



Full wwPDB EM Validation Report ⓘ

Mar 3, 2024 – 12:46 PM EST

PDB ID : 6AWC
EMDB ID : EMD-7015
Title : Structure of 30S ribosomal subunit and RNA polymerase complex in 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 : 7.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

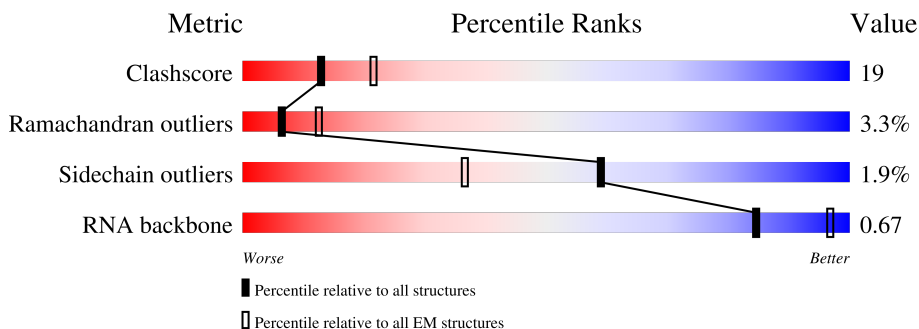
EMDB validation analysis : 0.0.1.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance

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

The reported resolution of this entry is 7.90 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	
3	03	1340	
4	04	1369	
5	05	59	
6	B	153	

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Mol	Chain	Length	Quality of chain
7	E	218	44% 43% 10% 9%
8	F	206	67% 31% 9%
9	G	205	56% 40%
10	H	157	61% 39% 9%
11	I	100	62% 38% 9%
12	J	151	60% 38% 9%
13	K	129	62% 36% 7%
14	L	127	49% 49% 7%
15	M	98	58% 40% 7%
16	N	116	57% 41% 7%
17	O	123	66% 33% 7%
18	P	114	54% 46% 7%
19	Q	100	52% 45%
20	R	88	70% 28% 7%
21	S	82	62% 32% 6% 5%
22	T	80	65% 35% 7%
23	U	65	55% 42% 8%
24	V	79	70% 30% 5%
25	W	85	45% 51% 5% 7%
26	X	65	57% 34% 8% 7%

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 75169 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
			Total	C	N	O	P		
1	A	1443	30955	13808	5681	10024	1442	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	J	151	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		

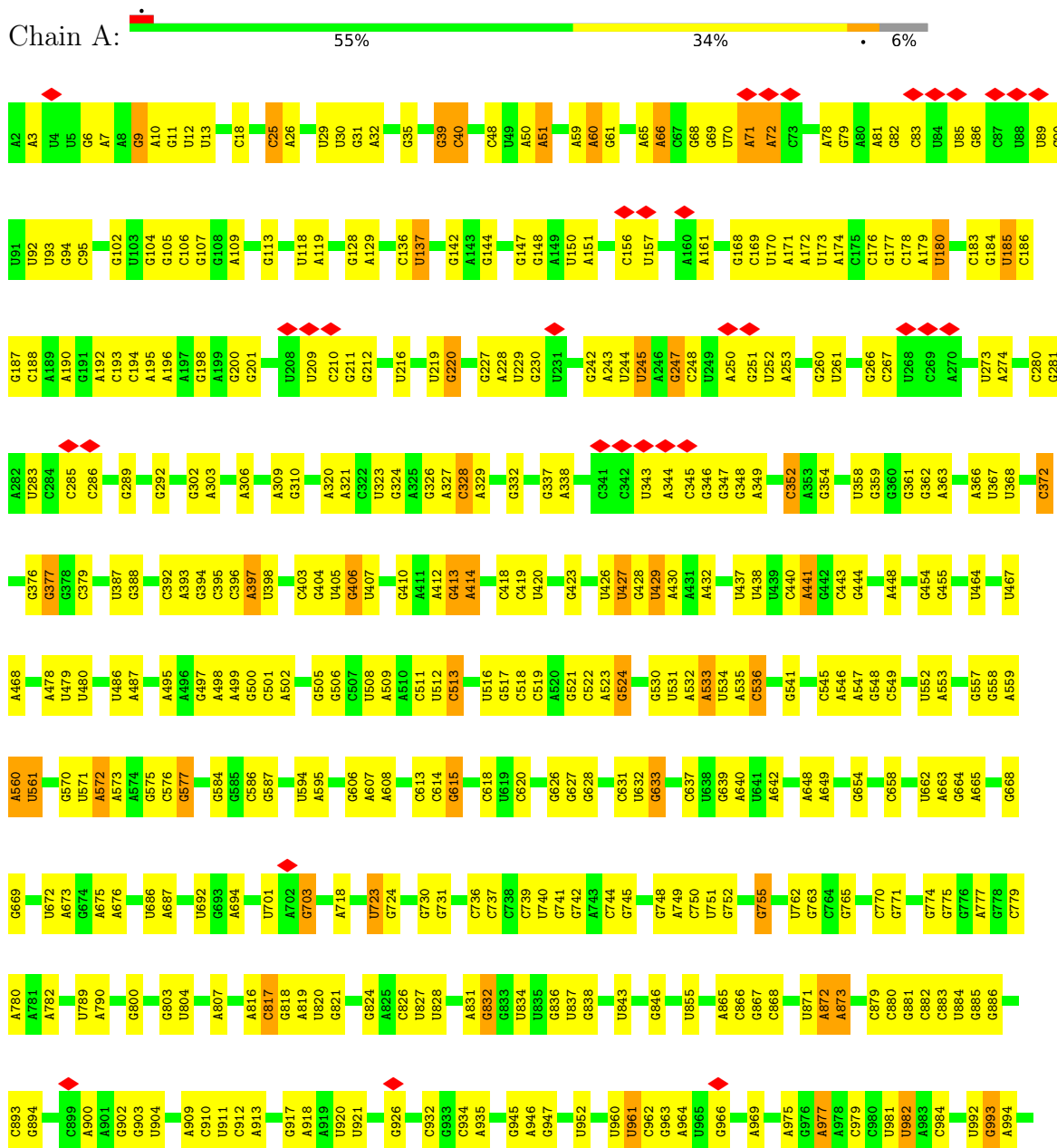
- Molecule 26 is a protein called 30S ribosomal protein S21.

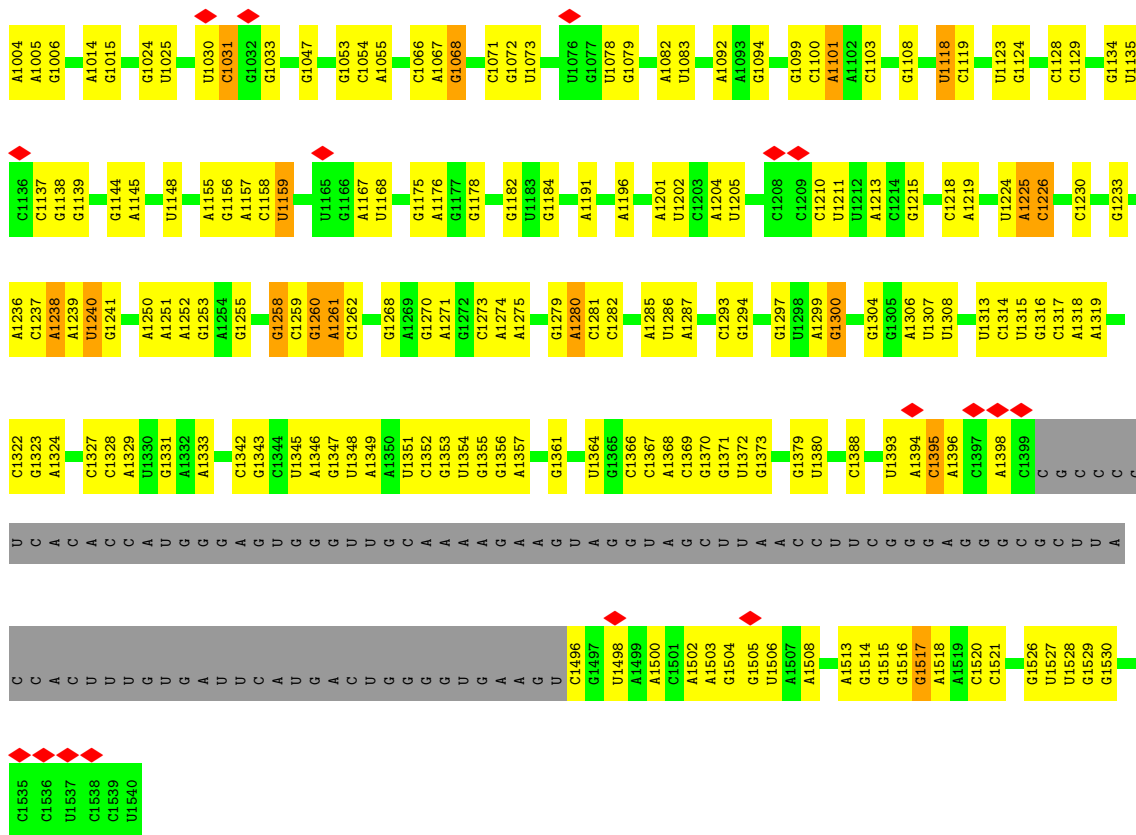
Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

