:J:25:PHE:HB2	12:J:100:MET:SD	2.58	0.44
14:L:76:GLY:HA2	14:L:79:ARG:HG2	2.00	0.44
21:S:57:ILE:O	21:S:61:VAL:HG23	2.17	0.44
1:A:668:G:O2'	20:R:45:HIS:HB3	2.18	0.43
2:02:152:TYR:O	2:02:154:PRO:HD3	2.17	0.43
3:03:360:LEU:O	3:03:364:VAL:HG23	2.18	0.43
3:03:680:LEU:HD23	3:03:680:LEU:C	2.42	0.43
3:03:775:GLU:HA	3:03:776:PRO:HD3	1.84	0.43
3:03:782:VAL:C	3:03:783:LEU:HD22	2.42	0.43
3:03:1180:MET:O	3:03:1182:ILE:HG13	2.18	0.43
4:04:58:CYS:HB3	4:04:61:ILE:HB	2.00	0.43
4:04:436:ALA:HB3	4:04:485:MET:HA	2.00	0.43
4:04:1165:PHE:HZ	4:04:1198:VAL:HG11	1.80	0.43
5:05:62:GLN:HB3	5:05:63:ILE:HD12	2.00	0.43
9:G:187:ARG:HH11	9:G:187:ARG:HG3	1.82	0.43
12:J:92:PRO:HA	12:J:95:ARG:HD2	2.00	0.43
17:O:3:VAL:CG1	22:T:35:LYS:HD2	2.47	0.43
17:O:28:GLN:OE1	17:O:82:ARG:HA	2.18	0.43
21:S:80:LYS:HG2	21:S:80:LYS:O	2.18	0.43
24:V:40:PHE:CG	24:V:41:PRO:HD2	2.53	0.43
25:W:3:ILE:HG22	25:W:4:LYS:N	2.33	0.43
1:A:252:U:O2	1:A:253:A:C8	2.71	0.43
1:A:1328:C:H2'	1:A:1329:A:C8	2.53	0.43
2:01:19:VAL:HG13	2:01:20:SER:N	2.33	0.43
2:02:25:LYS:HA	2:02:203:ILE:O	2.18	0.43
2:02:181:GLU:HA	4:04:535:ARG:HE	1.81	0.43
3:03:204:LEU:HD11	3:03:369:MET:HB2	2.00	0.43
3:03:210:LEU:O	3:03:215:TYR:HB2	2.18	0.43
3:03:1113:LEU:CD2	3:03:1195:ILE:HD13	2.49	0.43
4:04:582:ILE:HG23	4:04:623:GLN:HB3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:877:VAL:O	4:04:877:VAL:HG13	2.19	0.43
5:05:32:VAL:C	5:05:34:GLY:N	2.76	0.43
6:B:230:UNK:O	6:B:232:UNK:N	2.51	0.43
11:I:81:ASN:ND2	11:I:83:ALA:HB3	2.33	0.43
13:K:98:LEU:HD12	13:K:98:LEU:N	2.33	0.43
1:A:666:G:H2'	1:A:667:G:C8	2.53	0.43
2:01:208:ASN:HD21	2:01:210:THR:HG23	1.83	0.43
2:02:86:LYS:HD3	2:02:174:ASP:H	1.83	0.43
2:02:179:PRO:HG2	2:02:219:ARG:HH12	1.83	0.43
3:03:317:LEU:HD22	3:03:325:LEU:HD13	2.00	0.43
3:03:974:ARG:HG3	3:03:1014:LEU:HD13	2.00	0.43
3:03:976:ARG:HG2	3:03:976:ARG:HH11	1.84	0.43
4:04:218:THR:HA	4:04:221:ILE:CG2	2.48	0.43
4:04:838:ARG:HH22	4:04:1235:ASN:HD21	1.64	0.43
4:04:975:ILE:O	4:04:1028:ILE:HD11	2.18	0.43
4:04:1259:GLN:OE1	4:04:1259:GLN:HA	2.18	0.43
9:G:71:PHE:CZ	9:G:89:LEU:HD21	2.52	0.43
19:Q:62:ARG:CZ	19:Q:69:PRO:HB3	2.48	0.43
24:V:63:ASP:O	24:V:66:VAL:HG13	2.18	0.43
1:A:503:C:O2'	1:A:504:C:H5'	2.18	0.43
1:A:1285:A:H4'	1:A:1286:U:C5'	2.46	0.43
2:02:13:LEU:HD23	2:02:13:LEU:N	2.33	0.43
3:03:580:GLN:O	3:03:588:GLU:N	2.51	0.43
3:03:696:ASP:C	3:03:795:ALA:HB1	2.43	0.43
4:04:47:ARG:NE	4:04:47:ARG:HA	2.33	0.43
4:04:349:TYR:CE2	4:04:472:LEU:HD13	2.53	0.43
4:04:990:ARG:O	4:04:990:ARG:HG3	2.17	0.43
9:G:91:ALA:HB1	9:G:184:LYS:HG3	1.99	0.43
10:H:17:VAL:HA	10:H:33:THR:O	2.18	0.43
10:H:81:GLN:HB2	10:H:146:MET:SD	2.59	0.43
12:J:137:ARG:HD2	12:J:137:ARG:C	2.44	0.43
17:O:71:HIS:C	17:O:72:ASN:HD22	2.27	0.43
22:T:26:ARG:HG2	22:T:26:ARG:HH11	1.83	0.43
25:W:80:ALA:HA	25:W:83:ASN:HD22	1.83	0.43
1:A:122:G:N2	1:A:290:C:H4'	2.34	0.43
1:A:176:C:H5''	25:W:19:HIS:NE2	2.34	0.43
1:A:212:G:O2'	1:A:213:G:H5'	2.18	0.43
1:A:980:C:O2	19:Q:58:ARG:HA	2.18	0.43
1:A:1319:A:H4'	1:A:1320:C:H5	1.84	0.43
1:A:1322:C:H5''	18:P:98:GLY:HA3	2.00	0.43
2:01:12:ARG:HB3	2:01:30:PRO:HG2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:75:GLN:HB3	2:01:132:HIS:HB2	1.99	0.43
2:02:148:ARG:C	2:02:148:ARG:HD3	2.43	0.43
3:03:11:ILE:N	3:03:1172:LEU:HD11	2.28	0.43
3:03:951:MET:O	3:03:951:MET:HE3	2.19	0.43
3:03:1113:LEU:HA	4:04:641:ILE:CG1	2.48	0.43
3:03:1223:ARG:NH2	4:04:721:SER:OG	2.52	0.43
4:04:132:LEU:HD13	4:04:132:LEU:O	2.19	0.43
4:04:263:SER:C	4:04:265:LEU:H	2.26	0.43
4:04:673:VAL:HG12	4:04:677:GLU:OE2	2.17	0.43
4:04:1231:ARG:HG2	4:04:1231:ARG:NH1	2.31	0.43
7:E:35:ARG:HA	7:E:39:HIS:HA	2.01	0.43
7:E:192:ASP:HA	7:E:193:PRO:HD3	1.91	0.43
10:H:153:ALA:O	10:H:158:LYS:HA	2.19	0.43
18:P:5:GLY:O	18:P:6:ILE:CG2	2.63	0.43
19:Q:62:ARG:HB2	19:Q:68:ARG:O	2.18	0.43
24:V:7:GLY:HA3	24:V:8:PRO:HD2	1.83	0.43
25:W:27:MET:SD	25:W:66:ILE:HG13	2.58	0.43
26:X:45:ARG:HA	26:X:45:ARG:HD2	1.85	0.43
1:A:689:C:H2'	1:A:690:G:O4'	2.19	0.43
1:A:885:G:H1'	1:A:914:A:C2	2.54	0.43
2:02:124:VAL:HG21	2:02:209:GLY:O	2.19	0.43
2:02:223:ILE:O	2:02:226:GLU:HB3	2.19	0.43
3:03:10:ARG:HG3	3:03:10:ARG:NH1	2.34	0.43
3:03:158:ASP:HB2	3:03:173:ASN:OD1	2.18	0.43
3:03:555:TYR:CE1	4:04:769:VAL:HG21	2.54	0.43
4:04:435:GLN:HE21	4:04:489:ASN:HB2	1.83	0.43
4:04:531:LYS:O	4:04:534:GLU:HB3	2.18	0.43
4:04:812:ASP:OD2	4:04:911:LYS:HE3	2.18	0.43
4:04:819:GLY:HA2	4:04:884:SER:H	1.83	0.43
8:F:23:ALA:HB3	8:F:28:PHE:HD1	1.84	0.43
8:F:190:THR:HG21	8:F:195:ILE:HD12	2.00	0.43
12:J:103:ILE:HD13	12:J:123:LEU:HD13	2.01	0.43
14:L:12:LYS:C	14:L:14:SER:H	2.26	0.43
15:M:52:LEU:HD13	19:Q:80:ARG:HD2	2.00	0.43
15:M:88:MET:C	15:M:90:LEU:H	2.25	0.43
18:P:30:LYS:HA	18:P:40:GLU:OE2	2.19	0.43
19:Q:68:ARG:HE	19:Q:70:HIS:HB2	1.83	0.43
1:A:1210:C:C2'	1:A:1211:U:H5'	2.48	0.43
2:01:81:ILE:O	2:01:85:LEU:HG	2.19	0.43
3:03:569:ILE:C	3:03:569:ILE:HD12	2.44	0.43
3:03:1319:MET:C	3:03:1321:GLU:N	2.77	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:137:ARG:HG2	4:04:137:ARG:HH11	1.83	0.43
4:04:361:LEU:HD11	4:04:448:GLN:CB	2.48	0.43
4:04:868:TRP:O	4:04:872:LEU:HG	2.19	0.43
9:G:58:GLN:O	9:G:62:ARG:HG2	2.19	0.43
9:G:109:THR:HG22	9:G:110:ARG:N	2.34	0.43
20:R:84:LEU:HD23	20:R:86:LEU:HB3	1.99	0.43
22:T:69:THR:HG22	22:T:69:THR:O	2.19	0.43
24:V:38:THR:HB	24:V:69:LYS:HD3	2.00	0.43
1:A:998:C:O2'	1:A:999:C:H5'	2.19	0.43
1:A:1277:C:O2'	1:A:1278:G:H4'	2.19	0.43
2:02:116:THR:HG23	2:02:116:THR:O	2.19	0.43
3:03:1321:GLU:O	3:03:1325:VAL:HG23	2.19	0.43
4:04:18:ASP:O	4:04:19:ALA:C	2.62	0.43
4:04:514:THR:HG23	4:04:596:LEU:HB2	2.01	0.43
4:04:841:GLY:HA2	4:04:901:ARG:CZ	2.49	0.43
4:04:1141:VAL:HA	4:04:1144:LEU:CD1	2.49	0.43
4:04:1267:VAL:CG2	4:04:1303:SER:HB2	2.49	0.43
9:G:80:ARG:HD2	9:G:80:ARG:C	2.44	0.43
16:N:107:THR:HG23	16:N:108:ASN:N	2.33	0.43
18:P:82:LEU:HD11	24:V:65:MET:HG3	2.01	0.43
24:V:40:PHE:HB3	24:V:42:ASN:OD1	2.18	0.43
25:W:56:ILE:N	25:W:56:ILE:CD1	2.80	0.43
26:X:59:LYS:HD3	26:X:62:ARG:HE	1.84	0.43
1:A:250:A:H4'	1:A:252:U:C5	2.54	0.43
1:A:564:C:H5'	22:T:33:TYR:HE1	1.84	0.43
1:A:1066:C:H2'	1:A:1067:A:H5'	2.00	0.43
2:01:182:ARG:HH11	2:01:182:ARG:HG3	1.84	0.43
3:03:341:LEU:HD23	3:03:341:LEU:C	2.44	0.43
3:03:1258:PRO:HD3	4:04:345:LYS:CB	2.49	0.43
4:04:190:LYS:NZ	4:04:190:LYS:HB3	2.33	0.43
4:04:425:ARG:CG	4:04:427:PRO:HD2	2.40	0.43
4:04:835:LEU:HD21	4:04:880:VAL:HG23	2.00	0.43
4:04:1040:MET:HB3	4:04:1046:ILE:HD13	1.99	0.43
7:E:160:ALA:C	7:E:161:LEU:HD12	2.44	0.43
8:F:40:GLN:O	8:F:44:LYS:HG2	2.19	0.43
8:F:42:LEU:HD21	8:F:67:ILE:CD1	2.48	0.43
9:G:196:GLU:C	9:G:198:LEU:H	2.26	0.43
14:L:100:ALA:HB3	14:L:102:PHE:CE2	2.54	0.43
15:M:8:ILE:HD11	15:M:87:LEU:CD2	2.48	0.43
15:M:52:LEU:CD2	15:M:59:LYS:HZ2	2.30	0.43
19:Q:65:GLN:HG3	19:Q:66:THR:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:S:19:VAL:H	21:S:38:PHE:HA	1.84	0.43
1:A:238:A:O2'	1:A:239:U:H5'	2.18	0.43
1:A:427:U:H5''	1:A:428:G:H2'	1.99	0.43
1:A:687:A:H62	1:A:703:G:H21	1.66	0.43
1:A:824:G:H2'	1:A:825:A:C8	2.52	0.43
1:A:946:A:H2'	1:A:947:G:H8	1.84	0.43
1:A:959:A:H2'	1:A:960:U:C4'	2.49	0.43
3:03:524:ILE:HD11	3:03:712:SER:HB2	2.01	0.43
3:03:647:ARG:HD3	3:03:648:ASP:N	2.34	0.43
4:04:33:TRP:O	4:04:102:MET:O	2.37	0.43
4:04:41:PRO:CB	4:04:270:ARG:HG3	2.49	0.43
4:04:201:LEU:HD22	4:04:217:LEU:HD13	2.01	0.43
4:04:694:SER:C	4:04:696:ALA:N	2.69	0.43
10:H:97:PRO:HG2	10:H:98:ALA:H	1.84	0.43
10:H:108:GLY:O	10:H:109:ALA:HB3	2.18	0.43
10:H:159:SER:HB3	10:H:162:GLU:CB	2.49	0.43
14:L:43:ALA:HB1	14:L:46:VAL:CG1	2.48	0.43
24:V:14:LEU:HD13	24:V:34:SER:CB	2.47	0.43
1:A:192:A:O2'	25:W:55:PRO:HB3	2.19	0.42
2:02:83:LEU:HA	2:02:86:LYS:NZ	2.34	0.42
3:03:633:LEU:HD12	3:03:633:LEU:C	2.44	0.42
3:03:1085:MET:HA	3:03:1086:PRO:HD3	1.85	0.42
4:04:45:ASN:HB2	4:04:50:LYS:HB2	2.01	0.42
4:04:123:ARG:HD2	4:04:1337:VAL:HG11	2.00	0.42
4:04:820:ILE:HD12	4:04:1231:ARG:HB3	2.01	0.42
4:04:1005:LYS:HG3	4:04:1011:VAL:HG22	2.01	0.42
4:04:1016:THR:HG22	4:04:1019:ASN:HB2	2.01	0.42
5:05:69:ARG:HA	5:05:72:GLN:OE1	2.18	0.42
7:E:65:GLY:HA2	7:E:159:ASP:OD2	2.19	0.42
8:F:69:THR:CB	8:F:75:VAL:HG21	2.49	0.42
13:K:28:SER:CB	13:K:58:LEU:HB2	2.40	0.42
16:N:111:ASP:HB2	26:X:20:LYS:HD3	1.99	0.42
25:W:23:ARG:HG3	25:W:63:LYS:NZ	2.33	0.42
1:A:393:A:H5'	1:A:483:C:O2'	2.19	0.42
1:A:1126:U:H1'	1:A:1281:C:H1'	2.02	0.42
1:A:1394:A:H3'	1:A:1395:C:H5'	2.01	0.42
2:02:32:GLU:H	2:02:35:PHE:HB2	1.84	0.42
3:03:22:LEU:HD23	3:03:22:LEU:C	2.44	0.42
3:03:150:HIS:HD2	3:03:454:ARG:NH1	2.17	0.42
3:03:325:LEU:HD23	3:03:325:LEU:HA	1.73	0.42
3:03:690:VAL:HA	3:03:691:PRO:HD3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:817:LEU:HD13	3:03:817:LEU:C	2.44	0.42
3:03:963:GLU:O	3:03:967:LEU:HD13	2.20	0.42
4:04:582:ILE:HG22	4:04:620:PHE:CE1	2.54	0.42
5:05:53:GLU:HA	5:05:58:LEU:HD21	2.00	0.42
7:E:35:ARG:HB3	7:E:39:HIS:CE1	2.54	0.42
8:F:9:ILE:HG13	19:Q:97:LYS:NZ	2.34	0.42
11:I:64:VAL:HG22	11:I:65:GLU:N	2.34	0.42
24:V:13:HIS:CD2	24:V:36:ARG:HH21	2.37	0.42
1:A:224:U:OP1	25:W:64:GLY:HA2	2.19	0.42
1:A:392:C:H2'	1:A:393:A:H8	1.82	0.42
1:A:744:C:H2'	1:A:745:G:H8	1.84	0.42
2:01:165:GLU:HG3	2:01:165:GLU:O	2.19	0.42
3:03:522:SER:HA	3:03:525:THR:CG2	2.49	0.42
4:04:199:GLU:O	4:04:203:GLU:HG3	2.19	0.42
7:E:26:LYS:O	7:E:28:LYS:N	2.52	0.42
7:E:67:ILE:HD13	7:E:160:ALA:HB3	2.02	0.42
8:F:32:LEU:HD11	19:Q:76:PHE:HD1	1.83	0.42
9:G:18:LEU:HD11	9:G:63:ILE:HA	2.00	0.42
10:H:51:LYS:HE2	10:H:61:LYS:HZ3	1.82	0.42
17:O:34:THR:O	17:O:53:ARG:HB3	2.17	0.42
18:P:75:SER:O	18:P:78:ARG:HB3	2.19	0.42
20:R:84:LEU:HD23	20:R:86:LEU:HD23	2.01	0.42
1:A:72:A:N1	1:A:99:C:H1'	2.35	0.42
1:A:168:G:O2'	1:A:169:C:H5'	2.19	0.42
2:02:67:GLU:HG3	2:02:68:TYR:HD1	1.85	0.42
3:03:18:ARG:HE	3:03:19:PRO:CD	2.32	0.42
4:04:132:LEU:HA	4:04:135:ILE:HD12	2.00	0.42
4:04:155:GLU:HG3	4:04:156:ARG:N	2.34	0.42
4:04:665:GLN:O	4:04:669:GLN:HG3	2.20	0.42
4:04:1167:LYS:HE3	4:04:1174:ARG:HG3	2.01	0.42
9:G:8:LEU:HD22	9:G:27:ILE:HA	2.01	0.42
9:G:178:GLU:HG2	9:G:179:GLY:H	1.84	0.42
12:J:24:LYS:HB3	12:J:24:LYS:NZ	2.33	0.42
12:J:113:LYS:HB3	12:J:114:SER:H	1.54	0.42
21:S:5:ARG:HG2	21:S:5:ARG:NH1	2.34	0.42
1:A:634:C:H2'	1:A:635:A:C8	2.55	0.42
1:A:718:A:H4'	26:X:31:GLU:OE1	2.19	0.42
1:A:782:A:H62	1:A:800:G:N2	2.10	0.42
1:A:1514:G:H2'	1:A:1515:G:C8	2.55	0.42
2:02:194:GLN:HG3	4:04:406:ALA:CB	2.47	0.42
4:04:175:GLU:HG3	4:04:175:GLU:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:739:GLN:HA	4:04:744:ARG:HA	2.01	0.42