3 Residue-property plots [i](#)

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

• Molecule 1: 16S rRNA

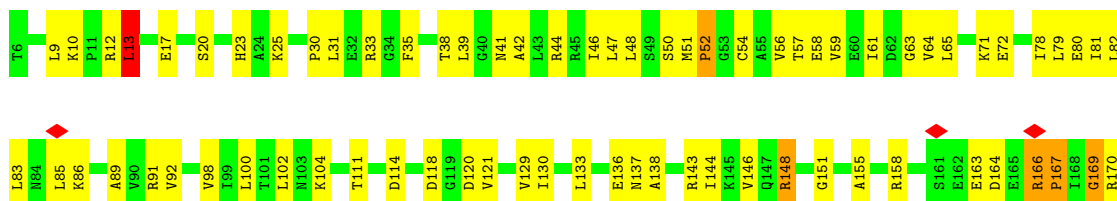


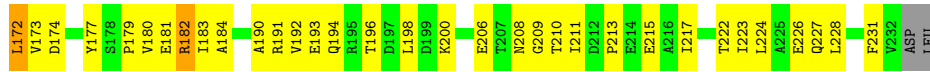


• Molecule 2: DNA-directed RNA polymerase subunit alpha

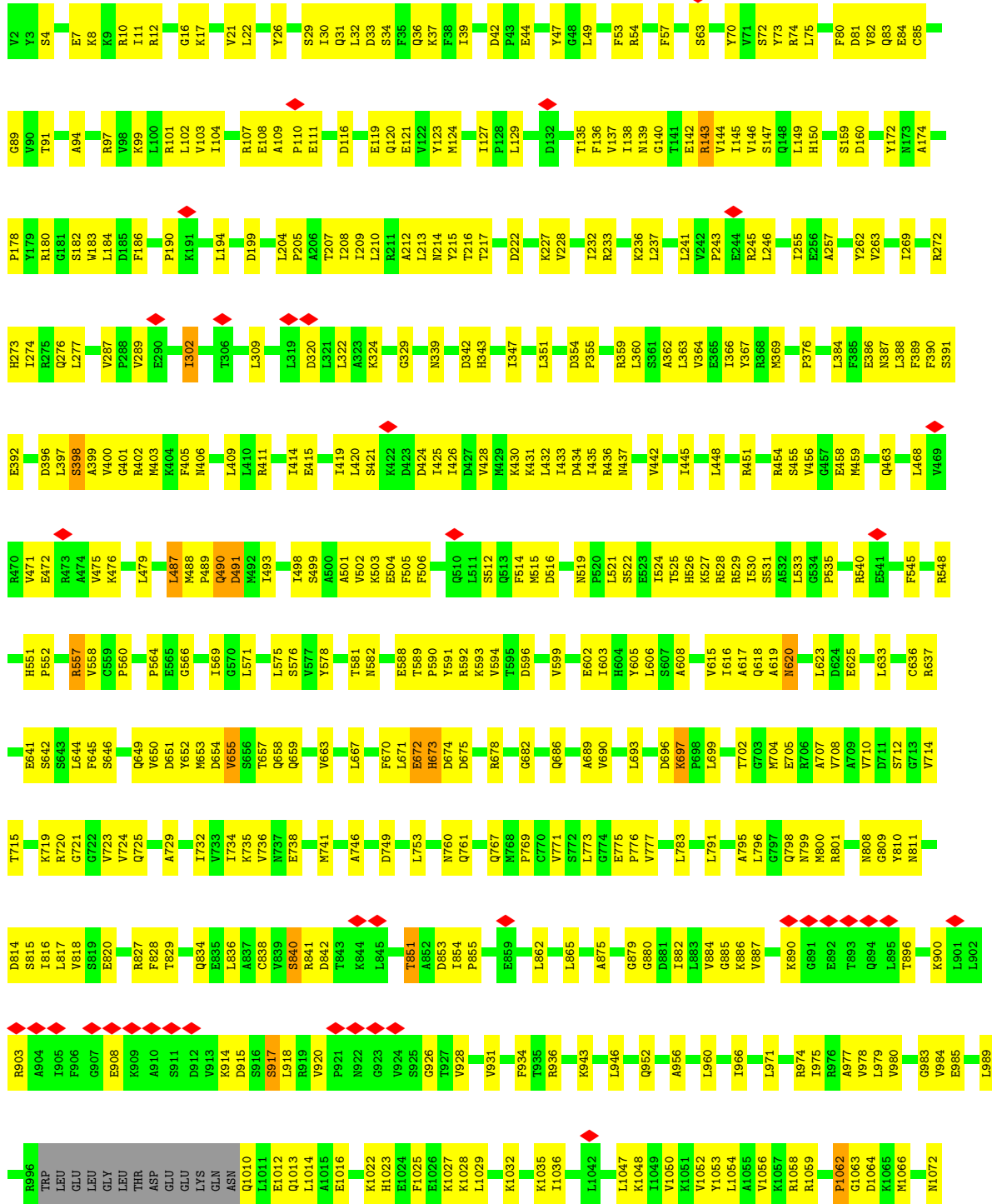


• Molecule 2: DNA-directed RNA polymerase subunit alpha





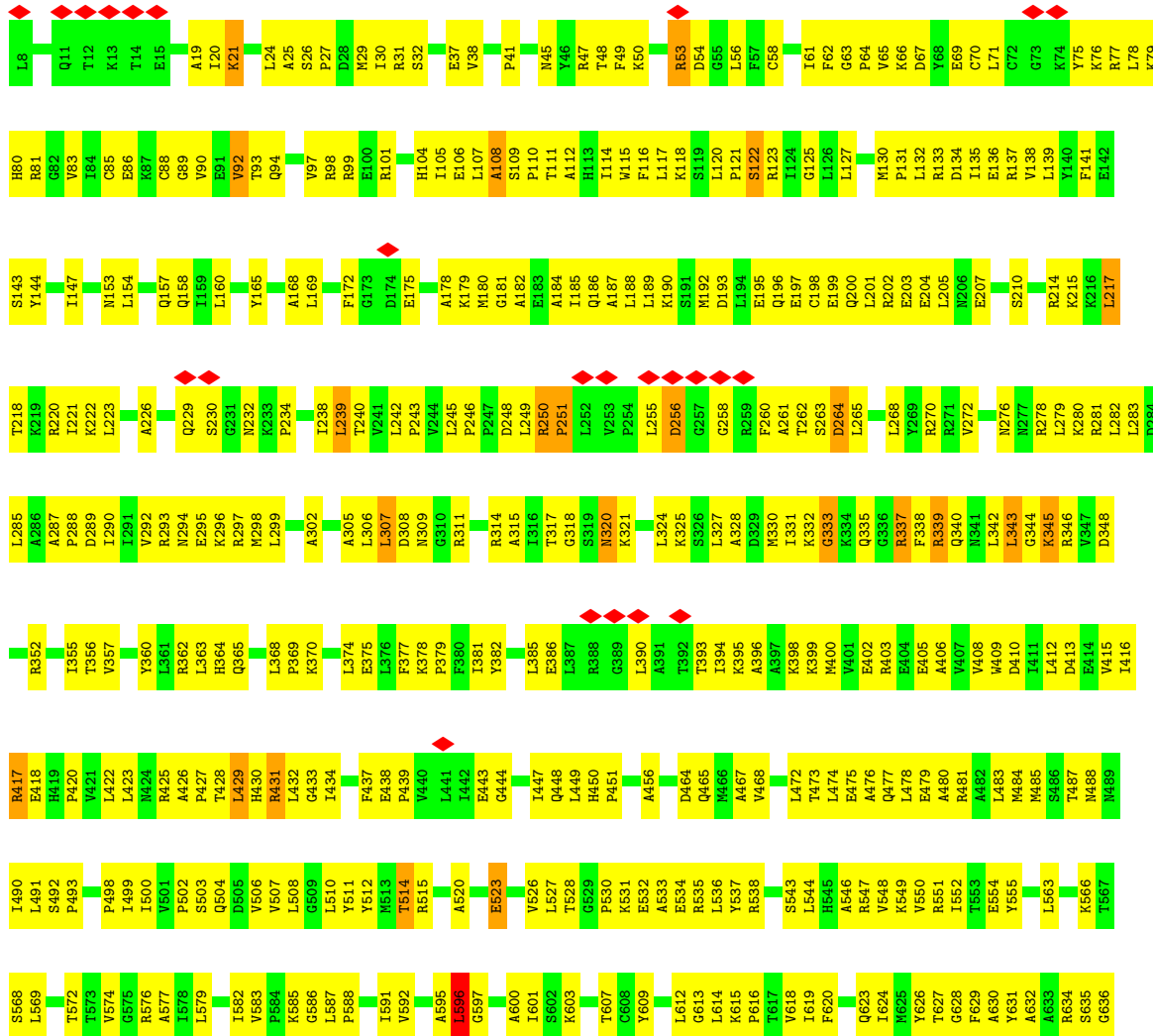
• Molecule 3: DNA-directed RNA polymerase subunit beta

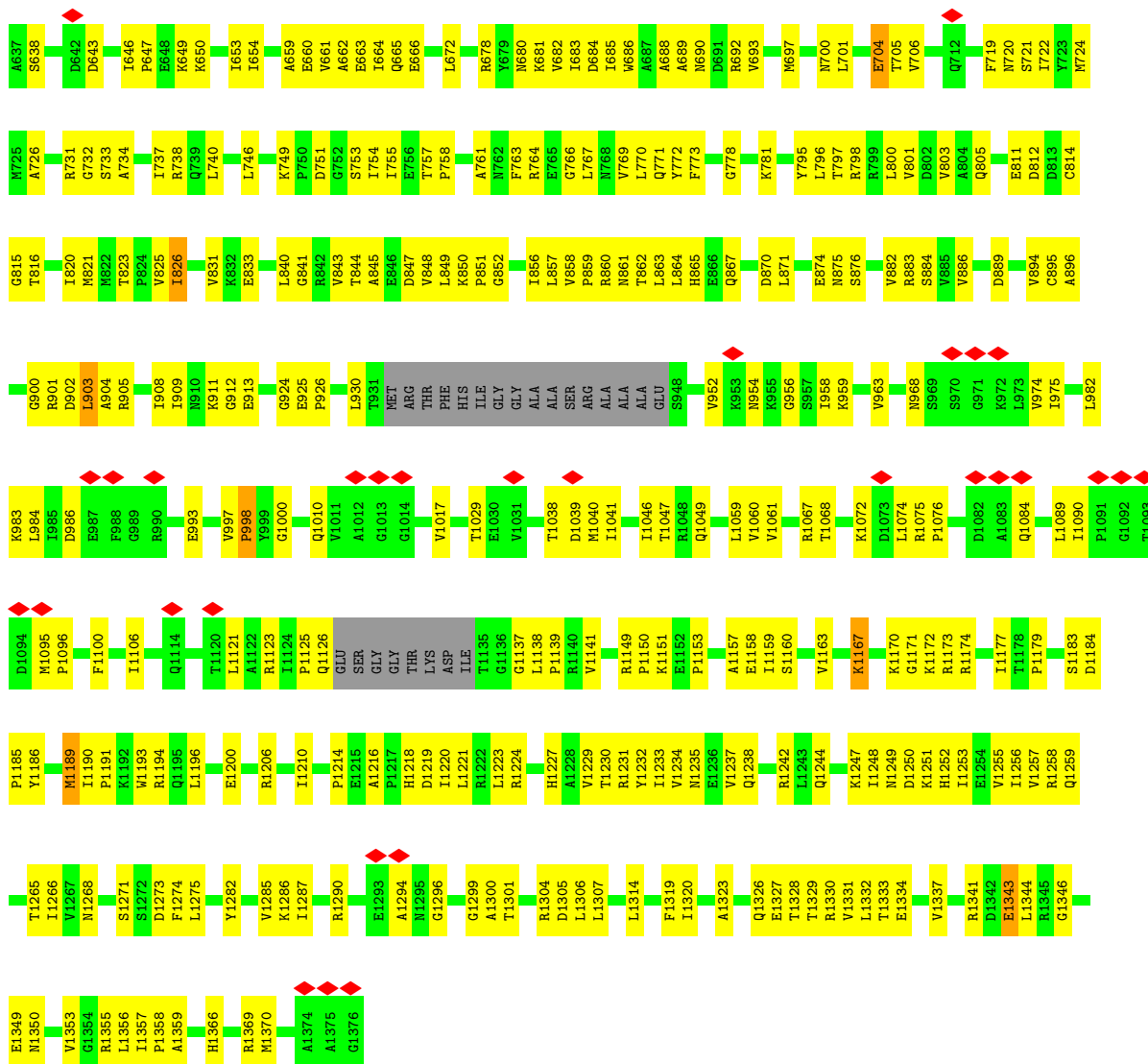




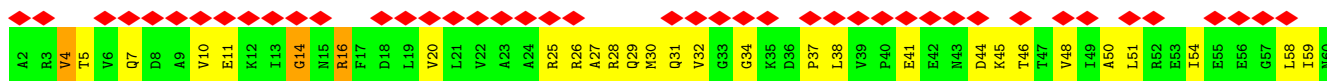
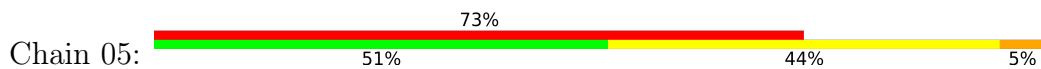
• Molecule 4: DNA-directed RNA polymerase subunit beta'

Chain 04:

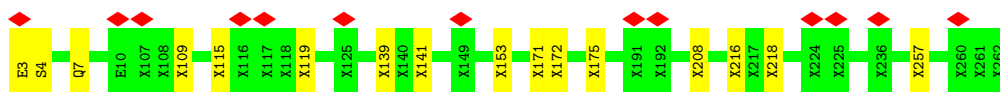
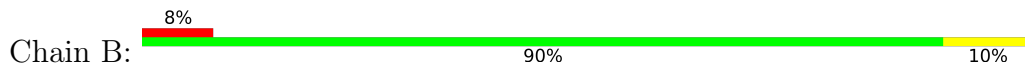




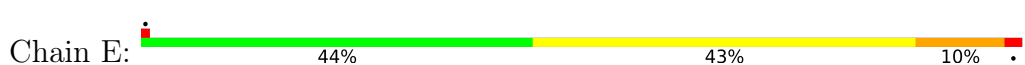
• Molecule 5: DNA-directed RNA polymerase subunit omega

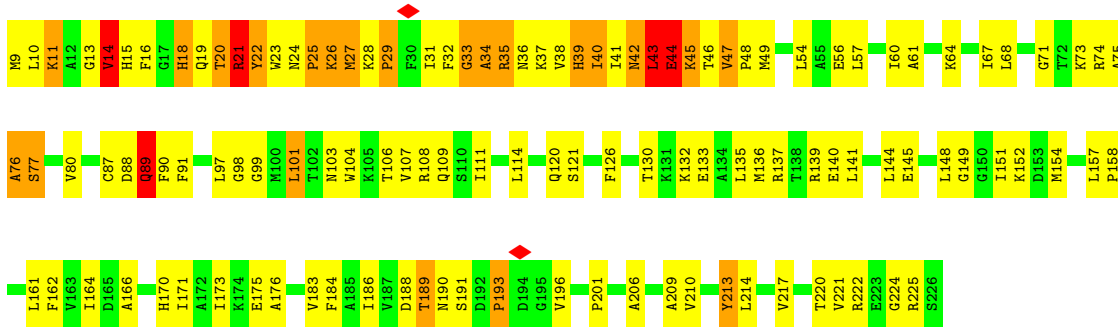


• Molecule 6: 30S ribosomal protein S1

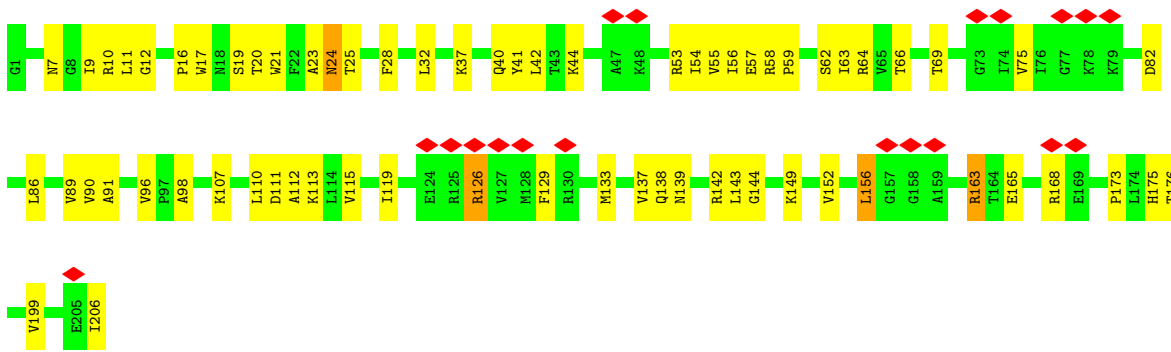


• Molecule 7: 30S ribosomal protein S2





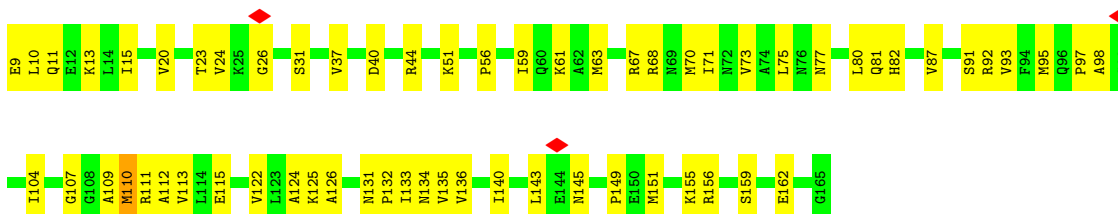
• Molecule 8: 30S ribosomal protein S3



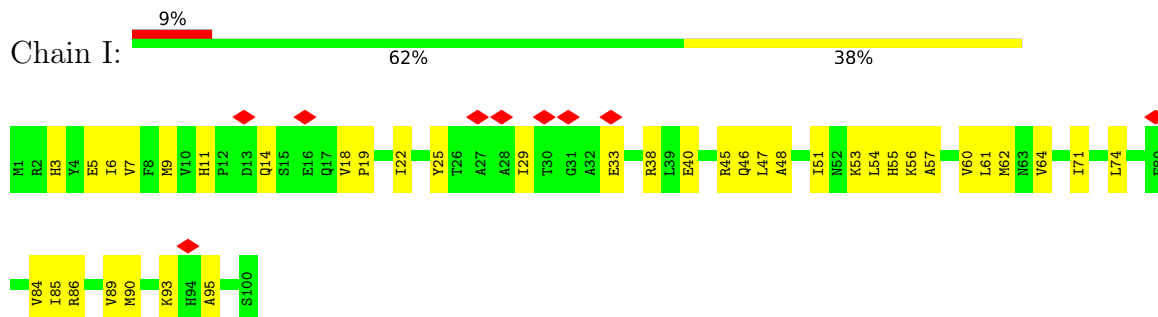
• Molecule 9: 30S ribosomal protein S4



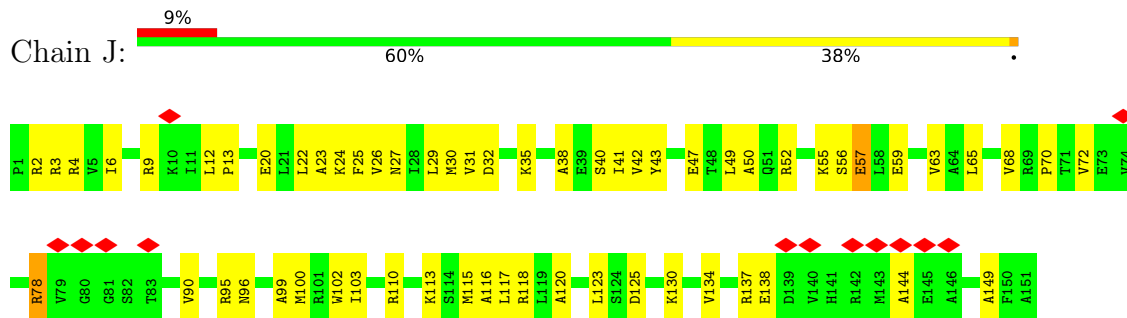
• Molecule 10: 30S ribosomal protein S5



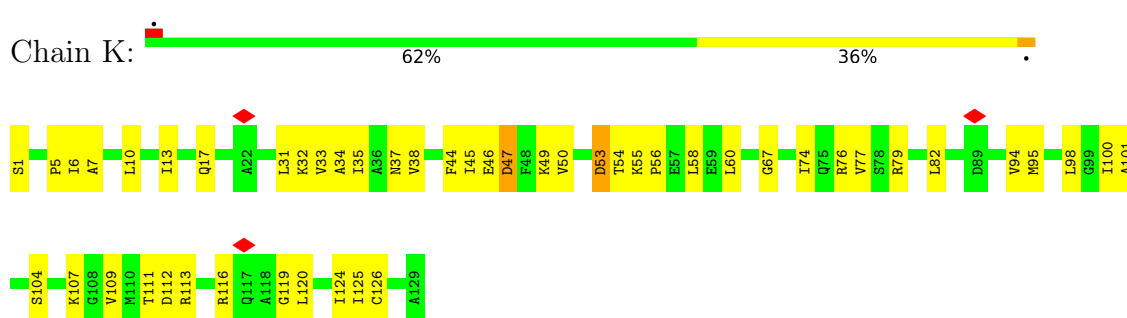
• Molecule 11: 30S ribosomal protein S6



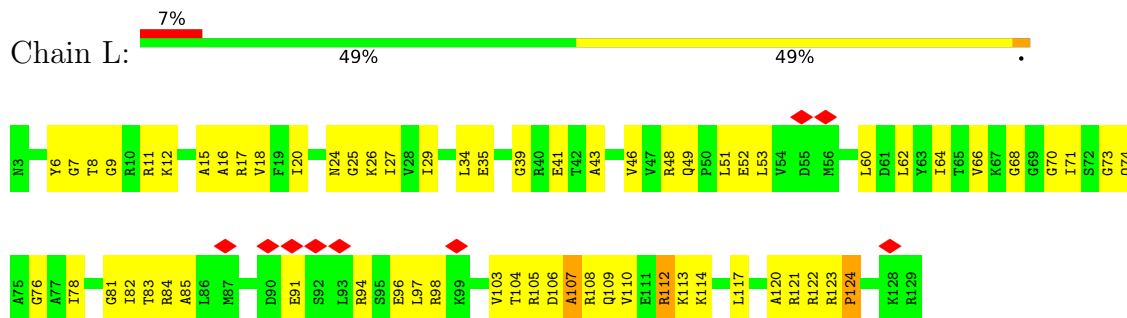
• Molecule 12: 30S ribosomal protein S7



• Molecule 13: 30S ribosomal protein S8

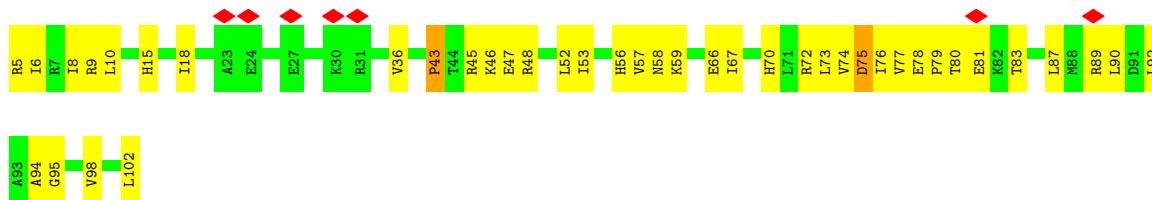


• Molecule 14: 30S ribosomal protein S9

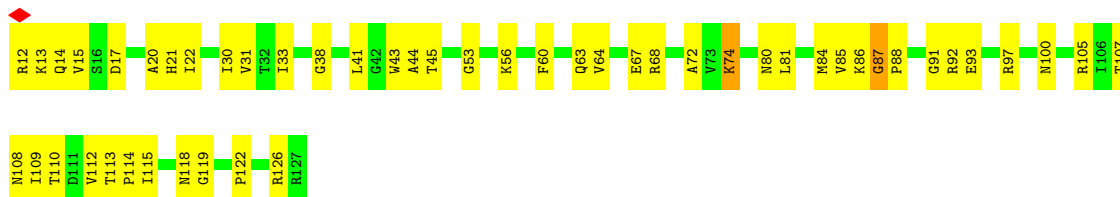


• Molecule 15: 30S ribosomal protein S10

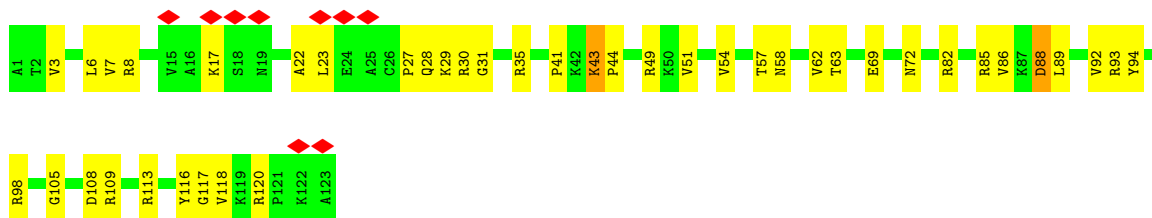




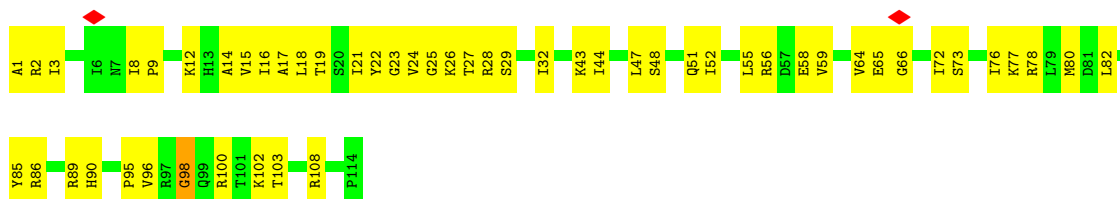
• Molecule 16: 30S ribosomal protein S11



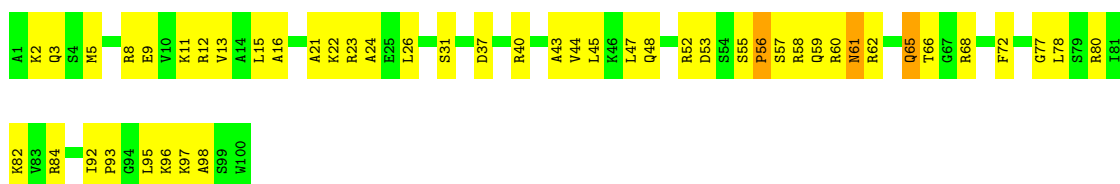
• Molecule 17: 30S ribosomal protein S12



• Molecule 18: 30S ribosomal protein S13



• Molecule 19: 30S ribosomal protein S14



- Molecule 20: 30S ribosomal protein S15

Chain R:  70% 28%



- Molecule 21: 30S ribosomal protein S16

Chain S:  5% 62% 32% 6%



- Molecule 22: 30S ribosomal protein S17

Chain T:  65% 35%



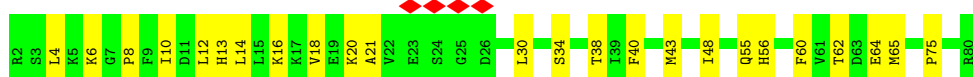
- Molecule 23: 30S ribosomal protein S18