4:04:885:VAL:HG21	4:04:1255:VAL:HG12	2.01	0.42
7:E:15:HIS:CG	7:E:16:PHE:N	2.88	0.42
7:E:36:ASN:O	7:E:38:VAL:N	2.52	0.42
7:E:141:LEU:O	7:E:145:GLU:HG3	2.20	0.42
7:E:179:LEU:HD12	7:E:179:LEU:N	2.35	0.42
8:F:77:GLY:HA3	8:F:82:ASP:HB3	2.02	0.42
9:G:88:ASN:O	9:G:92:LEU:HD13	2.20	0.42
10:H:10:LEU:CD2	10:H:67:ARG:HH21	2.32	0.42
10:H:51:LYS:H	10:H:61:LYS:HD3	1.85	0.42
11:I:10:VAL:CG2	11:I:58:HIS:HB3	2.49	0.42
11:I:40:GLU:OE1	11:I:61:LEU:HD22	2.19	0.42
15:M:45:ARG:HH11	15:M:45:ARG:HG2	1.85	0.42
1:A:738:C:O2'	1:A:739:C:H5'	2.20	0.42
1:A:1006:G:O2'	1:A:1007:U:H5'	2.19	0.42
1:A:1268:G:H1'	1:A:1327:C:H5'	2.01	0.42
3:03:851:THR:CB	3:03:869:GLY:HA3	2.49	0.42
3:03:1169:VAL:HG12	3:03:1169:VAL:O	2.20	0.42
3:03:1319:MET:HA	3:03:1320:PRO:HD3	1.91	0.42
4:04:270:ARG:HG2	4:04:270:ARG:HH11	1.83	0.42
4:04:527:LEU:O	4:04:550:VAL:HA	2.19	0.42
4:04:848:VAL:O	4:04:857:LEU:HD23	2.20	0.42
4:04:1230:THR:O	4:04:1234:VAL:HG13	2.19	0.42
5:05:27:ALA:O	5:05:30:MET:HB2	2.19	0.42
8:F:4:VAL:HG22	8:F:5:HIS:N	2.34	0.42
8:F:19:SER:HB3	8:F:39:ARG:HH22	1.84	0.42
9:G:82:LYS:N	9:G:82:LYS:HD2	2.35	0.42
12:J:128:GLU:HB2	12:J:130:LYS:NZ	2.34	0.42
13:K:124:ILE:HG13	13:K:124:ILE:O	2.20	0.42
21:S:52:LEU:HD13	21:S:75:ILE:HD13	2.00	0.42
22:T:12:VAL:O	22:T:54:ILE:HD13	2.20	0.42
1:A:34:C:H2'	1:A:35:G:C8	2.54	0.42
1:A:62:U:H4'	1:A:378:G:N2	2.34	0.42
1:A:326:G:H2'	1:A:327:A:H5'	2.01	0.42
1:A:648:A:H2'	1:A:649:A:C8	2.54	0.42
1:A:803:G:O2'	1:A:804:U:H5'	2.19	0.42
1:A:1201:A:H4'	1:A:1203:C:OP2	2.20	0.42
2:01:195:ARG:HA	2:01:195:ARG:HE	1.85	0.42
2:01:208:ASN:HD21	2:01:210:THR:CG2	2.32	0.42
3:03:302:ILE:O	3:03:330:HIS:HE1	2.03	0.42
3:03:725:GLN:HG3	3:03:735:LYS:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:24:LEU:HD22	4:04:24:LEU:N	2.35	0.42
4:04:71:LEU:C	4:04:71:LEU:HD13	2.44	0.42
4:04:287:ALA:HB3	4:04:292:VAL:HG13	2.02	0.42
4:04:418:GLU:CG	5:05:44:ASP:HA	2.46	0.42
4:04:504:GLN:HG3	4:04:505:ASP:N	2.34	0.42
4:04:912:GLY:O	4:04:1360:GLY:N	2.53	0.42
4:04:1125:PRO:HB2	4:04:1126:GLN:H	1.62	0.42
5:05:63:ILE:O	5:05:67:ARG:HG2	2.20	0.42
8:F:131:ARG:HH21	8:F:135:ARG:NH1	2.16	0.42
9:G:103:ARG:O	9:G:167:PRO:HG2	2.19	0.42
15:M:41:PRO:HG2	15:M:42:LEU:H	1.83	0.42
16:N:24:ALA:HB1	16:N:90:PRO:HD2	2.01	0.42
18:P:32:ILE:HD12	18:P:58:GLU:HG3	2.01	0.42
23:U:30:LYS:NZ	23:U:30:LYS:CB	2.82	0.42
24:V:74:ALA:O	24:V:76:THR:HG23	2.20	0.42
1:A:250:A:H4'	1:A:252:U:C6	2.54	0.42
3:03:50:GLU:O	3:03:54:ARG:HB2	2.19	0.42
3:03:206:ALA:O	3:03:209:ILE:HG22	2.18	0.42
3:03:243:PRO:CB	3:03:274:ILE:HG23	2.48	0.42
3:03:896:THR:O	3:03:900:LYS:HG3	2.20	0.42
4:04:166:LEU:O	4:04:170:GLU:HG3	2.20	0.42
4:04:744:ARG:HH21	4:04:747:MET:HE2	1.85	0.42
4:04:984:LEU:H	4:04:991:THR:HG23	1.85	0.42
4:04:1036:ARG:O	4:04:1036:ARG:HG3	2.19	0.42
7:E:107:VAL:O	7:E:111:ILE:HG12	2.20	0.42
8:F:183:TYR:HD1	8:F:199:VAL:O	2.03	0.42
19:Q:32:ASP:HB2	19:Q:34:ASN:ND2	2.35	0.42
19:Q:55:SER:HA	19:Q:56:PRO:HA	1.63	0.42
20:R:80:LEU:HG	20:R:86:LEU:HD21	2.02	0.42
24:V:11:ASP:OD2	24:V:36:ARG:HG2	2.19	0.42
25:W:24:ARG:HB3	25:W:28:ARG:HH12	1.84	0.42
1:A:570:G:H5'	1:A:820:U:O4'	2.20	0.42
1:A:918:A:H2'	1:A:919:A:O4'	2.19	0.42
1:A:1306:A:O2'	1:A:1307:U:H5'	2.20	0.42
2:02:58:GLU:HB3	2:02:170:ARG:HH21	1.84	0.42
3:03:257:ALA:HB3	3:03:262:TYR:CE2	2.54	0.42
3:03:521:LEU:HB2	3:03:794:LEU:HD21	2.00	0.42
3:03:1171:ARG:O	3:03:1175:ASN:ND2	2.52	0.42
3:03:1196:LYS:O	3:03:1200:LYS:HG3	2.20	0.42
4:04:68:TYR:HB2	4:04:78:LEU:HA	2.02	0.42
4:04:91:GLU:HG3	4:04:91:GLU:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:105:ILE:HD12	4:04:242:LEU:HD23	2.00	0.42
4:04:504:GLN:HG3	4:04:505:ASP:H	1.85	0.42
4:04:518:VAL:HG22	4:04:709:ARG:HG2	2.02	0.42
4:04:1198:VAL:HG13	4:04:1198:VAL:O	2.20	0.42
7:E:176:ALA:C	7:E:178:ASN:H	2.28	0.42
9:G:160:LEU:O	9:G:160:LEU:HG	2.20	0.42
9:G:200:VAL:HG13	9:G:201:GLU:HG3	2.02	0.42
12:J:130:LYS:N	12:J:134:VAL:HG11	2.34	0.42
24:V:36:ARG:HG3	24:V:36:ARG:NH1	2.35	0.42
1:A:3:A:N1	1:A:629:A:H4'	2.35	0.42
1:A:670:G:H2'	1:A:671:G:C8	2.55	0.42
1:A:881:G:O2'	1:A:882:C:H5'	2.20	0.42
1:A:1150:A:H1'	15:M:41:PRO:HB2	2.02	0.42
1:A:1377:A:C2	12:J:4:ARG:HG3	2.55	0.42
2:02:9:LEU:C	2:02:10:LYS:HD2	2.45	0.42
3:03:53:PHE:O	3:03:56:VAL:HG12	2.20	0.42
3:03:146:VAL:HG13	3:03:529:ARG:HB3	2.02	0.42
3:03:671:LEU:H	3:03:1186:VAL:CG1	2.33	0.42
3:03:725:GLN:CG	3:03:735:LYS:HB2	2.49	0.42
4:04:876:SER:HA	4:04:990:ARG:HH21	1.85	0.42
4:04:975:ILE:HD13	4:04:980:THR:HG21	2.02	0.42
4:04:1095:MET:HA	4:04:1096:PRO:HD3	1.84	0.42
7:E:178:ASN:HD22	10:H:68:ARG:HH21	1.67	0.42
10:H:51:LYS:O	10:H:51:LYS:HD2	2.20	0.42
14:L:58:GLU:OE1	14:L:58:GLU:N	2.53	0.42
14:L:66:VAL:HG11	14:L:74:GLN:HB3	2.02	0.42
1:A:8:A:H1'	10:H:107:GLY:CA	2.50	0.41
1:A:1038:C:H2'	1:A:1039:G:C8	2.55	0.41
1:A:1395:C:H2'	1:A:1396:A:C8	2.55	0.41
2:01:89:ALA:HB3	2:01:124:VAL:HG11	2.02	0.41
2:01:102:LEU:HB3	2:01:142:MET:HG2	2.02	0.41
2:01:227:GLN:HA	2:02:11:PRO:HG3	2.02	0.41
3:03:241:LEU:C	3:03:243:PRO:HD3	2.45	0.41
3:03:246:LEU:HA	3:03:249:GLU:OE1	2.20	0.41
7:E:45:LYS:HD2	7:E:201:PRO:HG2	2.02	0.41
8:F:111:ASP:O	8:F:115:VAL:HG23	2.20	0.41
11:I:61:LEU:HD12	11:I:61:LEU:N	2.35	0.41
12:J:58:LEU:C	12:J:58:LEU:HD23	2.45	0.41
14:L:112:ARG:HD2	19:Q:100:TRP:OXT	2.20	0.41
15:M:57:VAL:HG13	15:M:58:ASN:N	2.35	0.41
16:N:81:LEU:HD23	16:N:106:ILE:HA	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:O:17:LYS:HB2	17:O:17:LYS:HZ2	1.84	0.41
20:R:67:ASP:O	20:R:71:ARG:HG3	2.20	0.41
21:S:69:ASP:HA	21:S:72:ALA:HB3	2.01	0.41
24:V:31:ARG:HG2	24:V:31:ARG:HH11	1.85	0.41
1:A:1252:A:H61	1:A:1285:A:N6	2.09	0.41
3:03:521:LEU:O	3:03:521:LEU:HD13	2.20	0.41
3:03:1067:ALA:HB3	3:03:1235:LEU:HD11	2.02	0.41
4:04:223:LEU:O	4:04:226:ALA:HB3	2.20	0.41
4:04:247:PRO:C	4:04:249:LEU:H	2.29	0.41
4:04:718:SER:HB3	4:04:720:ASN:OD1	2.20	0.41
4:04:787:ALA:C	4:04:788:LEU:HD12	2.45	0.41
4:04:793:SER:O	4:04:796:LEU:HB3	2.20	0.41
8:F:72:PRO:O	8:F:76:ILE:HG12	2.19	0.41
9:G:117:VAL:O	9:G:130:ASN:HA	2.20	0.41
9:G:146:GLU:C	9:G:148:ALA:H	2.27	0.41
10:H:87:VAL:HA	10:H:91:SER:O	2.20	0.41
12:J:122:GLU:OE1	12:J:132:THR:HG22	2.20	0.41
13:K:74:ILE:HD12	13:K:128:VAL:HG13	2.02	0.41
18:P:32:ILE:HG23	18:P:58:GLU:CB	2.45	0.41
24:V:16:LYS:HD3	24:V:16:LYS:C	2.46	0.41
24:V:29:PRO:HB2	24:V:49:ALA:HB2	2.02	0.41
1:A:552:U:H4'	17:O:82:ARG:NH1	2.34	0.41
1:A:586:C:H2'	1:A:587:G:O4'	2.20	0.41
1:A:880:C:H2'	1:A:881:G:C8	2.55	0.41
2:02:55:ALA:HB2	2:02:176:CYS:O	2.20	0.41
2:02:152:TYR:CE2	2:02:154:PRO:HG3	2.54	0.41
3:03:153:PRO:HD2	3:03:452:ARG:HD2	2.02	0.41
3:03:178:PRO:HD2	3:03:183:TRP:HD1	1.84	0.41
3:03:487:LEU:HD23	3:03:487:LEU:H	1.85	0.41
3:03:747:GLY:C	3:03:748:ILE:HD12	2.45	0.41
3:03:888:THR:HA	3:03:889:PRO:HD3	1.92	0.41
3:03:928:VAL:HG23	3:03:928:VAL:O	2.20	0.41
3:03:1084:ASP:C	3:03:1085:MET:HE2	2.45	0.41
3:03:1099:ASN:HA	3:03:1100:PRO:HD3	1.81	0.41
4:04:56:LEU:H	4:04:56:LEU:CD1	2.33	0.41
4:04:72:CYS:SG	4:04:74:LYS:HB2	2.60	0.41
4:04:510:LEU:N	4:04:510:LEU:HD12	2.34	0.41
4:04:722:ILE:HD11	4:04:737:ILE:HG21	2.02	0.41
4:04:1331:VAL:HA	4:04:1334:GLU:HB3	2.01	0.41
7:E:10:LEU:HD23	7:E:10:LEU:HA	1.84	0.41
11:I:36:ILE:CD1	11:I:39:LEU:HB2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:52:LEU:N	15:M:52:LEU:HD12	2.35	0.41
15:M:93:ALA:HB3	15:M:96:VAL:CG2	2.50	0.41
16:N:124:LYS:HA	26:X:35:ARG:H	1.85	0.41
1:A:147:G:H2'	1:A:148:G:C8	2.56	0.41
1:A:241:G:H2'	1:A:242:G:C8	2.56	0.41
1:A:383:A:H2'	1:A:384:G:O4'	2.20	0.41
1:A:555:U:H2'	1:A:556:C:C6	2.56	0.41
2:O2:83:LEU:O	4:O4:528:THR:HB	2.20	0.41
3:O3:269:ILE:HG23	3:O3:273:HIS:HB2	2.02	0.41
3:O3:798:GLN:HB3	3:O3:827:ARG:NH2	2.35	0.41
3:O3:817:LEU:HB3	3:O3:1097:VAL:HB	2.01	0.41
3:O3:1076:ILE:HG23	3:O3:1076:ILE:O	2.21	0.41
4:O4:850:LYS:HG3	4:O4:855:ASP:O	2.21	0.41
4:O4:915:ILE:O	4:O4:918:ILE:HG12	2.21	0.41
4:O4:1218:HIS:O	4:O4:1221:LEU:HB3	2.19	0.41
7:E:11:LYS:HG2	7:E:212:LEU:HD21	2.01	0.41
7:E:28:LYS:N	7:E:29:PRO:HD2	2.36	0.41
7:E:101:LEU:HD21	7:E:181:ILE:HD11	2.02	0.41
8:F:72:PRO:HG2	8:F:73:GLY:H	1.85	0.41
9:G:91:ALA:O	9:G:94:GLU:HB3	2.21	0.41
10:H:145:ASN:O	10:H:145:ASN:ND2	2.53	0.41
11:I:6:ILE:HG12	11:I:89:VAL:HG12	2.02	0.41
12:J:138:GLU:HB3	12:J:142:ARG:NH1	2.36	0.41
17:O:34:THR:O	17:O:35:ARG:HB3	2.20	0.41
18:P:24:VAL:HG22	18:P:25:GLY:N	2.35	0.41
1:A:12:U:H2'	1:A:13:U:H5''	2.01	0.41
1:A:178:C:H2'	1:A:179:A:H4'	2.03	0.41
1:A:546:A:OP2	9:G:67:LEU:HB3	2.21	0.41
1:A:1270:G:H2'	1:A:1271:A:C8	2.55	0.41
3:O3:21:VAL:HG13	3:O3:22:LEU:N	2.35	0.41
3:O3:489:PRO:O	3:O3:490:GLN:HB3	2.19	0.41
3:O3:647:ARG:HD3	3:O3:647:ARG:C	2.45	0.41
3:O3:708:VAL:HG21	3:O3:794:LEU:HD22	2.02	0.41
3:O3:718:ALA:HB2	3:O3:783:LEU:HD21	2.02	0.41
4:O4:101:ARG:O	4:O4:246:PRO:HA	2.21	0.41
4:O4:130:MET:HE2	4:O4:135:ILE:CG1	2.50	0.41
4:O4:722:ILE:HG23	4:O4:723:TYR:H	1.85	0.41
4:O4:1089:LEU:HD23	4:O4:1094:ASP:HA	2.01	0.41
4:O4:1262:ARG:HH11	4:O4:1262:ARG:HG3	1.86	0.41
5:O5:10:VAL:HA	5:O5:14:GLY:HA2	2.03	0.41
9:G:59:LYS:O	9:G:63:ILE:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:72:VAL:HG21	12:J:144:ALA:CB	2.46	0.41
14:L:62:LEU:HD12	14:L:62:LEU:H	1.86	0.41
16:N:47:GLY:HA3	16:N:56:LYS:HE3	2.02	0.41
16:N:93:GLU:C	16:N:95:THR:H	2.27	0.41
26:X:8:GLU:OE2	26:X:16:LEU:HD13	2.20	0.41
1:A:284:C:H2'	1:A:285:C:C6	2.55	0.41
1:A:620:C:O2	9:G:131:ILE:HG13	2.19	0.41
1:A:695:A:H2'	1:A:696:A:O4'	2.20	0.41
2:01:42:ALA:O	2:01:46:ILE:HG12	2.20	0.41
3:03:32:LEU:HD12	3:03:130:MET:SD	2.60	0.41
3:03:179:TYR:CB	3:03:397:LEU:HA	2.51	0.41
3:03:352:ARG:HG2	3:03:352:ARG:HH11	1.85	0.41
3:03:719:LYS:NZ	3:03:751:TYR:HE1	2.18	0.41
3:03:1151:LEU:CG	3:03:1152:GLY:H	2.32	0.41
3:03:1202:GLY:C	3:03:1204:LEU:H	2.28	0.41
4:04:417:ARG:HE	5:05:43:ASN:HB3	1.84	0.41
4:04:750:PRO:HA	4:04:777:HIS:CE1	2.56	0.41
4:04:822:MET:HB2	4:04:880:VAL:O	2.19	0.41
4:04:835:LEU:HD22	4:04:878:ASP:C	2.46	0.41
4:04:848:VAL:HB	4:04:858:VAL:HG12	2.01	0.41
8:F:4:VAL:O	8:F:6:PRO:HD3	2.21	0.41
9:G:1:ALA:HB1	9:G:114:ARG:HH22	1.85	0.41
15:M:50:THR:CG2	15:M:62:ARG:HD3	2.51	0.41
17:O:109:ARG:HB3	17:O:118:VAL:HG21	2.02	0.41
2:01:82:LEU:HA	2:01:85:LEU:HD12	2.01	0.41
2:01:190:ALA:HB2	2:01:199:ASP:C	2.45	0.41
2:02:82:LEU:HD21	2:02:171:LEU:HD13	2.03	0.41
3:03:94:ALA:HB2	3:03:129:LEU:HD11	2.02	0.41
3:03:346:TYR:HE2	3:03:437:ASN:HD21	1.68	0.41
3:03:363:LEU:HB3	3:03:381:ALA:HB1	2.01	0.41
3:03:532:ALA:HB3	3:03:571:LEU:CA	2.50	0.41
3:03:742:TYR:C	3:03:744:GLY:H	2.27	0.41
3:03:842:ASP:CA	3:03:847:PRO:HA	2.48	0.41
3:03:945:ALA:O	3:03:949:GLU:HG3	2.21	0.41