Chain U:  8% 55% 42%



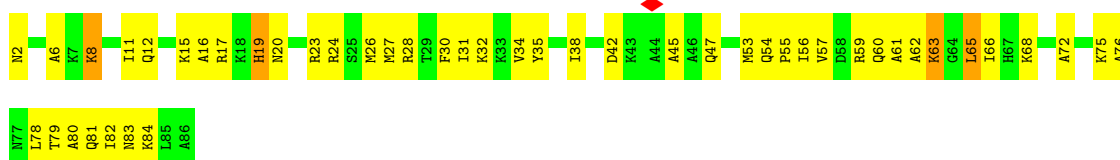
- Molecule 24: 30S ribosomal protein S19

Chain V:  5% 70% 30%

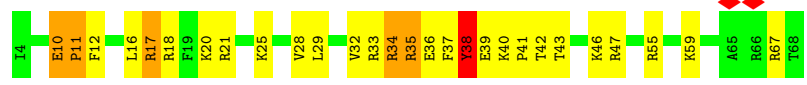


- Molecule 25: 30S ribosomal protein S20

Chain W:  45% 51% 5%



- 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	10090	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	9.739	Depositor
Minimum map value	-3.633	Depositor
Average map value	-0.011	Depositor
Map value standard deviation	0.655	Depositor
Recommended contour level	2.0	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	0.25	0/34660	0.66	0/54067
2	01	0.25	0/1774	0.62	0/2405
2	02	0.28	0/1779	0.70	0/2411
3	03	0.28	0/10433	0.67	1/14101 (0.0%)
4	04	0.28	0/10528	0.68	2/14224 (0.0%)
5	05	0.28	0/460	0.73	1/620 (0.2%)
6	B	0.43	0/65	0.60	0/86
7	E	0.36	0/1736	0.82	3/2338 (0.1%)
8	F	0.26	0/1652	0.58	0/2225
9	G	0.26	0/1665	0.59	0/2227
10	H	0.27	0/1170	0.57	0/1573
11	I	0.28	0/836	0.64	0/1128
12	J	0.27	0/1196	0.61	0/1602
13	K	0.29	0/989	0.68	1/1326 (0.1%)
14	L	0.26	0/1034	0.56	0/1375
15	M	0.27	0/797	0.61	1/1077 (0.1%)
16	N	0.28	0/886	0.62	0/1195
17	O	0.26	0/969	0.64	1/1300 (0.1%)
18	P	0.25	0/893	0.60	0/1193
19	Q	0.28	0/817	0.58	0/1088
20	R	0.26	0/722	0.58	0/964
21	S	0.30	0/659	0.60	0/884
22	T	0.27	0/658	0.60	0/881
23	U	0.31	0/545	0.70	0/731
24	V	0.29	0/653	0.60	0/877
25	W	0.29	0/671	0.58	0/888
26	X	0.39	0/551	0.65	0/728
All	All	0.27	0/78798	0.66	10/113514 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
7	E	0	1
All	All	0	4

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	E	26	LYS	N-CA-C	-9.24	86.05	111.00
4	04	339	ARG	N-CA-C	-6.41	93.70	111.00
7	E	44	GLU	N-CA-C	5.60	126.12	111.00
4	04	1296	GLY	N-CA-C	-5.41	99.57	113.10
13	K	67	GLY	N-CA-C	-5.32	99.81	113.10
3	03	516	ASP	CB-CG-OD2	5.25	123.02	118.30
15	M	45	ARG	N-CA-C	-5.23	96.89	111.00
5	05	14	GLY	N-CA-C	5.22	126.15	113.10
7	E	34	ALA	N-CA-C	-5.07	97.31	111.00
17	O	43	LYS	N-CA-C	5.07	124.68	111.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	25	C	Sidechain
1	A	872	A	Sidechain
1	A	9	G	Sidechain
7	E	22	TYR	Sidechain

5.2 Too-close contacts [\(i\)](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	30955	0	15586	432	0
2	01	1753	0	1780	96	0
2	02	1757	0	1778	95	0
3	03	10272	0	10138	477	0
4	04	10372	0	10512	614	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	05	458	0	476	31	0
6	B	774	0	201	9	0
7	E	1705	0	1732	163	0
8	F	1625	0	1699	49	0
9	G	1643	0	1710	71	0
10	H	1157	0	1199	48	0
11	I	818	0	808	36	0
12	J	1182	0	1240	48	0
13	K	979	0	1034	37	0
14	L	1022	0	1070	62	0
15	M	787	0	828	34	0
16	N	870	0	878	36	0
17	O	955	0	1019	31	0
18	P	884	0	944	51	0
19	Q	805	0	847	53	0
20	R	714	0	737	23	0
21	S	649	0	666	25	0
22	T	649	0	691	21	0
23	U	536	0	552	21	0
24	V	638	0	665	29	0
25	W	665	0	714	60	0
26	X	545	0	579	39	0
All	All	75169	0	60083	2504	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 19.