3:03:1054:LEU:HD12	3:03:1054:LEU:N	2.35	0.41
3:03:1132:LEU:HD11	3:03:1174:GLU:CG	2.47	0.41
3:03:1321:GLU:HG2	4:04:99:ARG:CZ	2.51	0.41
4:04:105:ILE:HG21	4:04:276:ASN:ND2	2.36	0.41
4:04:125:GLY:HA2	4:04:135:ILE:HD11	2.02	0.41
4:04:239:LEU:HD23	4:04:239:LEU:HA	1.89	0.41
4:04:370:LYS:O	4:04:373:ALA:HB3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:767:LEU:HA	4:04:771:GLN:OE1	2.20	0.41
7:E:199:VAL:HG22	7:E:201:PRO:HG3	2.02	0.41
9:G:30:LYS:O	9:G:31:CYS:SG	2.77	0.41
12:J:78:ARG:HD2	12:J:78:ARG:N	2.23	0.41
22:T:18:LYS:HG2	22:T:46:HIS:HE1	1.85	0.41
1:A:259:G:O2'	1:A:260:G:H5'	2.21	0.41
1:A:261:U:H2'	1:A:262:A:C8	2.56	0.41
1:A:520:A:H61	1:A:533:A:H61	1.69	0.41
1:A:1098:C:H2'	1:A:1099:G:O4'	2.20	0.41
3:03:160:ASP:HB3	3:03:164:THR:CB	2.51	0.41
3:03:395:TYR:OH	3:03:397:LEU:HD21	2.20	0.41
3:03:521:LEU:HG	3:03:686:GLN:NE2	2.23	0.41
3:03:798:GLN:HB2	3:03:828:PHE:CZ	2.55	0.41
3:03:1255:THR:HG22	3:03:1256:GLN:N	2.35	0.41
4:04:84:ILE:HA	4:04:90:VAL:O	2.21	0.41
4:04:534:GLU:O	4:04:538:ARG:HG3	2.21	0.41
4:04:552:ILE:HD12	4:04:552:ILE:C	2.45	0.41
4:04:563:LEU:HD12	4:04:563:LEU:N	2.35	0.41
7:E:46:THR:HA	7:E:201:PRO:HD2	2.01	0.41
9:G:1:ALA:HB3	9:G:2:ARG:HD3	2.03	0.41
10:H:157:GLY:HA3	10:H:163:ILE:CG2	2.50	0.41
12:J:12:LEU:N	12:J:12:LEU:HD12	2.36	0.41
14:L:93:LEU:HA	14:L:96:GLU:HB3	2.02	0.41
15:M:50:THR:HG23	15:M:62:ARG:HD3	2.03	0.41
1:A:67:C:H2'	1:A:68:G:C8	2.56	0.41
1:A:658:C:H1'	20:R:21:THR:HG21	2.01	0.41
1:A:1213:A:O2'	1:A:1214:C:H2'	2.20	0.41
1:A:1528:U:O4	26:X:43:THR:HG21	2.20	0.41
2:02:68:TYR:CD1	2:02:68:TYR:N	2.89	0.41
3:03:6:THR:HG23	3:03:781:ASP:OD1	2.21	0.41
3:03:109:ALA:O	3:03:111:GLU:N	2.46	0.41
3:03:722:GLY:HA3	3:03:735:LYS:O	2.21	0.41
3:03:791:LEU:CD2	3:03:791:LEU:O	2.69	0.41
3:03:1111:GLN:HB2	3:03:1230:MET:SD	2.61	0.41
3:03:1136:GLN:HA	3:03:1136:GLN:OE1	2.21	0.41
4:04:53:ARG:NH2	4:04:88:CYS:SG	2.94	0.41
4:04:133:ARG:O	4:04:137:ARG:HG3	2.21	0.41
4:04:227:PHE:O	4:04:231:GLY:N	2.48	0.41
4:04:409:TRP:O	4:04:412:LEU:HB3	2.20	0.41
4:04:433:GLY:HA2	4:04:457:TYR:CD1	2.56	0.41
4:04:490:ILE:HD13	4:04:614:LEU:CD1	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:525:MET:O	4:04:548:VAL:HG13	2.21	0.41
4:04:582:ILE:CD1	4:04:627:THR:HG21	2.51	0.41
4:04:583:VAL:CG1	4:04:587:LEU:HD23	2.51	0.41
4:04:912:GLY:CA	4:04:1360:GLY:H	2.34	0.41
4:04:1003:LEU:HA	4:04:1017:VAL:O	2.21	0.41
4:04:1102:PRO:CG	4:04:1124:ILE:HD11	2.51	0.41
4:04:1222:ARG:O	4:04:1222:ARG:HD2	2.20	0.41
7:E:151:ILE:O	7:E:151:ILE:HG12	2.21	0.41
9:G:94:GLU:CG	9:G:185:PRO:HG3	2.43	0.41
9:G:149:LYS:HG3	9:G:177:MET:HE1	2.03	0.41
11:I:76:THR:O	11:I:79:ARG:HB3	2.21	0.41
12:J:131:GLY:O	12:J:135:LYS:HB2	2.21	0.41
13:K:31:LEU:O	13:K:35:ILE:HG13	2.21	0.41
13:K:45:ILE:HD11	13:K:60:LEU:HB3	2.02	0.41
16:N:111:ASP:O	26:X:4:ILE:HG23	2.21	0.41
16:N:125:LYS:HG3	16:N:126:ARG:N	2.35	0.41
19:Q:79:SER:O	19:Q:83:VAL:HG23	2.21	0.41
20:R:69:LEU:HD23	20:R:77:TYR:HD1	1.86	0.41
26:X:6:VAL:HG11	26:X:16:LEU:O	2.21	0.41
26:X:14:VAL:HG22	26:X:15:ALA:N	2.36	0.41
1:A:37:U:O2'	1:A:38:G:H5'	2.20	0.41
1:A:240:G:H2'	1:A:241:G:C8	2.56	0.41
1:A:1220:G:H5''	24:V:36:ARG:HD2	2.03	0.41
1:A:1323:G:H2'	1:A:1324:A:H8	1.86	0.41
2:01:166:ARG:N	2:01:167:PRO:CD	2.83	0.41
2:02:82:LEU:HA	2:02:85:LEU:HD12	2.02	0.41
2:02:208:ASN:CG	2:02:209:GLY:H	2.29	0.41
3:03:156:PHE:O	3:03:175:ARG:N	2.53	0.41
3:03:212:ALA:C	3:03:214:ASN:H	2.29	0.41
4:04:836:ARG:NH2	4:04:866:GLU:OE2	2.53	0.41
4:04:1327:GLU:OE1	4:04:1330:ARG:HB2	2.21	0.41
11:I:29:ILE:HD13	11:I:64:VAL:HG11	2.03	0.41
11:I:97:THR:HG23	11:I:98:GLU:HG3	2.02	0.41
13:K:79:ARG:HD2	13:K:79:ARG:H	1.86	0.41
14:L:114:LYS:HD2	14:L:117:LEU:HD12	2.02	0.41
16:N:88:PRO:CB	16:N:92:ARG:HD2	2.50	0.41
17:O:118:VAL:HG12	17:O:119:LYS:N	2.33	0.41
18:P:15:VAL:O	18:P:19:THR:HG23	2.20	0.41
1:A:1118:U:OP1	14:L:105:ARG:HG3	2.21	0.40
2:01:128:HIS:O	2:01:130:ILE:HD12	2.21	0.40
3:03:27:LEU:HB2	3:03:711:ASP:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:257:ALA:HB3	3:03:262:TYR:CD2	2.56	0.40
3:03:545:PHE:HZ	4:04:781:LYS:HA	1.85	0.40
3:03:816:ILE:O	3:03:1076:ILE:HD12	2.20	0.40
3:03:878:THR:OG1	3:03:879:GLY:N	2.54	0.40
3:03:1088:ASP:HB2	3:03:1210:ILE:HG21	2.03	0.40
3:03:1118:GLY:HA3	3:03:1229:TYR:O	2.21	0.40
3:03:1156:ARG:HG3	3:03:1156:ARG:NH1	2.35	0.40
4:04:125:GLY:HA2	4:04:135:ILE:CD1	2.51	0.40
4:04:510:LEU:O	4:04:514:THR:HG22	2.21	0.40
4:04:755:ILE:C	4:04:757:THR:H	2.29	0.40
4:04:1138:LEU:CB	4:04:1139:PRO:HD3	2.41	0.40
4:04:1261:LEU:O	4:04:1280:VAL:HG21	2.21	0.40
4:04:1356:LEU:HD12	4:04:1365:TYR:CD2	2.56	0.40
7:E:143:LYS:HA	7:E:146:ASN:ND2	2.35	0.40
9:G:101:VAL:HA	9:G:104:MET:HG3	2.04	0.40
11:I:45:ARG:HG2	11:I:45:ARG:HH11	1.85	0.40
12:J:63:VAL:O	12:J:66:GLU:HG2	2.21	0.40
13:K:34:ALA:O	13:K:38:VAL:HG23	2.22	0.40
17:O:43:LYS:CG	17:O:44:PRO:HD3	2.51	0.40
22:T:10:ARG:HG3	22:T:10:ARG:HH11	1.86	0.40
23:U:48:ARG:HD3	23:U:51:TYR:HD2	1.85	0.40
23:U:51:TYR:O	23:U:55:LEU:HG	2.20	0.40
26:X:21:ARG:HA	26:X:25:LYS:HB2	2.02	0.40
1:A:39:G:H2'	1:A:40:C:C5'	2.48	0.40
1:A:170:U:O2'	1:A:171:A:H5'	2.21	0.40
1:A:190:A:N1	25:W:47:GLN:HB3	2.37	0.40
1:A:576:C:H3'	1:A:577:G:H5''	2.02	0.40
2:01:100:LEU:HD12	2:01:100:LEU:N	2.36	0.40
3:03:297:VAL:CG2	3:03:298:ALA:N	2.84	0.40
3:03:694:ARG:HA	3:03:694:ARG:HD3	1.80	0.40
4:04:584:PRO:O	4:04:585:LYS:C	2.65	0.40
4:04:766:GLY:C	4:04:767:LEU:HD12	2.46	0.40
4:04:785:ASP:O	4:04:789:LYS:HG2	2.21	0.40
4:04:1350:ASN:ND2	4:04:1357:ILE:HA	2.37	0.40
9:G:9:LYS:O	9:G:9:LYS:HD2	2.20	0.40
13:K:4:ASP:HA	13:K:5:PRO:HD2	1.85	0.40
16:N:12:ARG:C	16:N:14:GLN:H	2.30	0.40
21:S:2:VAL:O	21:S:66:THR:HG22	2.21	0.40
26:X:17:ARG:HH11	26:X:17:ARG:HG3	1.87	0.40
1:A:118:U:H2'	1:A:119:A:H5'	2.04	0.40
2:02:29:GLU:HA	2:02:30:PRO:HA	1.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:02:104:LYS:HG2	2:02:110:VAL:HG22	2.03	0.40
3:03:150:HIS:HB3	3:03:454:ARG:HH12	1.85	0.40
3:03:482:GLY:HA3	3:03:487:LEU:HD22	2.03	0.40
3:03:976:ARG:CD	3:03:989:LEU:HD23	2.51	0.40
3:03:1222:GLU:O	3:03:1223:ARG:HB3	2.21	0.40
4:04:53:ARG:HH11	4:04:53:ARG:HG2	1.86	0.40
4:04:81:ARG:HA	4:04:92:VAL:HG23	2.04	0.40
4:04:425:ARG:HG2	4:04:426:ALA:H	1.85	0.40
4:04:573:THR:OG1	4:04:576:ARG:HG2	2.20	0.40
4:04:749:LYS:HB3	4:04:755:ILE:CG1	2.49	0.40
4:04:848:VAL:HG21	4:04:880:VAL:HG13	2.03	0.40
4:04:1184:ASP:N	4:04:1185:PRO:HD2	2.36	0.40
4:04:1243:LEU:N	4:04:1243:LEU:HD12	2.37	0.40
4:04:1346:GLY:HA3	4:04:1349:GLU:OE1	2.21	0.40
5:05:67:ARG:O	5:05:71:GLU:HG3	2.21	0.40
9:G:151:GLN:O	9:G:152:SER:HB3	2.21	0.40
14:L:118:ARG:HH11	14:L:118:ARG:HG3	1.87	0.40
15:M:18:ILE:O	15:M:22:THR:HG23	2.21	0.40
15:M:45:ARG:HG2	15:M:45:ARG:NH1	2.36	0.40
16:N:54:SER:O	16:N:57:SER:HB3	2.21	0.40
19:Q:25:GLU:C	19:Q:27:LYS:N	2.80	0.40
1:A:36:C:H4'	17:O:113:ARG:HG3	2.04	0.40
1:A:402:G:H5''	9:G:70:GLN:HE21	1.86	0.40
1:A:1346:A:H4'	14:L:121:ARG:HH22	1.84	0.40
2:01:100:LEU:HD21	2:01:121:VAL:HG21	2.02	0.40
2:01:172:LEU:N	2:01:172:LEU:HD12	2.36	0.40
2:02:209:GLY:C	2:02:211:ILE:N	2.80	0.40
3:03:150:HIS:CE1	3:03:452:ARG:HB3	2.56	0.40
3:03:672:GLU:O	4:04:767:LEU:HD13	2.21	0.40
3:03:695:ALA:HB1	3:03:795:ALA:O	2.21	0.40
3:03:724:VAL:HG22	3:03:775:GLU:H	1.85	0.40
3:03:812:PHE:CZ	4:04:503:SER:HB2	2.55	0.40
3:03:1209:GLN:O	3:03:1224:PRO:HB3	2.22	0.40
4:04:70:CYS:SG	4:04:85:CYS:HB2	2.61	0.40
4:04:272:VAL:O	4:04:276:ASN:HB2	2.21	0.40
4:04:390:LEU:N	4:04:390:LEU:HD12	2.37	0.40
7:E:11:LYS:HZ2	7:E:212:LEU:HD11	1.86	0.40
7:E:108:ARG:HA	7:E:111:ILE:CG1	2.51	0.40
8:F:32:LEU:HD23	8:F:32:LEU:C	2.46	0.40
9:G:110:ARG:O	9:G:114:ARG:HG3	2.20	0.40
14:L:74:GLN:O	14:L:78:ILE:HG13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:65:GLN:HE21	19:Q:78:LEU:HD22	1.86	0.40
19:Q:92:ILE:HA	19:Q:93:PRO:HD3	1.82	0.40
1:A:108:G:C2	25:W:6:ALA:HB1	2.56	0.40
1:A:219:U:C3'	1:A:220:G:H5''	2.52	0.40
1:A:509:A:H5''	9:G:48:SER:OG	2.21	0.40
1:A:811:C:H2'	1:A:812:G:H5'	2.03	0.40
1:A:1097:C:H2'	1:A:1098:C:C6	2.57	0.40
1:A:1343:G:O2'	14:L:122:ARG:HA	2.22	0.40
2:01:104:LYS:HG2	2:01:110:VAL:HG22	2.04	0.40
2:01:230:ALA:HA	2:01:233:ASP:HB3	2.03	0.40
2:02:208:ASN:CG	2:02:209:GLY:N	2.79	0.40
3:03:720:ARG:HH21	3:03:749:ASP:CG	2.29	0.40
3:03:735:LYS:HD2	3:03:735:LYS:HA	1.90	0.40
3:03:865:LEU:HA	3:03:870:ILE:O	2.21	0.40
3:03:944:ARG:O	3:03:948:ILE:HG13	2.22	0.40
3:03:1262:LYS:HD3	3:03:1262:LYS:HA	1.89	0.40
4:04:45:ASN:HD22	4:04:50:LYS:HD2	1.87	0.40
4:04:50:LYS:HA	4:04:51:PRO:HD2	1.78	0.40
4:04:66:LYS:HG2	4:04:67:ASP:N	2.37	0.40
4:04:98:ARG:HA	4:04:101:ARG:CG	2.49	0.40
4:04:146:VAL:HA	4:04:178:ALA:CB	2.51	0.40
4:04:410:ASP:O	4:04:413:ASP:HB2	2.22	0.40
4:04:447:ILE:HD13	4:04:468:VAL:HG13	2.03	0.40
4:04:801:VAL:HG23	4:04:802:ASP:N	2.37	0.40
4:04:1162:ILE:HG22	4:04:1178:THR:O	2.21	0.40
7:E:23:TRP:CD2	7:E:25:PRO:HG3	2.54	0.40
8:F:156:LEU:HD12	8:F:156:LEU:O	2.22	0.40
17:O:56:LEU:HD12	17:O:60:PHE:HB2	2.02	0.40
18:P:77:LYS:HB3	18:P:77:LYS:HZ2	1.86	0.40
22:T:26:ARG:O	22:T:26:ARG:HD3	2.22	0.40
24:V:68:HIS:HB2	24:V:73:PHE:CE2	2.55	0.40
25:W:54:GLN:C	25:W:56:ILE:H	2.30	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%)	183 (81%)	38 (17%)	4 (2%)	6	34
2	02	225/229 (98%)	177 (79%)	37 (16%)	11 (5%)	1	16
3	03	1323/1340 (99%)	1053 (80%)	221 (17%)	49 (4%)	2	19
4	04	1339/1369 (98%)	1091 (82%)	205 (15%)	43 (3%)	3	21
5	05	74/76 (97%)	60 (81%)	13 (18%)	1 (1%)	9	40
6	B	6/153 (4%)	6 (100%)	0	0	100	100
7	E	216/218 (99%)	161 (74%)	40 (18%)	15 (7%)	1	11
8	F	204/206 (99%)	178 (87%)	24 (12%)	2 (1%)	12	48
9	G	203/205 (99%)	158 (78%)	38 (19%)	7 (3%)	3	21
10	H	155/157 (99%)	119 (77%)	33 (21%)	3 (2%)	6	32
11	I	98/100 (98%)	78 (80%)	15 (15%)	5 (5%)	1	15
12	J	149/151 (99%)	126 (85%)	20 (13%)	3 (2%)	6	31
13	K	127/129 (98%)	110 (87%)	14 (11%)	3 (2%)	4	27
14	L	125/127 (98%)	94 (75%)	28 (22%)	3 (2%)	4	27
15	M	96/98 (98%)	79 (82%)	11 (12%)	6 (6%)	1	12
16	N	114/116 (98%)	96 (84%)	14 (12%)	4 (4%)	3	20
17	O	121/123 (98%)	87 (72%)	25 (21%)	9 (7%)	1	10
18	P	112/114 (98%)	93 (83%)	12 (11%)	7 (6%)	1	12
19	Q	98/100 (98%)	66 (67%)	28 (29%)	4 (4%)	2	18
20	R	86/88 (98%)	74 (86%)	12 (14%)	0	100	100
21	S	80/82 (98%)	61 (76%)	15 (19%)	4 (5%)	1	16
22	T	78/80 (98%)	61 (78%)	13 (17%)	4 (5%)	1	15
23	U	63/65 (97%)	48 (76%)	11 (18%)	4 (6%)	1	12
24	V	77/79 (98%)	59 (77%)	17 (22%)	1 (1%)	9	42
25	W	83/85 (98%)	68 (82%)	10 (12%)	5 (6%)	1	13
26	X	63/65 (97%)	49 (78%)	9 (14%)	5 (8%)	1	9
All	All	5540/5784 (96%)	4435 (80%)	903 (16%)	202 (4%)	4	20