All (2504) 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:25:PRO:HB2	7:E:28:LYS:HB2	1.30	1.13
25:W:54:GLN:HA	25:W:57:VAL:HG12	1.39	1.03
7:E:23:TRP:CZ3	7:E:25:PRO:HB3	1.96	1.00
3:03:979:LEU:HD21	3:03:989:LEU:HD22	1.43	0.99
7:E:19:GLN:H	7:E:40:ILE:HA	1.27	0.98
1:A:1304:G:H21	1:A:1333:A:H62	1.08	0.97
7:E:39:HIS:O	7:E:40:ILE:HG23	1.63	0.97
7:E:87:CYS:HB2	7:E:89:GLN:HE22	1.30	0.97
25:W:38:ILE:HG21	25:W:81:GLN:HE21	1.28	0.96
4:04:705:THR:HG21	4:04:719:PHE:H	1.32	0.94
4:04:94:GLN:HB2	4:04:97:VAL:HG23	1.50	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:47:VAL:HB	7:E:48:PRO:HD3	1.49	0.94
3:03:1267:GLY:H	4:04:346:ARG:HH21	1.14	0.93
7:E:11:LYS:HB2	7:E:15:HIS:HB3	1.50	0.92
2:01:11:PRO:HA	2:01:30:PRO:HB2	1.52	0.92
4:04:327:LEU:HA	4:04:330:MET:HB2	1.49	0.92
3:03:397:LEU:HB3	3:03:401:GLY:HA3	1.51	0.92
3:03:588:GLU:HB3	3:03:605:TYR:HB3	1.52	0.91
4:04:290:ILE:H	4:04:290:ILE:HD12	1.36	0.91
4:04:845:ALA:HA	4:04:883:ARG:HG3	1.50	0.91
7:E:26:LYS:O	7:E:29:PRO:HD2	1.71	0.91
1:A:427:U:H1'	1:A:541:G:H5''	1.50	0.90
2:02:35:PHE:HA	2:02:38:THR:HG22	1.53	0.90
3:03:1058:ARG:HD2	3:03:1238:LEU:HD13	1.52	0.90
7:E:19:GLN:N	7:E:40:ILE:HA	1.88	0.89
3:03:137:VAL:HG22	3:03:142:GLU:HG3	1.55	0.88
3:03:1149:TYR:HB3	3:03:1159:VAL:HG12	1.54	0.88
1:A:961:U:H3	1:A:1201:A:H61	1.23	0.87
3:03:1082:ILE:H	3:03:1082:ILE:HD12	1.38	0.87
3:03:241:LEU:HD21	3:03:277:LEU:HD13	1.56	0.86
3:03:1320:PRO:HG2	3:03:1323:PHE:HB2	1.55	0.86
4:04:109:SER:HB2	4:04:279:LEU:HD13	1.55	0.86
3:03:149:LEU:HD11	3:03:451:ARG:HB3	1.57	0.86
2:02:83:LEU:HB3	4:04:528:THR:HB	1.58	0.86
19:Q:60:ARG:HG2	19:Q:62:ARG:HH21	1.40	0.86
18:P:3:ILE:HD13	18:P:21:ILE:HD11	1.58	0.85
7:E:90:PHE:HB3	7:E:151:ILE:HA	1.58	0.85
4:04:909:ILE:HD11	4:04:913:GLU:HG2	1.59	0.85
1:A:363:A:H5'	17:O:30:ARG:HB2	1.57	0.84
3:03:502:VAL:HG13	3:03:503:LYS:HD2	1.59	0.84
14:L:24:ASN:HB3	14:L:26:LYS:HE2	1.59	0.83
1:A:1259:C:H3'	1:A:1260:G:H5''	1.61	0.83
3:03:673:HIS:HA	4:04:763:PHE:O	1.78	0.83
10:H:133:ILE:HD12	10:H:133:ILE:H	1.41	0.83
10:H:24:VAL:HG23	10:H:26:GLY:H	1.44	0.83
3:03:420:LEU:HB3	3:03:425:ILE:HD11	1.62	0.82
3:03:1255:THR:HG22	3:03:1256:GLN:H	1.42	0.82
4:04:20:ILE:O	4:04:1343:GLU:HA	1.80	0.82
25:W:8:LYS:NZ	25:W:8:LYS:HB3	1.93	0.81
3:03:237:LEU:HD12	3:03:289:VAL:HA	1.63	0.81
1:A:1230:C:H41	18:P:103:THR:HG21	1.46	0.80
4:04:1366:HIS:HA	4:04:1369:ARG:HB2	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:24:LYS:HA	12:J:27:ASN:HD22	1.44	0.80
4:04:1191:PRO:HB2	4:04:1194:ARG:HD3	1.64	0.80
1:A:92:U:H2'	1:A:93:U:H4'	1.63	0.80
4:04:272:VAL:HG22	4:04:302:ALA:HB1	1.64	0.80
17:O:43:LYS:HG3	17:O:44:PRO:HD3	1.63	0.80
24:V:62:THR:H	24:V:65:MET:HE3	1.46	0.80
3:03:519:ASN:ND2	3:03:521:LEU:HB3	1.97	0.79
1:A:1329:A:H5''	18:P:25:GLY:H	1.47	0.79
3:03:190:PRO:HG3	3:03:436:ARG:HH21	1.45	0.79
3:03:723:VAL:HG22	3:03:776:PRO:HG3	1.65	0.79
4:04:19:ALA:HB1	4:04:1343:GLU:HB3	1.63	0.79
3:03:74:ARG:HB2	3:03:99:LYS:HE3	1.65	0.78
2:02:65:LEU:HB3	2:02:169:GLY:HA2	1.66	0.78
3:03:1258:PRO:HB3	4:04:346:ARG:HH11	1.49	0.78
4:04:337:ARG:H	4:04:337:ARG:HD2	1.48	0.78
4:04:844:THR:HG23	4:04:864:LEU:HD11	1.64	0.78
2:01:180:VAL:HB	2:01:183:ILE:HD11	1.65	0.78
9:G:129:VAL:HG12	9:G:131:ILE:H	1.49	0.78
2:01:100:LEU:HD21	2:01:121:VAL:HG11	1.66	0.78
2:02:166:ARG:HB2	2:02:167:PRO:HD3	1.63	0.78
1:A:1103:C:H4'	7:E:97:LEU:HD22	1.65	0.77
2:02:193:GLU:HB3	4:04:406:ALA:HB1	1.66	0.77
4:04:1242:ARG:HH12	4:04:1247:LYS:HG2	1.49	0.77
7:E:33:GLY:HA2	7:E:41:ILE:O	1.84	0.77
7:E:54:LEU:HD22	7:E:220:THR:HG21	1.63	0.77
18:P:16:ILE:HD12	18:P:16:ILE:H	1.48	0.77
18:P:72:ILE:O	18:P:76:ILE:HG13	1.83	0.77
2:01:207:THR:HG22	2:01:209:GLY:H	1.48	0.77
4:04:1327:GLU:HB3	4:04:1330:ARG:HG3	1.67	0.77
4:04:849:LEU:HD23	4:04:849:LEU:H	1.49	0.77
3:03:241:LEU:HD11	3:03:246:LEU:HD11	1.64	0.77
3:03:729:ALA:HA	3:03:769:PRO:HG2	1.67	0.77
4:04:958:ILE:HD12	4:04:982:LEU:HD11	1.65	0.77
2:01:29:GLU:HB3	2:01:30:PRO:HD3	1.67	0.77
3:03:1109:ILE:HG21	4:04:764:ARG:HA	1.66	0.77
7:E:166:ALA:HB3	7:E:191:SER:HB3	1.67	0.77
10:H:80:LEU:HG	10:H:81:GLN:H	1.49	0.77
14:L:114:LYS:HB2	14:L:117:LEU:HD12	1.67	0.77
1:A:419:C:H5'	1:A:513:C:H4'	1.67	0.76
3:03:592:ARG:HG3	3:03:655:VAL:HG22	1.66	0.76
3:03:1063:GLY:H	3:03:1076:ILE:HG23	1.50	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:526:VAL:HG12	4:04:549:LYS:HB2	1.67	0.76
14:L:18:VAL:HG21	14:L:81:GLY:HA3	1.68	0.76
14:L:83:THR:HG21	14:L:103:VAL:HG22	1.67	0.76
2:02:89:ALA:HB1	2:02:210:THR:HG23	1.67	0.76
1:A:244:U:H4'	1:A:245:U:H5'	1.67	0.76
5:05:4:VAL:HG13	5:05:5:THR:HG23	1.68	0.76
1:A:1250:A:H4'	14:L:68:GLY:HA2	1.66	0.76
1:A:426:U:H1'	9:G:39:GLN:HE21	1.48	0.76
3:03:1335:ILE:HA	4:04:24:LEU:HD13	1.68	0.76
3:03:82:VAL:HG13	3:03:137:VAL:HG21	1.67	0.76
6:B:109:UNK:HA	6:B:153:UNK:HA	1.65	0.75
3:03:207:THR:HG21	3:03:351:LEU:HD23	1.69	0.75
3:03:732:ILE:HG13	3:03:753:LEU:HD11	1.69	0.75
9:G:84:ASN:HD22	9:G:87:GLU:HG3	1.51	0.75
7:E:21:ARG:O	7:E:23:TRP:HD1	1.70	0.75
1:A:614:C:H2'	1:A:615:G:H5''	1.68	0.75
1:A:1158:C:H4'	7:E:132:LYS:HD3	1.69	0.75
3:03:448:LEU:HB2	3:03:608:ALA:HB3	1.68	0.75
7:E:23:TRP:HE3	7:E:189:THR:HB	1.52	0.75
2:02:164:ASP:HB2	2:02:170:ARG:HB2	1.68	0.74
1:A:161:A:H61	1:A:347:G:H21	1.35	0.74
3:03:209:ILE:HA	3:03:212:ALA:HB3	1.69	0.74
4:04:1173:ARG:HH21	4:04:1196:LEU:HD23	1.51	0.74
9:G:7:LYS:HE3	9:G:20:LEU:HD22	1.68	0.74
1:A:1322:C:H5''	18:P:98:GLY:HA3	1.69	0.74
8:F:9:ILE:HG13	19:Q:97:LYS:HD3	1.68	0.74
3:03:1320:PRO:O	3:03:1322:SER:N	2.19	0.74
21:S:54:LEU:HD23	21:S:57:ILE:HD12	1.67	0.74
3:03:406:ASN:HB3	3:03:411:ARG:HB2	1.70	0.74
4:04:814:CYS:HB2	4:04:889:ASP:HB3	1.67	0.74
20:R:28:VAL:HG22	20:R:65:LEU:HD23	1.69	0.74
1:A:396:C:O2'	1:A:397:A:H5'	1.86	0.74
4:04:393:THR:HG23	4:04:396:ALA:H	1.51	0.74
3:03:364:VAL:HG13	3:03:376:PRO:HG3	1.70	0.74
4:04:555:TYR:HB3	4:04:563:LEU:HB3	1.68	0.74
4:04:1314:LEU:HD12	4:04:1326:GLN:HE21	1.53	0.74
4:04:925:GLU:HB3	4:04:926:PRO:HD3	1.68	0.74
21:S:52:LEU:HD13	21:S:75:ILE:HD13	1.70	0.74
11:I:6:ILE:HG12	11:I:89:VAL:HG12	1.69	0.73
25:W:42:ASP:HB3	25:W:45:ALA:HB3	1.69	0.73
2:02:190:ALA:HB2	2:02:200:LYS:HB2	1.68	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:30:ILE:H	3:03:30:ILE:HD12	1.51	0.73
4:04:80:HIS:HB3	4:04:92:VAL:HG21	1.70	0.73
4:04:154:LEU:HD21	4:04:160:LEU:HD21	1.71	0.73
4:04:342:LEU:O	4:04:343:LEU:HB2	1.88	0.73
11:I:29:ILE:HG21	11:I:64:VAL:HG21	1.70	0.73
2:01:32:GLU:HB2	2:01:35:PHE:HD2	1.52	0.73
2:02:23:HIS:HB3	2:02:206:GLU:HG2	1.70	0.73
4:04:485:MET:HB3	4:04:488:ASN:HD22	1.52	0.73
15:M:57:VAL:HG22	15:M:58:ASN:H	1.53	0.73
8:F:163:ARG:H	8:F:163:ARG:HD3	1.53	0.73
3:03:434:ASP:HA	3:03:437:ASN:HD22	1.53	0.73
4:04:344:GLY:O	4:04:345:LYS:CB	2.37	0.73
8:F:59:PRO:HB3	15:M:94:ALA:HA	1.71	0.73
2:02:56:VAL:HG21	2:02:144:ILE:HD11	1.69	0.73
3:03:1169:VAL:HA	3:03:1172:LEU:HB2	1.70	0.73
1:A:1202:U:H4'	19:Q:68:ARG:HD2	1.69	0.72
4:04:120:LEU:HB3	4:04:121:PRO:HD3	1.71	0.72
7:E:89:GLN:NE2	7:E:89:GLN:H	1.86	0.72
4:04:327:LEU:CA	4:04:330:MET:HB2	2.19	0.72
13:K:35:ILE:HG12	13:K:109:VAL:HG11	1.71	0.72
1:A:1252:A:H61	1:A:1285:A:H61	1.35	0.72
4:04:490:ILE:HD12	4:04:491:LEU:HG	1.71	0.72
1:A:1502:A:H8	1:A:1505:G:H22	1.38	0.72
3:03:1331:ARG:HG2	4:04:243:PRO:HG2	1.71	0.72
4:04:1190:ILE:HG21	4:04:1196:LEU:HD11	1.71	0.72
4:04:1320:ILE:HB	4:04:1349:GLU:HG3	1.72	0.72
1:A:414:A:H62	1:A:430:A:H61	1.37	0.72
4:04:116:PHE:HE1	4:04:1333:THR:HA	1.53	0.72
4:04:749:LYS:HD3	4:04:753:SER:HB2	1.69	0.72
25:W:59:ARG:O	25:W:63:LYS:HB2	1.90	0.72