All (202) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	02	13	LEU
2	02	62	ASP
2	02	135	ASP
2	02	193	GLU
3	03	288	PRO
3	03	638	SER
3	03	866	ASP
3	03	1013	GLN
3	03	1321	GLU
4	04	47	ARG
4	04	234	PRO
4	04	264	ASP
4	04	325	LYS
4	04	345	LYS
4	04	357	VAL
4	04	585	LYS
4	04	712	GLN
4	04	860	ARG
4	04	1051	ASP
4	04	1065	ALA
4	04	1067	ARG
4	04	1343	GLU
7	E	39	HIS
7	E	40	ILE
7	E	43	LEU
9	G	31	CYS
17	O	24	GLU
18	P	4	ALA
18	P	6	ILE
18	P	26	LYS
21	S	27	ALA
23	U	20	GLU
25	W	6	ALA
26	X	10	GLU
26	X	38	TYR
2	02	20	SER
3	03	63	SER
3	03	200	ARG
3	03	201	ARG
3	03	268	ARG
3	03	270	THR
3	03	483	ASP
3	03	655	VAL

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Mol	Chain	Res	Type
3	03	660	VAL
3	03	842	ASP
3	03	852	ALA
3	03	872	TYR
3	03	879	GLY
3	03	937	ASP
3	03	1101	LEU
4	04	89	GLY
4	04	122	SER
4	04	289	ASP
4	04	586	GLY
4	04	596	LEU
4	04	637	ALA
4	04	1125	PRO
4	04	1292	LEU
7	E	17	GLY
7	E	22	TYR
7	E	25	PRO
7	E	33	GLY
7	E	37	LYS
7	E	151	ILE
8	F	205	GLU
9	G	4	LEU
11	I	92	THR
13	K	56	PRO
15	M	57	VAL
15	M	75	ASP
17	O	27	PRO
17	O	33	CYS
17	O	108	ASP
18	P	5	GLY
21	S	28	ARG
21	S	44	SER
22	T	50	ASN
23	U	72	ASP
25	W	7	LYS
2	01	195	ARG
3	03	132	ASP
3	03	188	PHE
3	03	343	HIS
3	03	440	GLY
3	03	596	ASP

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Mol	Chain	Res	Type
3	03	659	GLN
3	03	984	VAL
3	03	1151	LEU
3	03	1161	LEU
3	03	1224	PRO
4	04	309	ASN
4	04	463	GLY
4	04	756	GLU
4	04	815	GLY
4	04	1084	GLN
4	04	1167	LYS
7	E	88	ASP
8	F	28	PHE
9	G	182	LYS
10	H	26	GLY
10	H	98	ALA
11	I	53	LYS
11	I	93	LYS
12	J	16	LYS
12	J	57	GLU
16	N	25	SER
16	N	123	PRO
16	N	126	ARG
17	O	41	PRO
17	O	101	LEU
18	P	109	LYS
19	Q	2	LYS
19	Q	51	PRO
21	S	81	ALA
22	T	34	GLY
23	U	70	TYR
26	X	8	GLU
26	X	36	GLU
2	01	62	ASP
2	02	162	GLU
2	02	213	PRO
3	03	202	ARG
3	03	357	ASN
3	03	627	GLY
3	03	729	ALA
3	03	1186	VAL
4	04	112	ALA

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Mol	Chain	Res	Type
4	04	248	ASP
4	04	499	ILE
4	04	695	LYS
4	04	734	ALA
4	04	832	LYS
4	04	1169	THR
4	04	1185	PRO
5	05	33	GLY
7	E	21	ARG
7	E	29	PRO
7	E	101	LEU
9	G	34	GLU
10	H	24	VAL
11	I	56	LYS
15	M	41	PRO
15	M	42	LEU
17	O	2	THR
17	O	15	VAL
18	P	23	GLY
18	P	104	ASN
19	Q	31	SER
23	U	24	LYS
25	W	17	ARG
25	W	76	ALA
26	X	25	LYS
2	02	166	ARG
2	02	211	ILE
3	03	575	LEU
3	03	841	ARG
3	03	994	ARG
3	03	1334	GLY
4	04	51	PRO
4	04	236	TRP
7	E	201	PRO
9	G	45	PRO
11	I	33	GLU
13	K	20	ASN
14	L	12	LYS
19	Q	55	SER
22	T	48	GLU
25	W	3	ILE
2	01	168	ILE

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Mol	Chain	Res	Type
3	03	438	GLY
3	03	567	PRO
3	03	630	VAL
3	03	1223	ARG
3	03	1265	PHE
4	04	313	GLY
4	04	496	GLY
9	G	47	LEU
9	G	167	PRO
14	L	25	GLY
14	L	107	ALA
16	N	94	SER
2	01	167	PRO
3	03	1100	PRO
4	04	825	VAL
4	04	1176	VAL
15	M	78	GLU
3	03	747	GLY
3	03	1320	PRO
4	04	1150	PRO
7	E	98	GLY
17	O	62	VAL
24	V	75	PRO
2	02	167	PRO
2	02	209	GLY
3	03	809	GLY
3	03	874	GLY
22	T	4	ILE
3	03	294	GLY
4	04	561	GLY
12	J	81	GLY
13	K	50	VAL
15	M	43	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	01	194/197 (98%)	193 (100%)	1 (0%)	81	83
2	02	194/197 (98%)	190 (98%)	4 (2%)	47	65
3	03	1098/1155 (95%)	1086 (99%)	12 (1%)	65	76
4	04	1103/1141 (97%)	1087 (98%)	16 (2%)	57	72
5	05	65/65 (100%)	65 (100%)	0	100	100
6	B	6/7 (86%)	6 (100%)	0	100	100
7	E	180/180 (100%)	172 (96%)	8 (4%)	25	47
8	F	170/170 (100%)	167 (98%)	3 (2%)	51	68
9	G	172/172 (100%)	170 (99%)	2 (1%)	63	75
10	H	119/119 (100%)	117 (98%)	2 (2%)	53	69
11	I	87/87 (100%)	86 (99%)	1 (1%)	65	76
12	J	124/124 (100%)	123 (99%)	1 (1%)	73	80
13	K	104/104 (100%)	102 (98%)	2 (2%)	50	67
14	L	105/105 (100%)	103 (98%)	2 (2%)	50	67
15	M	86/86 (100%)	86 (100%)	0	100	100
16	N	89/89 (100%)	88 (99%)	1 (1%)	65	76
17	O	103/103 (100%)	98 (95%)	5 (5%)	22	43
18	P	92/92 (100%)	92 (100%)	0	100	100
19	Q	83/83 (100%)	83 (100%)	0	100	100
20	R	76/76 (100%)	75 (99%)	1 (1%)	61	74
21	S	65/65 (100%)	63 (97%)	2 (3%)	35	56
22	T	74/74 (100%)	73 (99%)	1 (1%)	59	72
23	U	56/56 (100%)	54 (96%)	2 (4%)	31	52
24	V	70/70 (100%)	68 (97%)	2 (3%)	37	58
25	W	65/65 (100%)	60 (92%)	5 (8%)	12	32
26	X	55/55 (100%)	53 (96%)	2 (4%)	31	52
All	All	4635/4737 (98%)	4560 (98%)	75 (2%)	54	70