4:04:108:ALA:HB1	4:04:283:LEU:HD11	1.70	0.71
8:F:107:LYS:HD2	8:F:110:LEU:HD22	1.72	0.71
19:Q:8:ARG:HB3	19:Q:12:ARG:HH12	1.54	0.71
2:02:33:ARG:H	2:02:33:ARG:HD3	1.55	0.71
3:03:1099:ASN:HD21	3:03:1101:LEU:HB2	1.55	0.71
3:03:1101:LEU:HD21	4:04:508:LEU:HD22	1.72	0.71
4:04:107:LEU:HD23	4:04:276:ASN:ND2	2.06	0.71
4:04:425:ARG:HG2	4:04:427:PRO:HD2	1.73	0.71
18:P:90:HIS:HA	18:P:108:ARG:HH22	1.55	0.71
3:03:810:TYR:HB3	3:03:817:LEU:HD23	1.72	0.71
4:04:114:ILE:HG13	4:04:118:LYS:HE2	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:U:H3	1:A:171:A:H62	1.39	0.70
1:A:1158:C:H2'	1:A:1159:U:H4'	1.71	0.70
4:04:1344:LEU:HD12	4:04:1349:GLU:HB3	1.73	0.70
3:03:39:ILE:HD11	3:03:75:LEU:HD21	1.73	0.70
3:03:102:LEU:HD22	3:03:489:PRO:HD3	1.72	0.70
3:03:479:LEU:HD23	3:03:487:LEU:HD13	1.73	0.70
4:04:963:VAL:HG21	4:04:975:ILE:HG23	1.73	0.70
9:G:33:ILE:HG13	9:G:34:GLU:HG3	1.72	0.70
3:03:697:LYS:H	3:03:697:LYS:HD3	1.57	0.70
21:S:23:ASP:HB2	21:S:26:ASN:ND2	2.06	0.70
4:04:534:GLU:HG3	4:04:538:ARG:HD3	1.74	0.70
7:E:23:TRP:HA	7:E:190:ASN:HB3	1.73	0.70
4:04:246:PRO:HD2	4:04:249:LEU:HD12	1.72	0.70
14:L:60:LEU:O	14:L:60:LEU:HD12	1.92	0.70
1:A:831:A:H3'	1:A:832:G:H5''	1.73	0.70
7:E:43:LEU:O	7:E:46:THR:HB	1.91	0.70
15:M:102:LEU:HD23	15:M:102:LEU:H	1.55	0.70
4:04:504:GLN:HE22	4:04:731:ARG:HD2	1.56	0.69
4:04:504:GLN:HA	4:04:507:VAL:HG22	1.74	0.69
7:E:76:ALA:O	7:E:80:VAL:HG23	1.92	0.69
3:03:548:ARG:HD3	3:03:569:ILE:HG13	1.74	0.69
4:04:123:ARG:HD2	4:04:1337:VAL:HG21	1.74	0.69
1:A:188:C:H5	25:W:83:ASN:HD22	1.40	0.69
2:02:54:CYS:HB2	2:02:91:ARG:HA	1.74	0.69
5:05:58:LEU:HG	5:05:59:ILE:HG12	1.74	0.69
9:G:70:GLN:HA	9:G:73:ASN:HD22	1.55	0.69
1:A:59:A:H3'	1:A:60:A:H5'	1.73	0.69
1:A:770:C:H1'	1:A:900:A:H2	1.57	0.69
2:02:56:VAL:HG22	2:02:146:VAL:HG22	1.73	0.69
10:H:44:ARG:HE	10:H:70:MET:HB3	1.57	0.69
4:04:456:ALA:HB2	4:04:500:ILE:HD11	1.75	0.69
4:04:472:LEU:HD23	4:04:472:LEU:H	1.56	0.69
23:U:55:LEU:O	23:U:59:ILE:HG13	1.93	0.69
1:A:410:G:H21	1:A:432:A:H62	1.39	0.69
3:03:678:ARG:NH2	3:03:1106:ARG:HG2	2.07	0.69
1:A:1219:A:H5''	19:Q:52:ARG:HG2	1.75	0.68
3:03:263:VAL:HG11	3:03:269:ILE:HG12	1.74	0.68
4:04:903:LEU:HG	4:04:904:ALA:H	1.56	0.68
7:E:26:LYS:O	7:E:29:PRO:CD	2.41	0.68
13:K:33:VAL:HG22	13:K:58:LEU:HD13	1.75	0.68
1:A:1148:U:H1'	14:L:17:ARG:HD3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:02:80:GLU:HB3	4:04:551:ARG:HH21	1.58	0.68
9:G:113:ALA:O	9:G:117:VAL:HG23	1.93	0.68
1:A:321:A:H61	1:A:332:G:H1	1.40	0.68
3:03:174:ALA:O	3:03:186:PHE:HB2	1.94	0.68
2:02:118:ASP:H	2:02:121:VAL:HB	1.59	0.68
4:04:260:PHE:HB3	4:04:262:THR:HG22	1.76	0.68
7:E:21:ARG:O	7:E:23:TRP:CD1	2.47	0.68
17:O:29:LYS:HG3	17:O:30:ARG:H	1.59	0.68
1:A:12:U:H2'	1:A:13:U:H5''	1.76	0.68
1:A:142:G:H1'	1:A:195:A:H61	1.57	0.68
4:04:1067:ARG:HH12	4:04:1076:PRO:HD3	1.58	0.68
7:E:23:TRP:CD2	7:E:25:PRO:HD3	2.29	0.68
10:H:104:ILE:HG13	10:H:122:VAL:HG23	1.74	0.68
12:J:40:SER:HA	12:J:43:TYR:HD2	1.57	0.68
18:P:16:ILE:HD12	18:P:16:ILE:N	2.08	0.68
1:A:410:G:H2'	1:A:429:U:C5	2.30	0.67
1:A:981:U:H3'	1:A:982:U:H5''	1.75	0.67
3:03:673:HIS:CA	4:04:763:PHE:O	2.42	0.67
4:04:527:LEU:HD13	4:04:548:VAL:HG11	1.75	0.67
7:E:21:ARG:HD3	7:E:22:TYR:N	2.08	0.67
12:J:103:ILE:HD13	12:J:123:LEU:HD13	1.75	0.67
3:03:1082:ILE:HD12	3:03:1082:ILE:N	2.08	0.67
20:R:84:LEU:HD23	20:R:86:LEU:HD23	1.76	0.67
2:01:16:ILE:HG23	2:01:26:VAL:HA	1.77	0.67
4:04:826:ILE:HA	4:04:831:VAL:HA	1.76	0.67
2:01:228:LEU:HD21	2:02:224:LEU:HD22	1.75	0.67
3:03:799:ASN:HB3	3:03:1231:TYR:HD1	1.58	0.67
18:P:64:VAL:HG23	18:P:66:GLY:H	1.59	0.67
3:03:851:THR:H	3:03:887:VAL:HG23	1.60	0.67
13:K:77:VAL:HG23	13:K:126:CYS:HA	1.75	0.67
17:O:51:VAL:HG11	17:O:89:LEU:HD22	1.76	0.67
24:V:14:LEU:O	24:V:18:VAL:HG23	1.94	0.67
4:04:364:HIS:HB3	5:05:4:VAL:HG23	1.75	0.67
1:A:81:A:H2'	1:A:82:G:H4'	1.77	0.67
1:A:1053:G:H4'	1:A:1054:C:H3'	1.75	0.67
3:03:1292:THR:O	3:03:1296:ASP:HB3	1.95	0.67
4:04:328:ALA:C	4:04:330:MET:H	1.97	0.67
3:03:1336:ASN:HB3	4:04:25:ALA:HB3	1.77	0.67
4:04:395:LYS:HA	4:04:398:LYS:HE2	1.76	0.67
1:A:105:G:N2	1:A:379:C:H4'	2.09	0.66
3:03:159:SER:HB2	3:03:442:VAL:HG21	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:1335:ILE:N	3:03:1335:ILE:HD12	2.10	0.66
7:E:31:ILE:HB	7:E:42:ASN:HA	1.76	0.66
26:X:40:LYS:HB3	26:X:41:PRO:HD3	1.77	0.66
1:A:186:C:H5'	25:W:72:ALA:HA	1.76	0.66
2:01:184:ALA:HB2	3:03:1091:GLY:HA3	1.77	0.66
12:J:49:LEU:HD22	12:J:123:LEU:HB3	1.76	0.66
25:W:31:ILE:HG12	25:W:53:MET:HE3	1.77	0.66
4:04:97:VAL:HG12	4:04:101:ARG:HH12	1.59	0.66
1:A:1236:A:H4'	1:A:1304:G:H4'	1.77	0.66
3:03:433:ILE:HG22	3:03:437:ASN:HD21	1.60	0.66
3:03:1103:VAL:HB	3:03:1104:PRO:HD3	1.76	0.66
20:R:28:VAL:HG11	20:R:66:LEU:HD21	1.77	0.66
1:A:194:C:H4'	25:W:59:ARG:HG3	1.77	0.66
1:A:831:A:C3'	1:A:832:G:H5''	2.26	0.66
1:A:1226:C:N4	18:P:102:LYS:HE2	2.11	0.66
3:03:966:ILE:H	3:03:966:ILE:HD12	1.61	0.66
13:K:94:VAL:HG12	13:K:95:MET:HG3	1.78	0.66
14:L:18:VAL:HA	14:L:64:ILE:HG12	1.76	0.66
16:N:88:PRO:HA	16:N:92:ARG:HH11	1.59	0.66
26:X:28:VAL:O	26:X:32:VAL:HG22	1.96	0.66
3:03:228:VAL:HG22	3:03:245:ARG:HH11	1.59	0.66
3:03:1319:MET:HG3	3:03:1323:PHE:HD2	1.61	0.66
4:04:1179:PRO:HD2	4:04:1184:ASP:HA	1.77	0.66
4:04:1252:HIS:O	4:04:1255:VAL:HG22	1.95	0.66
3:03:616:ILE:HD12	3:03:616:ILE:N	2.10	0.66
4:04:609:TYR:HE1	4:04:614:LEU:HB2	1.59	0.66
14:L:94:ARG:O	14:L:98:ARG:HG3	1.96	0.66
1:A:440:C:H2'	1:A:441:A:H5''	1.77	0.66
16:N:53:GLY:H	16:N:56:LYS:HG3	1.61	0.66
3:03:498:ILE:H	3:03:498:ILE:HD12	1.61	0.65
12:J:78:ARG:H	12:J:78:ARG:HD2	1.59	0.65
9:G:88:ASN:O	9:G:92:LEU:HD13	1.97	0.65
14:L:27:ILE:HG21	14:L:34:LEU:HD12	1.78	0.65
1:A:718:A:H5'	16:N:118:ASN:HB2	1.78	0.65
2:01:195:ARG:HG2	2:01:198:LEU:HG	1.78	0.65
3:03:204:LEU:HD21	3:03:369:MET:HG3	1.78	0.65
1:A:1280:A:O2'	1:A:1281:C:H5'	1.96	0.65
5:05:58:LEU:HD23	5:05:58:LEU:H	1.62	0.65
8:F:69:THR:HG21	8:F:75:VAL:HG21	1.79	0.65
25:W:27:MET:O	25:W:31:ILE:HG13	1.96	0.65
1:A:65:A:H4'	1:A:66:A:H5'	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:761:GLN:HE22	3:03:1236:ASN:ND2	1.95	0.65
3:03:1141:LEU:HD12	3:03:1142:ARG:N	2.11	0.65
4:04:926:PRO:HG2	4:04:1248:ILE:HD11	1.79	0.65
9:G:90:LEU:HD23	9:G:93:LEU:HD12	1.78	0.65
1:A:1393:U:H2'	1:A:1395:C:H5	1.61	0.65
9:G:121:ALA:HB1	9:G:148:ALA:HB2	1.77	0.65
1:A:981:U:H4'	19:Q:62:ARG:HH22	1.61	0.65
3:03:817:LEU:HB3	3:03:1097:VAL:HB	1.79	0.65
10:H:73:VAL:HG21	10:H:143:LEU:HB3	1.77	0.65
24:V:4:LEU:HD23	24:V:4:LEU:H	1.61	0.65
1:A:25:C:H41	1:A:558:G:N2	1.95	0.65
4:04:377:PHE:O	4:04:381:ILE:HG13	1.97	0.65
1:A:252:U:O2	1:A:252:U:H2'	1.97	0.64
4:04:1041:ILE:HD12	4:04:1041:ILE:N	2.12	0.64
1:A:1285:A:H4'	1:A:1286:U:H5''	1.77	0.64
1:A:1526:G:OP2	26:X:39:GLU:HB2	1.97	0.64
3:03:54:ARG:NH1	3:03:54:ARG:HB2	2.13	0.64
4:04:86:GLU:HG3	7:E:74:ARG:HG3	1.79	0.64
4:04:506:VAL:HG23	4:04:628:GLY:HA3	1.78	0.64
1:A:179:A:H61	1:A:196:A:H62	1.45	0.64
14:L:109:GLN:HG2	14:L:110:VAL:H	1.62	0.64
1:A:885:G:H2'	1:A:886:G:C8	2.33	0.64
2:02:30:PRO:C	2:02:31:LEU:HD22	2.18	0.64
4:04:1029:THR:HG23	4:04:1121:LEU:HD11	1.79	0.64
7:E:18:HIS:HA	7:E:40:ILE:HG22	1.80	0.64
11:I:47:LEU:HD12	11:I:55:HIS:HA	1.80	0.64
3:03:54:ARG:HB2	3:03:54:ARG:HH11	1.63	0.64
12:J:29:LEU:HD23	12:J:42:VAL:HG22	1.78	0.64
1:A:614:C:C2'	1:A:615:G:H5''	2.28	0.64
4:04:811:GLU:HA	4:04:911:LYS:HE2	1.78	0.64
3:03:205:PRO:HD2	3:03:208:ILE:HB	1.80	0.64
6:B:218:UNK:HA	6:B:257:UNK:O	1.98	0.64
1:A:245:U:H3	1:A:283:U:H3	1.45	0.64
13:K:79:ARG:HG3	13:K:82:LEU:H	1.61	0.64