All (75) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	01	133	LEU
2	02	13	LEU
2	02	30	PRO

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Mol	Chain	Res	Type
2	02	172	LEU
2	02	213	PRO
3	03	54	ARG
3	03	143	ARG
3	03	194	LEU
3	03	647	ARG
3	03	1012	GLU
3	03	1082	ILE
3	03	1113	LEU
3	03	1127	LYS
3	03	1151	LEU
3	03	1211	ARG
3	03	1224	PRO
3	03	1253	LEU
4	04	53	ARG
4	04	77	ARG
4	04	102	MET
4	04	113	HIS
4	04	190	LYS
4	04	214	ARG
4	04	217	LEU
4	04	234	PRO
4	04	250	ARG
4	04	290	ILE
4	04	422	LEU
4	04	596	LEU
4	04	612	LEU
4	04	746	LEU
4	04	1231	ARG
4	04	1332	LEU
7	E	11	LYS
7	E	19	GLN
7	E	21	ARG
7	E	35	ARG
7	E	39	HIS
7	E	45	LYS
7	E	89	GLN
7	E	204	ASP
8	F	156	LEU
8	F	163	ARG
8	F	203	LYS
9	G	149	LYS

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Mol	Chain	Res	Type
9	G	167	PRO
10	H	51	LYS
10	H	75	LEU
11	I	14	GLN
12	J	24	LYS
13	K	8	ASP
13	K	113	ARG
14	L	60	LEU
14	L	62	LEU
16	N	110	THR
17	O	17	LYS
17	O	27	PRO
17	O	29	LYS
17	O	55	ARG
17	O	113	ARG
20	R	9	LYS
21	S	5	ARG
21	S	25	ARG
22	T	15	LYS
23	U	38	LYS
23	U	48	ARG
24	V	4	LEU
24	V	36	ARG
25	W	4	LYS
25	W	8	LYS
25	W	56	ILE
25	W	67	HIS
25	W	69	ASN
26	X	17	ARG
26	X	34	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (142) such sidechains are listed below:

Mol	Chain	Res	Type
2	01	18	GLN
2	01	41	ASN
2	01	227	GLN
2	02	37	HIS
2	02	75	GLN
2	02	93	GLN
2	02	103	ASN
2	02	147	GLN

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Mol	Chain	Res	Type
2	02	186	ASN
2	02	194	GLN
2	02	208	ASN
3	03	20	GLN
3	03	65	ASN
3	03	86	GLN
3	03	150	HIS
3	03	214	ASN
3	03	219	GLN
3	03	235	ASN
3	03	238	GLN
3	03	258	ASN
3	03	330	HIS
3	03	406	ASN
3	03	437	ASN
3	03	462	ASN
3	03	463	GLN
3	03	494	ASN
3	03	526	HIS
3	03	620	ASN
3	03	649	GLN
3	03	684	ASN
3	03	686	GLN
3	03	688	GLN
3	03	725	GLN
3	03	761	GLN
3	03	766	ASN
3	03	811	ASN
3	03	824	GLN
3	03	922	ASN
3	03	955	GLN
3	03	1017	GLN
3	03	1061	GLN
3	03	1070	HIS
3	03	1080	ASN
3	03	1090	ASN
3	03	1116	HIS
3	03	1175	ASN
3	03	1256	GLN
3	03	1257	GLN
3	03	1312	ASN
3	03	1314	GLN

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Mol	Chain	Res	Type
3	03	1324	ASN
4	04	45	ASN
4	04	266	ASN
4	04	300	GLN
4	04	320	ASN
4	04	335	GLN
4	04	435	GLN
4	04	448	GLN
4	04	450	HIS
4	04	458	ASN
4	04	469	HIS
4	04	488	ASN
4	04	545	HIS
4	04	594	GLN
4	04	708	ASN
4	04	736	GLN
4	04	861	ASN
4	04	954	ASN
4	04	1019	ASN
4	04	1084	GLN
4	04	1235	ASN
4	04	1279	GLN
4	04	1289	ASN
5	05	29	GLN
5	05	31	GLN
5	05	43	ASN
6	B	7	GLN
7	E	15	HIS
7	E	39	HIS
7	E	51	ASN
7	E	89	GLN
7	E	103	ASN
7	E	120	GLN
7	E	146	ASN
7	E	177	ASN
7	E	178	ASN
8	F	24	ASN
8	F	31	ASN
8	F	139	ASN
8	F	175	HIS
8	F	184	ASN
8	F	189	HIS

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Mol	Chain	Res	Type
9	G	39	GLN
9	G	70	GLN
9	G	73	ASN
9	G	88	ASN
9	G	115	GLN
9	G	125	ASN
9	G	130	ASN
9	G	195	ASN
10	H	72	ASN
10	H	76	ASN
10	H	81	GLN
10	H	82	HIS
10	H	96	GLN
10	H	134	ASN
10	H	145	ASN
10	H	147	ASN
11	I	52	ASN
11	I	68	GLN
11	I	81	ASN
12	J	121	ASN
12	J	129	ASN
13	K	15	ASN
13	K	37	ASN
14	L	24	ASN
14	L	30	ASN
14	L	49	GLN
14	L	74	GLN
15	M	58	ASN
16	N	21	HIS
16	N	100	ASN
16	N	118	ASN
17	O	71	HIS
17	O	72	ASN
18	P	51	GLN
19	Q	34	ASN
19	Q	48	GLN
19	Q	61	ASN
19	Q	65	GLN
19	Q	70	HIS
20	R	36	ASN
20	R	49	HIS
22	T	46	HIS

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Mol	Chain	Res	Type
23	U	31	ASN
23	U	52	GLN
23	U	74	HIS
24	V	42	ASN
25	W	2	ASN
25	W	12	GLN
25	W	69	ASN
25	W	83	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1441/1539 (93%)	170 (11%)	2 (0%)

All (170) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	7	A
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	66	A
1	A	68	G
1	A	70	U
1	A	71	A
1	A	72	A
1	A	79	G
1	A	83	C
1	A	85	U
1	A	86	G
1	A	87	C
1	A	89	U
1	A	90	C
1	A	93	U

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Mol	Chain	Res	Type
1	A	94	G
1	A	99	C
1	A	137	U
1	A	144	G
1	A	164	G
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	252	U
1	A	266	G
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

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Mol	Chain	Res	Type
1	A	479	U
1	A	480	U
1	A	486	U
1	A	487	A
1	A	495	A
1	A	497	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	572	A
1	A	573	A
1	A	575	G
1	A	576	C
1	A	577	G
1	A	633	G
1	A	642	A
1	A	665	A
1	A	701	U
1	A	703	G
1	A	723	U
1	A	724	G
1	A	734	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	844	G

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Mol	Chain	Res	Type
1	A	846	G
1	A	871	U
1	A	902	G
1	A	926	G
1	A	934	C
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	1053	G
1	A	1055	A
1	A	1094	G
1	A	1101	A
1	A	1118	U
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	1213	A
1	A	1215	G
1	A	1225	A
1	A	1226	C
1	A	1238	A
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	1280	A
1	A	1282	C
1	A	1287	A
1	A	1300	G
1	A	1303	C
1	A	1317	C
1	A	1347	G
1	A	1364	U
1	A	1394	A
1	A	1395	C
1	A	1398	A
1	A	1498	U
1	A	1499	A
1	A	1502	A
1	A	1503	A
1	A	1506	U
1	A	1517	G
1	A	1529	G
1	A	1530	G

All (2) RNA pucker outliers are listed below:

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

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
6	B	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	10:GLU	C	107:UNK	N	56.44
1	B	179:UNK	C	191:UNK	N	18.18

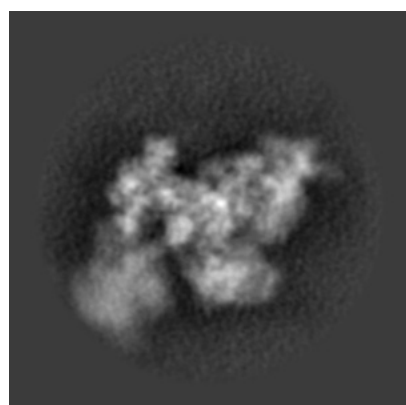
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7014. These allow visual inspection of the internal detail of the map and identification of artifacts.

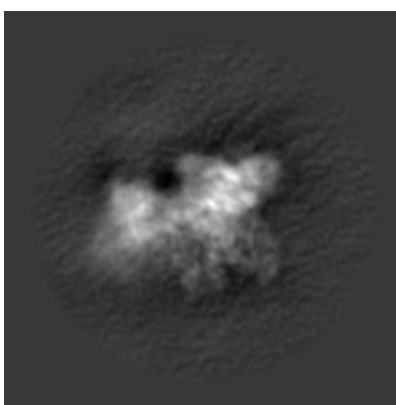
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

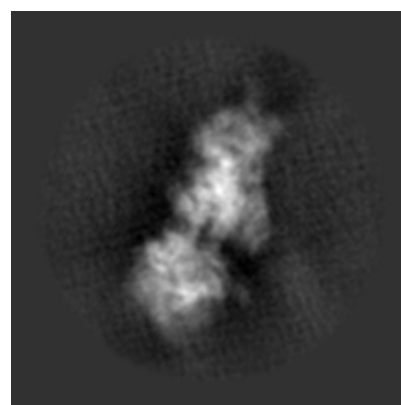
6.1.1 Primary map



X



Y

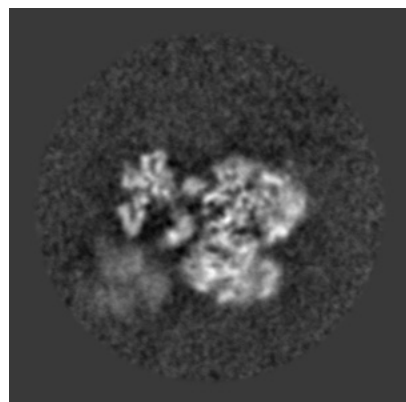


Z

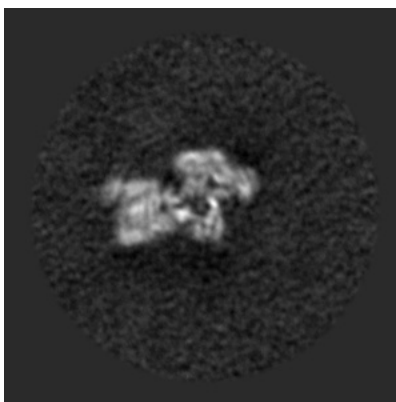
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

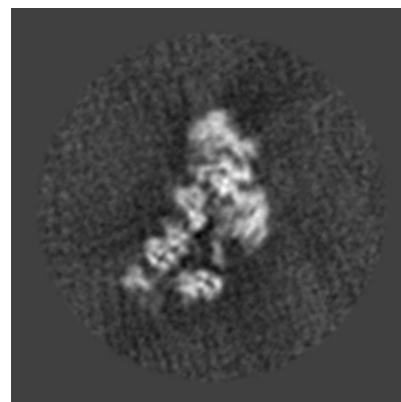
6.2.1 Primary map



X Index: 140



Y Index: 140

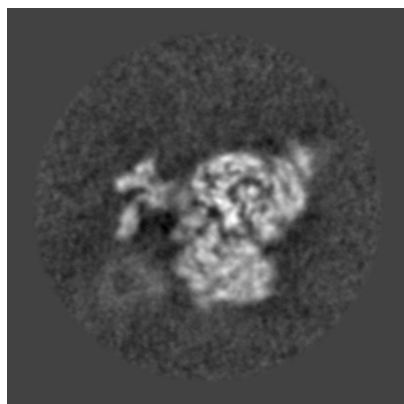


Z Index: 140

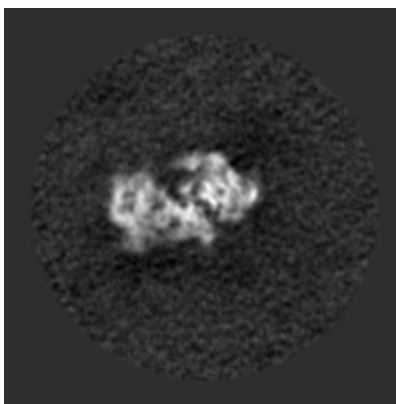
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