2:01:166:ARG:N	2:01:167:PRO:HD2	2.12	0.63
17:O:28:GLN:HE22	17:O:82:ARG:HG3	1.62	0.63
19:Q:2:LYS:HE2	19:Q:5:MET:HB2	1.80	0.63
19:Q:9:GLU:O	19:Q:13:VAL:HG23	1.97	0.63
4:04:814:CYS:SG	4:04:816:THR:HG22	2.39	0.63
7:E:41:ILE:HG22	7:E:43:LEU:H	1.62	0.63
9:G:190:LEU:HD12	9:G:192:ALA:H	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:55:SER:HA	19:Q:57:SER:H	1.61	0.63
24:V:40:PHE:H	24:V:43:MET:CE	2.12	0.63
1:A:1306:A:H61	1:A:1331:G:H1'	1.63	0.63
4:04:582:ILE:HD13	4:04:627:THR:HG21	1.81	0.63
4:04:678:ARG:O	4:04:682:VAL:HG23	1.99	0.63
4:04:812:ASP:HA	4:04:896:ALA:H	1.62	0.63
1:A:292:G:H21	1:A:608:A:H61	1.46	0.63
2:02:80:GLU:HB3	4:04:551:ARG:NH2	2.13	0.63
3:03:384:LEU:O	3:03:388:LEU:HG	1.97	0.63
4:04:112:ALA:HB2	4:04:182:ALA:HB2	1.81	0.63
4:04:195:GLU:HA	4:04:198:CYS:HB2	1.81	0.63
1:A:522:C:H5''	17:O:109:ARG:HH22	1.62	0.63
4:04:483:LEU:HD23	4:04:483:LEU:H	1.64	0.63
2:01:183:ILE:HD12	2:01:183:ILE:N	2.14	0.63
3:03:104:ILE:HD12	3:03:104:ILE:N	2.13	0.63
3:03:397:LEU:O	3:03:398:SER:O	2.17	0.63
7:E:13:GLY:O	7:E:14:VAL:HG13	1.99	0.63
16:N:87:GLY:H	16:N:114:PRO:HD2	1.62	0.63
1:A:405:U:H1'	1:A:498:A:H2'	1.80	0.63
1:A:884:U:H4'	1:A:885:G:H5''	1.81	0.63
2:01:45:ARG:HB2	2:02:38:THR:HB	1.81	0.63
4:04:520:ALA:HB3	4:04:523:GLU:HB2	1.81	0.63
4:04:600:ALA:HA	4:04:603:LYS:NZ	2.14	0.63
4:04:812:ASP:OD2	4:04:911:LYS:HE3	1.98	0.63
16:N:107:THR:HG23	16:N:108:ASN:OD1	1.99	0.63
17:O:98:ARG:HB3	17:O:105:GLY:HA2	1.81	0.63
3:03:80:PHE:HB2	3:03:85:CYS:SG	2.39	0.63
3:03:670:PHE:HB3	3:03:673:HIS:HD2	1.63	0.63
7:E:35:ARG:HD3	7:E:35:ARG:H	1.64	0.63
7:E:36:ASN:HB2	7:E:40:ILE:HD13	1.81	0.63
1:A:501:C:H2'	1:A:502:A:H8	1.64	0.62
3:03:836:LEU:HD13	3:03:1054:LEU:HD13	1.81	0.62
21:S:61:VAL:HA	21:S:65:ALA:HB3	1.80	0.62
1:A:523:A:H61	17:O:49:ARG:NH2	1.96	0.62
1:A:1297:G:H21	12:J:113:LYS:HB3	1.64	0.62
2:01:14:VAL:HG22	2:01:15:ASP:H	1.64	0.62
3:03:672:GLU:HB2	4:04:766:GLY:HA2	1.80	0.62
18:P:28:ARG:O	18:P:32:ILE:HG12	1.99	0.62
4:04:579:LEU:HD12	4:04:582:ILE:HD12	1.81	0.62
9:G:13:ARG:NH1	9:G:37:PRO:HB2	2.13	0.62
25:W:24:ARG:HB3	25:W:28:ARG:HH22	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:X:43:THR:HA	26:X:46:LYS:NZ	2.14	0.62
3:03:1272:GLU:HA	3:03:1275:VAL:HG23	1.80	0.62
5:05:25:ARG:HG2	5:05:28:ARG:HH21	1.65	0.62
21:S:5:ARG:HD3	21:S:5:ARG:H	1.65	0.62
1:A:501:C:H2'	1:A:502:A:C8	2.34	0.62
1:A:1224:U:H4'	18:P:100:ARG:HH12	1.64	0.62
3:03:979:LEU:HD13	3:03:985:GLU:HB2	1.81	0.62
18:P:19:THR:HA	18:P:25:GLY:HA2	1.81	0.62
1:A:59:A:H1'	1:A:354:G:N2	2.15	0.62
1:A:426:U:H1'	9:G:39:GLN:NE2	2.14	0.62
1:A:883:C:O2'	1:A:884:U:H5'	2.00	0.62
2:02:47:LEU:HD22	2:02:180:VAL:HG11	1.82	0.62
3:03:401:GLY:O	3:03:405:PHE:HB2	1.98	0.62
4:04:81:ARG:HB2	7:E:206:ALA:HB1	1.81	0.62
4:04:527:LEU:HB2	4:04:550:VAL:HG12	1.81	0.62
4:04:552:ILE:HD12	4:04:552:ILE:O	2.00	0.62
14:L:51:LEU:HD21	14:L:82:ILE:HG21	1.82	0.62
25:W:68:LYS:HB2	25:W:68:LYS:NZ	2.15	0.62
1:A:552:U:H2'	1:A:553:A:H8	1.64	0.62
12:J:68:VAL:HG23	12:J:99:ALA:HB1	1.81	0.62
1:A:151:A:H62	1:A:170:U:H3	1.46	0.62
1:A:437:U:O2'	1:A:438:U:H5'	1.99	0.62
2:02:41:ASN:HA	2:02:44:ARG:HG2	1.82	0.62
3:03:499:SER:HA	3:03:503:LYS:HD3	1.82	0.62
3:03:657:THR:HG23	3:03:658:GLN:HG3	1.81	0.62
16:N:92:ARG:HH21	26:X:20:LYS:HD3	1.64	0.62
2:02:172:LEU:HD23	2:02:172:LEU:H	1.64	0.62
2:01:48:LEU:HD21	2:01:183:ILE:HD13	1.82	0.61
3:03:557:ARG:HG2	3:03:558:VAL:HG23	1.82	0.61
3:03:886:LYS:HB3	3:03:917:SER:HA	1.82	0.61
19:Q:68:ARG:HH22	19:Q:80:ARG:HH21	1.48	0.61
1:A:614:C:C3'	1:A:615:G:H5''	2.30	0.61
9:G:94:GLU:HG2	9:G:185:PRO:HG3	1.82	0.61
13:K:34:ALA:O	13:K:38:VAL:HG23	2.00	0.61
14:L:105:ARG:O	14:L:105:ARG:HD3	1.99	0.61
19:Q:65:GLN:HE21	19:Q:82:LYS:HE2	1.66	0.61
3:03:1010:GLN:O	3:03:1014:LEU:HD13	2.00	0.61
4:04:64:PRO:HG2	4:04:93:THR:H	1.65	0.61
16:N:86:LYS:HB3	16:N:114:PRO:HD3	1.82	0.61
4:04:311:ARG:HH21	4:04:1329:THR:HB	1.64	0.61
4:04:1167:LYS:HE3	4:04:1174:ARG:HG3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:185:TYR:HB2	2:01:201:LEU:HD11	1.81	0.61
4:04:97:VAL:HG12	4:04:101:ARG:NH1	2.14	0.61
3:03:815:SER:OG	3:03:1077:SER:HB3	2.01	0.61
3:03:884:VAL:HG11	3:03:1050:VAL:HG11	1.83	0.61
5:05:7:GLN:O	5:05:11:GLU:HG2	2.01	0.61
1:A:216:U:H4'	1:A:464:U:H4'	1.82	0.61
2:02:59:VAL:HG21	2:02:85:LEU:HD13	1.82	0.61
3:03:838:CYS:HB3	3:03:1050:VAL:HB	1.82	0.61
9:G:100:VAL:O	9:G:104:MET:HG2	1.99	0.61
4:04:903:LEU:HB3	4:04:905:ARG:HG2	1.81	0.61
4:04:1137:GLY:O	4:04:1141:VAL:HG23	2.01	0.61
7:E:23:TRP:CE2	7:E:25:PRO:HD3	2.36	0.61
1:A:326:G:H2'	1:A:327:A:H5'	1.82	0.61
3:03:498:ILE:HD12	3:03:498:ILE:N	2.15	0.61
4:04:66:LYS:NZ	4:04:78:LEU:HD11	2.16	0.60
4:04:1159:ILE:HG21	4:04:1179:PRO:HG3	1.83	0.60
9:G:117:VAL:O	9:G:130:ASN:HA	2.01	0.60
13:K:45:ILE:HD11	13:K:60:LEU:HB3	1.83	0.60
22:T:35:LYS:NZ	22:T:35:LYS:HB3	2.15	0.60
1:A:516:U:H5	1:A:533:A:H62	1.47	0.60
2:01:32:GLU:HB2	2:01:35:PHE:CD2	2.35	0.60
3:03:26:TYR:HE2	3:03:32:LEU:HD13	1.66	0.60
3:03:623:LEU:HD12	3:03:623:LEU:O	2.01	0.60
4:04:117:LEU:HD22	4:04:139:LEU:HD12	1.82	0.60
4:04:583:VAL:HG21	4:04:592:VAL:HG11	1.83	0.60
25:W:26:MET:HG2	25:W:56:ILE:HG12	1.83	0.60
1:A:1343:G:H4'	14:L:123:ARG:HB3	1.83	0.60
9:G:36:ALA:HB1	9:G:38:GLY:O	2.01	0.60
18:P:15:VAL:HB	18:P:16:ILE:HD12	1.82	0.60
2:01:89:ALA:HB1	2:01:208:ASN:HD22	1.64	0.60
14:L:20:ILE:HG21	14:L:60:LEU:HD22	1.82	0.60
15:M:6:ILE:HD11	15:M:79:PRO:HB3	1.83	0.60
18:P:77:LYS:NZ	18:P:77:LYS:HB3	2.17	0.60
3:03:671:LEU:O	3:03:673:HIS:N	2.34	0.60
11:I:46:GLN:HA	11:I:56:LYS:HG2	1.81	0.60
18:P:55:LEU:HD12	18:P:56:ARG:N	2.15	0.60
12:J:41:ILE:HG23	12:J:116:ALA:HB2	1.84	0.60
15:M:80:THR:H	15:M:83:THR:HB	1.65	0.60
1:A:367:U:O2'	1:A:368:U:H4'	2.02	0.60
3:03:646:SER:HB3	3:03:649:GLN:HG3	1.82	0.60
4:04:1138:LEU:HB3	4:04:1139:PRO:HD3	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:24:ASN:ND2	8:F:25:THR:H	1.99	0.60
2:02:194:GLN:HG3	4:04:406:ALA:HB2	1.84	0.60
4:04:214:ARG:HA	4:04:217:LEU:HB2	1.84	0.60
7:E:11:LYS:CB	7:E:15:HIS:HB3	2.28	0.60
8:F:63:ILE:HG23	8:F:98:ALA:HA	1.84	0.60
25:W:79:THR:HA	25:W:82:ILE:HG12	1.84	0.60
2:01:31:LEU:HB2	2:01:199:ASP:O	2.02	0.60
3:03:136:PHE:O	3:03:143:ARG:HD2	2.02	0.60
3:03:616:ILE:HG13	3:03:652:TYR:HB2	1.84	0.60
4:04:530:PRO:HB3	4:04:577:ALA:O	2.02	0.60
4:04:554:GLU:HG3	4:04:566:LYS:HE3	1.83	0.60
4:04:959:LYS:HB3	4:04:983:LYS:HB2	1.82	0.60
1:A:244:U:H5'	1:A:894:G:N2	2.16	0.60
1:A:1239:A:H5''	1:A:1240:U:H5	1.66	0.60
3:03:74:ARG:HD2	3:03:75:LEU:N	2.17	0.60
3:03:402:ARG:HG3	3:03:406:ASN:ND2	2.17	0.60
3:03:488:MET:O	3:03:491:ASP:HB3	2.01	0.60
3:03:931:VAL:HG13	3:03:1052:VAL:HG22	1.83	0.60
4:04:99:ARG:HA	4:04:248:ASP:HB2	1.84	0.60
7:E:15:HIS:CE1	7:E:47:VAL:HG22	2.37	0.60
14:L:83:THR:HG23	14:L:97:LEU:HD23	1.84	0.59
15:M:52:LEU:HB2	19:Q:80:ARG:HD2	1.84	0.59
21:S:67:ILE:HD12	21:S:67:ILE:N	2.15	0.59
3:03:524:ILE:HD12	3:03:708:VAL:HG13	1.84	0.59
7:E:9:MET:HG3	7:E:10:LEU:HD23	1.84	0.59
7:E:106:THR:HA	7:E:109:GLN:HG3	1.84	0.59
16:N:88:PRO:HG2	26:X:29:LEU:HD22	1.85	0.59
2:02:42:ALA:O	2:02:46:ILE:HG13	2.02	0.59
3:03:34:SER:HA	3:03:37:LYS:NZ	2.18	0.59
3:03:143:ARG:HD2	3:03:143:ARG:H	1.66	0.59
12:J:113:LYS:HD2	12:J:117:LEU:CD2	2.33	0.59
16:N:20:ALA:HB2	16:N:33:ILE:HG22	1.84	0.59
4:04:86:GLU:HG2	26:X:67:ARG:HH22	1.67	0.59
4:04:1252:HIS:O	4:04:1256:ILE:HG12	2.02	0.59
1:A:885:G:H2'	1:A:886:G:H8	1.67	0.59
3:03:1235:LEU:H	3:03:1235:LEU:HD12	1.68	0.59
4:04:278:ARG:HD2	4:04:295:GLU:OE1	2.03	0.59
4:04:426:ALA:HB3	4:04:427:PRO:HD3	1.84	0.59