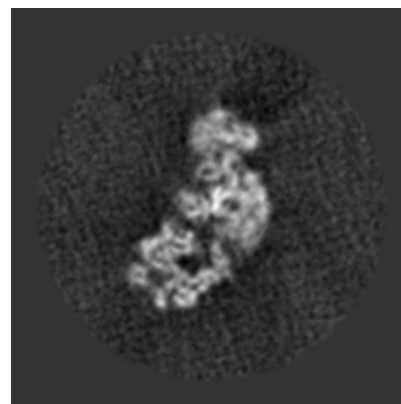
6.3.1 Primary map



X Index: 147



Y Index: 151

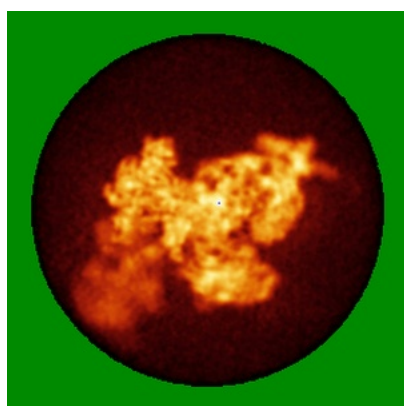


Z Index: 146

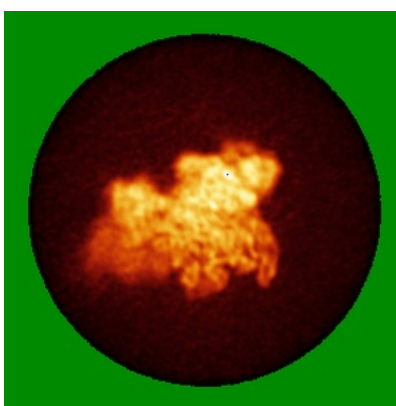
The images above show the largest variance slices of the map in three orthogonal directions.

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

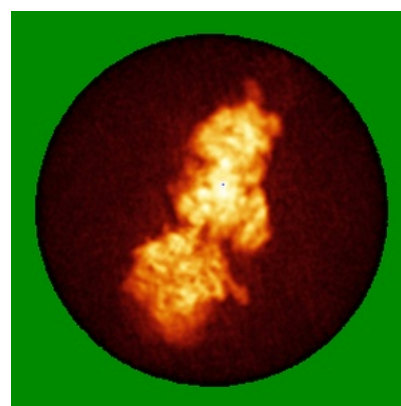
6.4.1 Primary map



X



Y

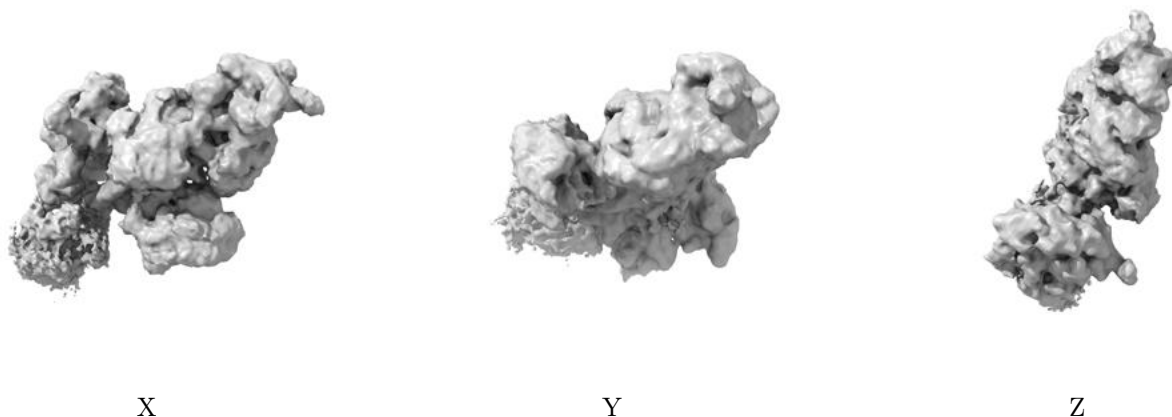


Z

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.

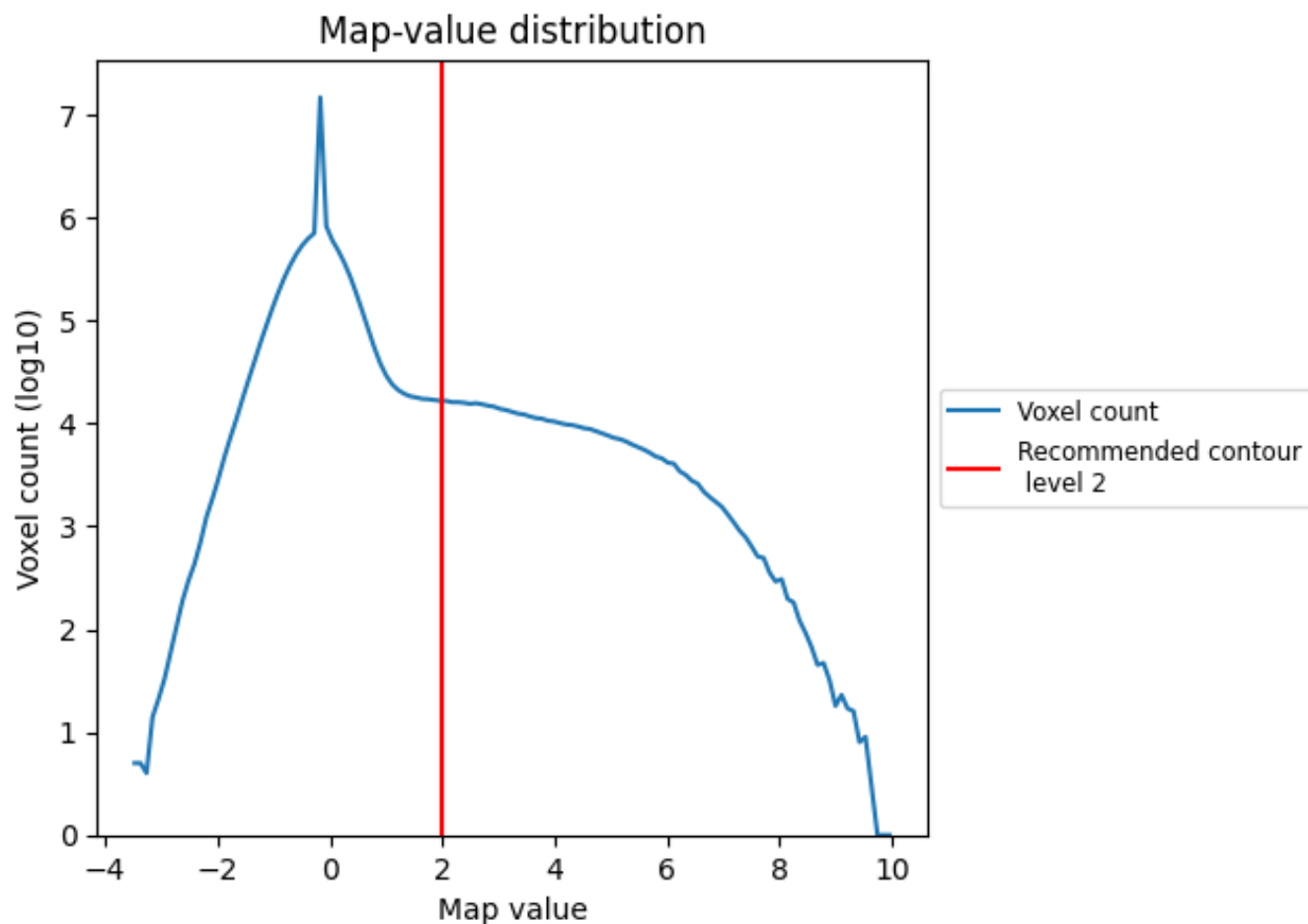
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

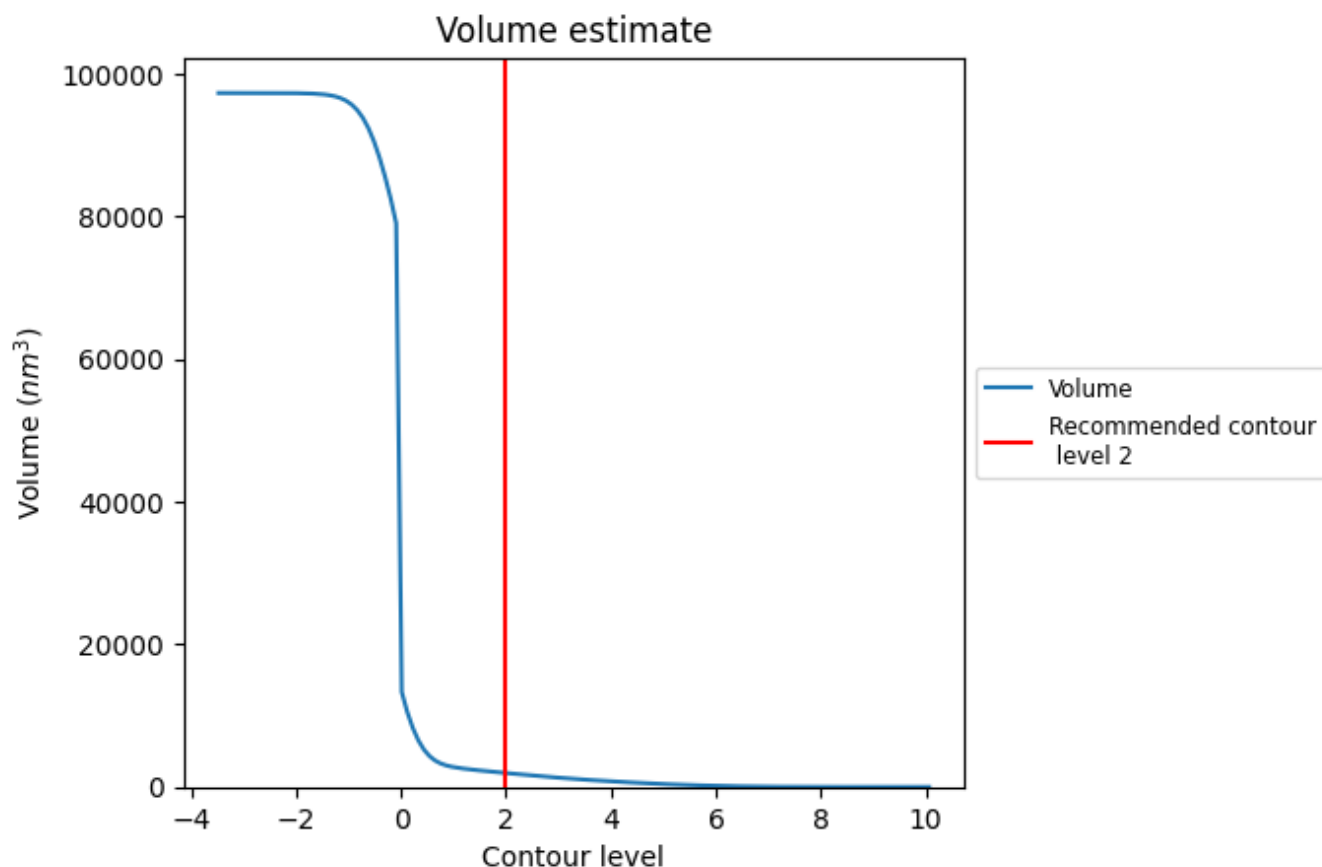
This section contains the results of statistical analysis of the map.

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.

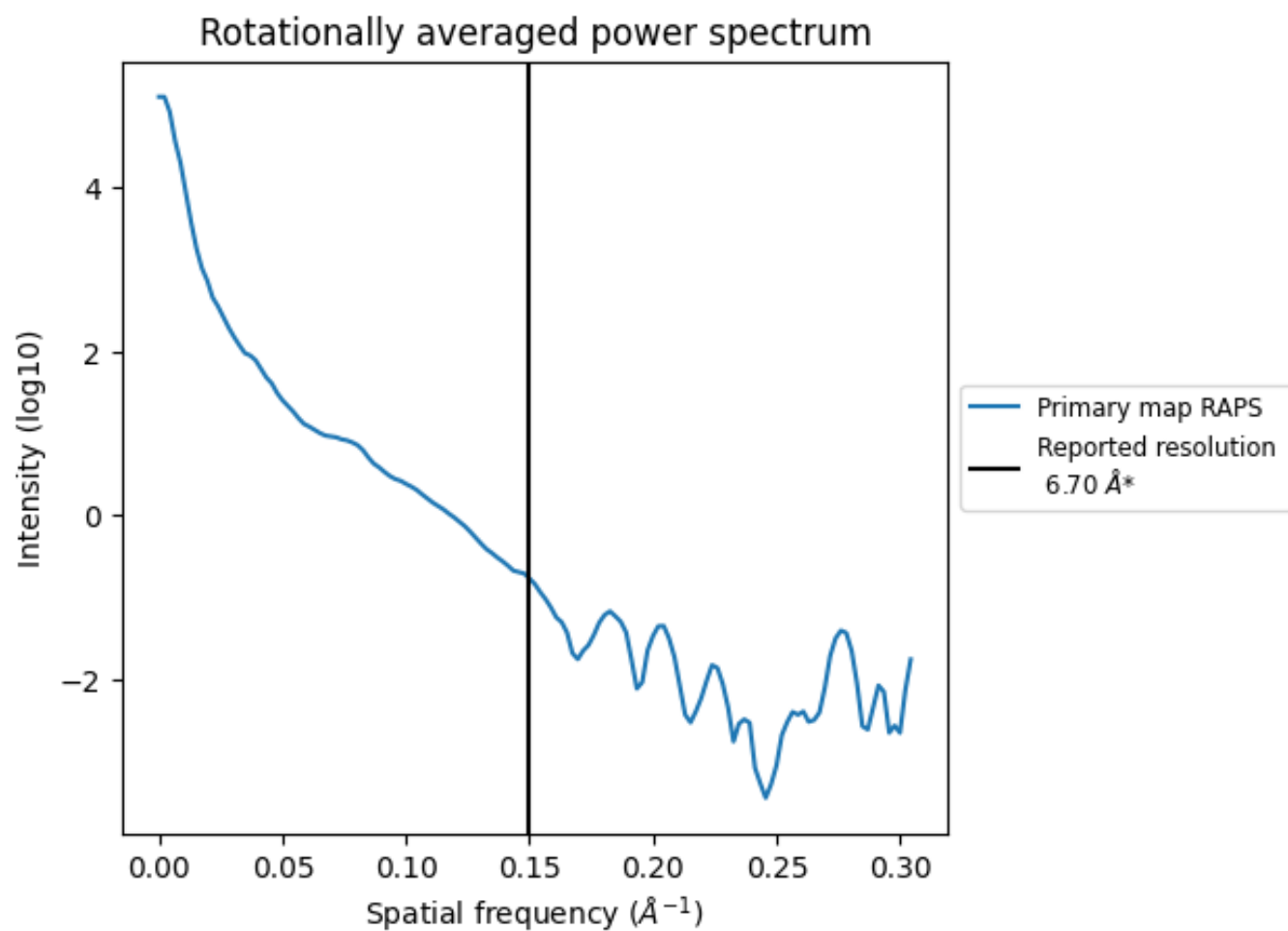
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1953 nm³; this corresponds to an approximate mass of 1764 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 0.149 Å⁻¹

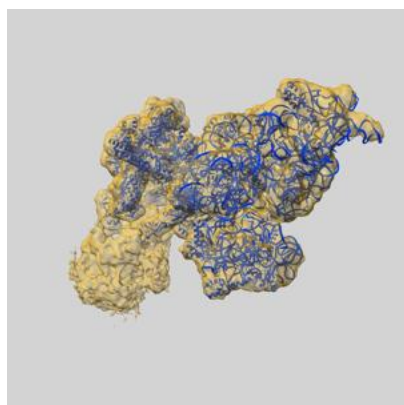
8 Fourier-Shell correlation ⓘ

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

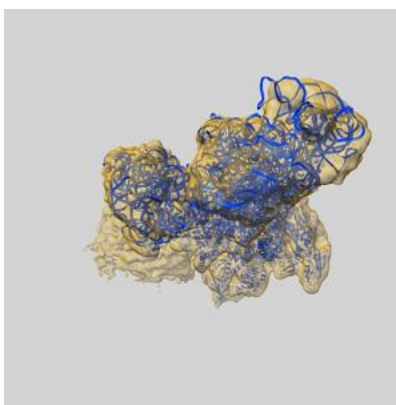
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7014 and PDB model 6AWB. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

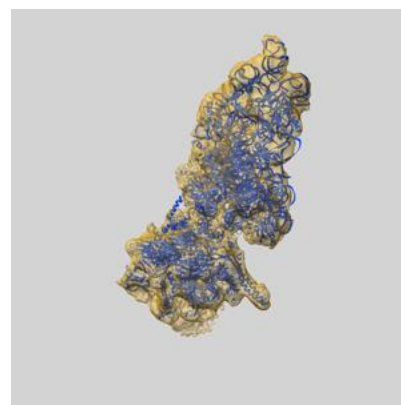
9.1 Map-model overlay [i](#)



X



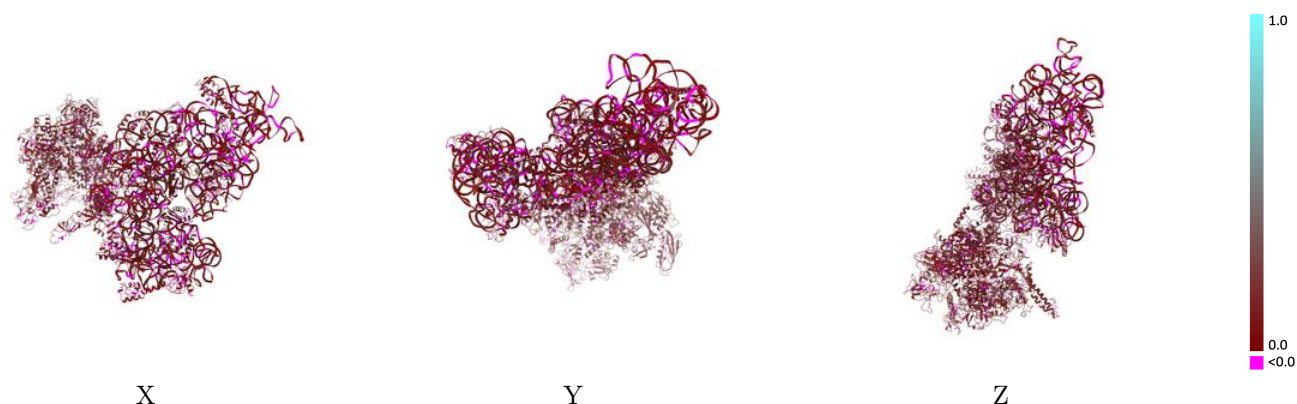
Y



Z

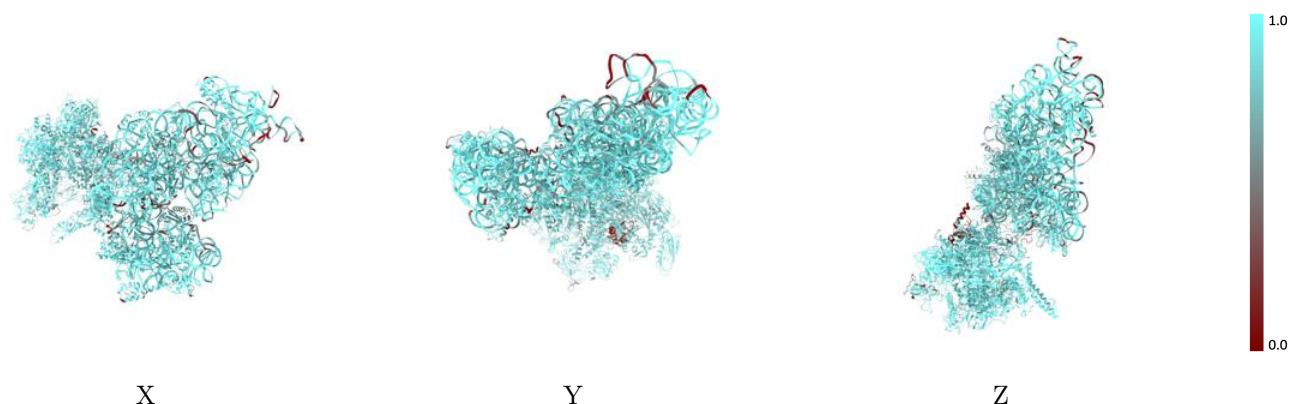
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



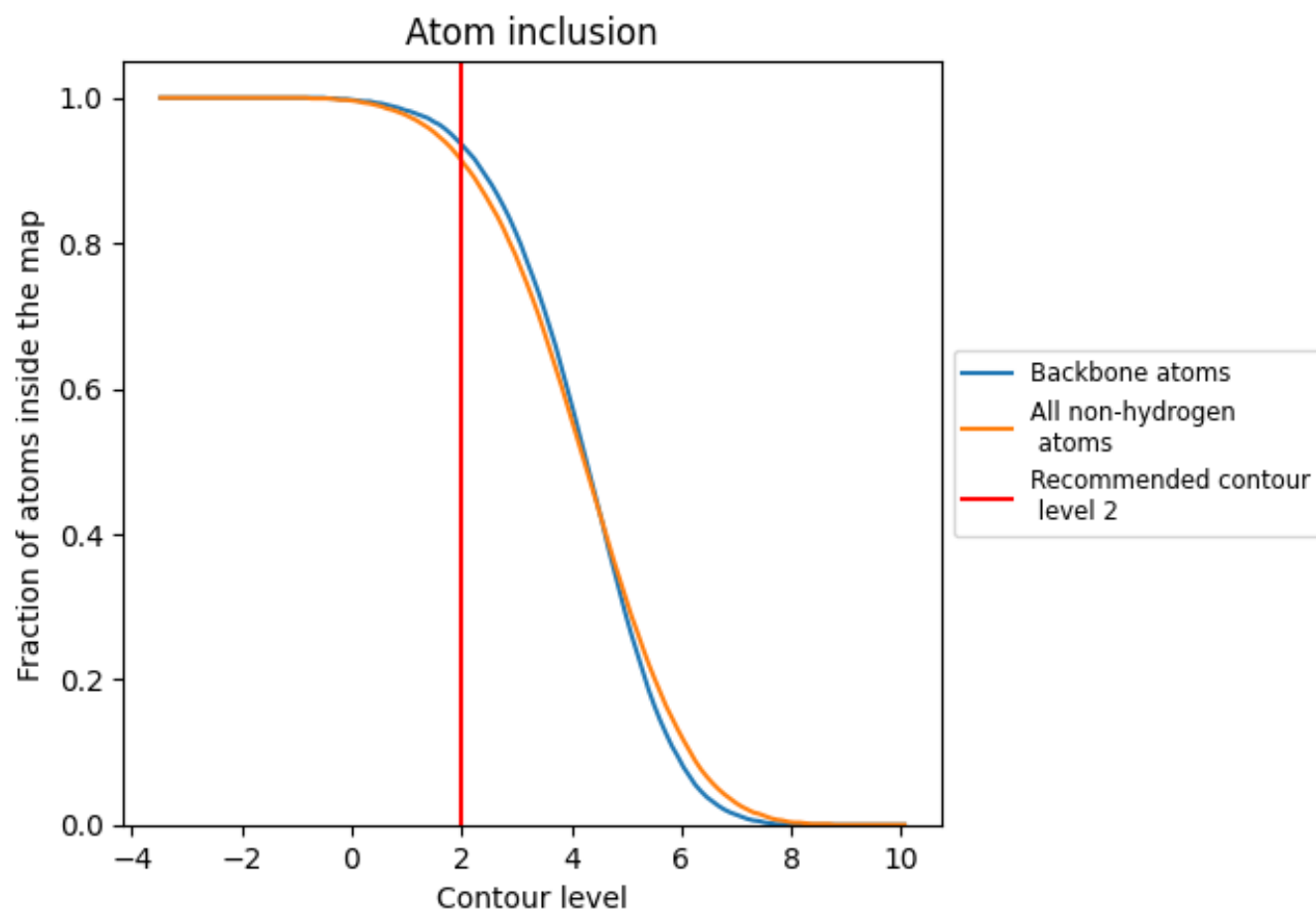
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 94% of all backbone atoms, 91% 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	 0.9140	 0.1080
01	 0.9600	 0.1560
02	 0.9630	 0.1390
03	 0.9140	 0.1350
04	 0.9270	 0.1400
05	 0.3000	 0.1070
A	 0.9150	 0.0930
B	 0.9350	 0.1120
E	 0.9590	 0.1330
F	 0.8540	 0.1090
G	 0.9280	 0.0810
H	 0.9150	 0.1360
I	 0.8650	 0.1080
J	 0.8410	 0.0770
K	 0.9540	 0.1260
L	 0.9040	 0.0610
M	 0.9050	 0.0690
N	 0.9470	 0.0820
O	 0.8730	 0.0770
P	 0.9040	 0.0590
Q	 0.9660	 0.0390
R	 0.9190	 0.1200
S	 0.9710	 0.0680
T	 0.9570	 0.0900
U	 0.9090	 0.0870
V	 0.9230	 0.0500
W	 0.9310	 0.0920
X	 0.8820	 0.1300