4:04:912:GLY:O	4:04:1359:ALA:HB1	2.03	0.59
26:X:34:ARG:HD3	26:X:34:ARG:H	1.67	0.59
4:04:483:LEU:HA	5:05:16:ARG:HH21	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:25:ARG:HD3	9:G:28:ASP:HA	1.83	0.59
1:A:1355:G:H2'	1:A:1356:G:C8	2.38	0.59
22:T:63:CYS:SG	22:T:64:ARG:N	2.75	0.59
25:W:76:ALA:C	25:W:78:LEU:H	2.05	0.59
1:A:71:A:H3'	1:A:72:A:H5''	1.85	0.59
3:O3:575:LEU:HG	3:O3:576:SER:H	1.68	0.59
10:H:159:SER:HB3	10:H:162:GLU:HB2	1.84	0.59
1:A:1047:G:H5''	19:Q:3:GLN:HG3	1.84	0.59
4:O4:415:VAL:HG23	4:O4:416:ILE:HG13	1.85	0.59
3:O3:94:ALA:HB2	3:O3:129:LEU:HD11	1.83	0.58
4:O4:342:LEU:O	4:O4:343:LEU:CB	2.48	0.58
4:O4:1153:PRO:HA	4:O4:1214:PRO:O	2.02	0.58
1:A:1345:U:H4'	1:A:1346:A:C8	2.38	0.58
2:O1:45:ARG:CB	2:O2:38:THR:HB	2.33	0.58
2:O1:48:LEU:HD23	2:O1:180:VAL:HG21	1.85	0.58
2:O2:12:ARG:C	2:O2:13:LEU:HD23	2.22	0.58
4:O4:45:ASN:C	4:O4:47:ARG:H	2.06	0.58
7:E:154:MET:HE3	7:E:158:PRO:HB3	1.84	0.58
2:O2:86:LYS:HG2	2:O2:174:ASP:H	1.67	0.58
3:O3:1132:LEU:HD23	3:O3:1132:LEU:O	2.02	0.58
4:O4:475:GLU:O	4:O4:479:GLU:HG3	2.03	0.58
4:O4:797:THR:HG22	4:O4:924:GLY:HA3	1.84	0.58
8:F:59:PRO:HD3	15:M:94:ALA:HB1	1.84	0.58
23:U:30:LYS:HA	23:U:33:ILE:HG12	1.85	0.58
3:O3:107:ARG:HG2	3:O3:108:GLU:HG3	1.84	0.58
3:O3:702:THR:HG23	3:O3:704:MET:H	1.67	0.58
1:A:440:C:C3'	1:A:441:A:H5''	2.32	0.58
2:O2:155:ALA:HB1	2:O2:172:LEU:HD12	1.86	0.58
3:O3:971:LEU:O	3:O3:975:ILE:HG13	2.03	0.58
4:O4:356:THR:HG23	4:O4:448:GLN:HG2	1.85	0.58
1:A:750:C:H2'	1:A:751:U:C6	2.39	0.58
1:A:1108:G:H5'	8:F:175:HIS:ND1	2.18	0.58
3:O3:426:ILE:HG22	3:O3:430:LYS:HE3	1.86	0.58
3:O3:738:GLU:HA	3:O3:741:MET:HB3	1.84	0.58
9:G:103:ARG:HB3	9:G:167:PRO:HG2	1.86	0.58
14:L:41:GLU:HG2	14:L:71:ILE:HG21	1.85	0.58
18:P:16:ILE:H	18:P:16:ILE:CD1	2.17	0.58
1:A:392:C:H2'	1:A:393:A:H8	1.68	0.58
4:O4:109:SER:CB	4:O4:279:LEU:HD13	2.30	0.58
4:O4:120:LEU:O	4:O4:122:SER:N	2.37	0.58
25:W:30:PHE:HB3	25:W:53:MET:HA	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:664:G:OP1	23:U:57:ARG:HD2	2.04	0.58
2:01:71:LYS:O	2:01:74:VAL:HG12	2.04	0.58
2:01:130:ILE:N	2:01:130:ILE:HD12	2.19	0.58
3:03:31:GLN:HE22	3:03:456:VAL:HG21	1.68	0.58
3:03:204:LEU:HD22	3:03:208:ILE:HD13	1.86	0.58
3:03:796:LEU:H	3:03:796:LEU:HD12	1.68	0.58
4:04:360:TYR:HA	4:04:626:TYR:HE1	1.69	0.58
4:04:847:ASP:HB3	4:04:856:ILE:HD13	1.85	0.58
7:E:34:ALA:H	7:E:41:ILE:HB	1.68	0.58
1:A:917:G:H2'	1:A:918:A:C8	2.39	0.58
2:02:33:ARG:HD3	2:02:33:ARG:N	2.17	0.58
4:04:1320:ILE:HG21	4:04:1349:GLU:HA	1.86	0.58
10:H:44:ARG:HA	10:H:71:ILE:O	2.04	0.58
17:O:89:LEU:HD12	17:O:89:LEU:N	2.18	0.58
3:03:1141:LEU:O	3:03:1145:ILE:HG12	2.04	0.58
4:04:1323:ALA:HA	4:04:1331:VAL:HG21	1.86	0.58
3:03:17:LYS:HD3	3:03:1155:VAL:HG21	1.86	0.57
3:03:322:LEU:O	3:03:322:LEU:HD23	2.04	0.57
4:04:30:ILE:HD13	4:04:243:PRO:HG3	1.85	0.57
4:04:520:ALA:HB1	4:04:546:ALA:HA	1.85	0.57
14:L:11:ARG:HG2	14:L:76:GLY:HA3	1.86	0.57
26:X:16:LEU:HA	26:X:18:ARG:HH11	1.67	0.57
1:A:867:G:H2'	1:A:868:C:C6	2.38	0.57
1:A:1304:G:N2	1:A:1333:A:H62	1.89	0.57
1:A:1345:U:H4'	1:A:1346:A:H8	1.69	0.57
3:03:10:ARG:HD3	3:03:1181:PRO:HG2	1.86	0.57
4:04:1060:VAL:HG13	4:04:1106:ILE:HA	1.87	0.57
12:J:68:VAL:HG21	12:J:103:ILE:HD11	1.86	0.57
22:T:70:LYS:HB2	22:T:70:LYS:NZ	2.19	0.57
1:A:1500:A:H5''	1:A:1508:A:H5''	1.84	0.57
2:02:222:THR:O	2:02:226:GLU:HG2	2.04	0.57
3:03:180:ARG:HB3	3:03:396:ASP:HB3	1.85	0.57
1:A:687:A:H62	1:A:703:G:H21	1.50	0.57
1:A:1225:A:H5'	1:A:1226:C:OP2	2.05	0.57
3:03:74:ARG:HD2	3:03:75:LEU:H	1.69	0.57
7:E:76:ALA:HB2	7:E:210:VAL:HG21	1.84	0.57
7:E:188:ASP:C	7:E:190:ASN:H	2.08	0.57
9:G:190:LEU:CD1	9:G:192:ALA:H	2.17	0.57
12:J:49:LEU:HD12	12:J:50:ALA:N	2.19	0.57
1:A:1118:U:H4'	14:L:84:ARG:HH12	1.69	0.57
2:01:111:THR:HA	2:01:129:VAL:HA	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:30:ILE:HD12	3:03:30:ILE:N	2.20	0.57
3:03:594:VAL:HG22	3:03:599:VAL:HG13	1.85	0.57
4:04:107:LEU:HD11	4:04:239:LEU:HD12	1.85	0.57
7:E:16:PHE:HD2	7:E:41:ILE:HG23	1.68	0.57
3:03:405:PHE:HE2	3:03:424:ASP:HB3	1.70	0.57
3:03:617:ALA:HB3	3:03:653:MET:HG3	1.86	0.57
4:04:1149:ARG:HD3	4:04:1150:PRO:O	2.05	0.57
10:H:149:PRO:HG3	13:K:98:LEU:HD21	1.86	0.57
14:L:91:GLU:HA	14:L:94:ARG:HB2	1.86	0.57
3:03:53:PHE:O	3:03:57:PHE:HB2	2.04	0.57
4:04:700:ASN:O	4:04:704:GLU:HB2	2.04	0.57
8:F:163:ARG:HD3	8:F:163:ARG:N	2.18	0.57
18:P:24:VAL:HG23	18:P:28:ARG:HB3	1.87	0.57
20:R:21:THR:HA	20:R:26:VAL:HG11	1.86	0.57
24:V:30:LEU:HD22	24:V:48:ILE:HG22	1.85	0.57
26:X:18:ARG:HA	26:X:21:ARG:HH11	1.68	0.57
2:02:100:LEU:HD21	2:02:121:VAL:HG21	1.85	0.57
4:04:65:VAL:HG22	4:04:98:ARG:NH1	2.19	0.57
4:04:597:GLY:H	4:04:600:ALA:HB3	1.68	0.57
4:04:609:TYR:HA	4:04:613:GLY:O	2.05	0.57
4:04:627:THR:HA	4:04:630:ALA:HB3	1.87	0.57
24:V:30:LEU:HD12	24:V:30:LEU:N	2.19	0.57
3:03:1255:THR:HG22	3:03:1256:GLN:N	2.15	0.57
7:E:103:ASN:O	7:E:107:VAL:HG23	2.05	0.57
16:N:74:LYS:HD3	16:N:74:LYS:H	1.69	0.57
21:S:4:ILE:HD12	21:S:67:ILE:HG13	1.87	0.57
25:W:75:LYS:HA	25:W:78:LEU:HB3	1.86	0.57
2:02:100:LEU:HD21	2:02:121:VAL:HG11	1.87	0.57
3:03:1109:ILE:O	3:03:1112:ILE:HG22	2.04	0.57
3:03:1275:VAL:O	3:03:1279:GLU:HG3	2.05	0.57
4:04:778:GLY:O	4:04:781:LYS:HB3	2.05	0.57
4:04:1157:ALA:HB2	4:04:1210:ILE:HD11	1.86	0.57
10:H:15:ILE:N	10:H:15:ILE:HD12	2.20	0.57
16:N:84:MET:HG2	16:N:110:THR:HB	1.86	0.57
1:A:39:G:C3'	1:A:40:C:H5''	2.35	0.56
1:A:632:U:H3'	1:A:633:G:H5'	1.85	0.56
2:01:13:LEU:HD23	2:01:13:LEU:H	1.70	0.56
4:04:952:VAL:HG22	4:04:954:ASN:H	1.69	0.56
4:04:1216:ALA:O	4:04:1220:ILE:HG12	2.05	0.56
5:05:32:VAL:C	5:05:34:GLY:H	2.08	0.56
8:F:133:MET:O	8:F:137:VAL:HG23	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:93:LYS:HB3	11:I:93:LYS:NZ	2.20	0.56
21:S:71:VAL:O	21:S:75:ILE:HG12	2.05	0.56
25:W:20:ASN:O	25:W:24:ARG:HG3	2.04	0.56
1:A:190:A:H2	25:W:47:GLN:HB3	1.69	0.56
2:01:78:ILE:O	2:01:82:LEU:HG	2.05	0.56
3:03:1082:ILE:H	3:03:1082:ILE:CD1	2.14	0.56
4:04:511:TYR:O	4:04:515:ARG:HB2	2.05	0.56
4:04:844:THR:CG2	4:04:864:LEU:HD11	2.35	0.56
1:A:50:A:H4'	1:A:51:A:H5'	1.87	0.56
1:A:376:G:H2'	1:A:377:G:C5'	2.35	0.56
1:A:1101:A:N7	7:E:171:ILE:HD13	2.19	0.56
1:A:1308:U:H5''	18:P:96:VAL:HG22	1.87	0.56
1:A:1323:G:H2'	1:A:1324:A:H8	1.68	0.56
3:03:243:PRO:HB3	3:03:274:ILE:HG23	1.87	0.56
3:03:405:PHE:O	3:03:409:LEU:HG	2.05	0.56
4:04:449:LEU:HG	4:04:450:HIS:H	1.69	0.56
4:04:865:HIS:HE1	4:04:867:GLN:HB2	1.70	0.56
7:E:157:LEU:HD12	7:E:157:LEU:O	2.05	0.56
15:M:77:VAL:HG12	15:M:78:GLU:N	2.21	0.56
19:Q:43:ALA:O	19:Q:47:LEU:HB2	2.05	0.56
26:X:36:GLU:HG3	26:X:38:TYR:H	1.71	0.56
1:A:1167:A:H2'	1:A:1167:A:N3	2.20	0.56
3:03:387:ASN:HA	3:03:391:SER:HB2	1.86	0.56
3:03:673:HIS:C	4:04:763:PHE:O	2.43	0.56
3:03:1109:ILE:HG12	4:04:764:ARG:HG3	1.87	0.56
3:03:1317:PRO:HB3	4:04:1355:ARG:HG2	1.86	0.56
4:04:205:LEU:HD23	4:04:217:LEU:HD12	1.88	0.56
4:04:418:GLU:HB3	5:05:45:LYS:HD3	1.87	0.56
1:A:250:A:H4'	1:A:252:U:C6	2.40	0.56
1:A:920:U:H2'	1:A:921:U:C6	2.39	0.56
3:03:409:LEU:HD21	3:03:428:VAL:HG22	1.88	0.56
3:03:431:LYS:O	3:03:435:ILE:HG13	2.06	0.56
3:03:1192:GLU:O	3:03:1196:LYS:HG2	2.06	0.56
3:03:1327:LEU:HG	3:03:1337:ILE:HG21	1.88	0.56
4:04:333:GLY:HA3	4:04:338:PHE:CZ	2.41	0.56
4:04:650:LYS:O	4:04:654:ILE:HG13	2.04	0.56
1:A:39:G:H2'	1:A:40:C:H5''	1.88	0.56
2:01:214:GLU:HA	2:01:217:ILE:HG22	1.88	0.56
3:03:1151:LEU:HD12	3:03:1152:GLY:N	2.21	0.56
4:04:530:PRO:O	4:04:533:ALA:HB3	2.06	0.56
16:N:22:ILE:HG23	16:N:31:VAL:HG22	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:109:ILE:HD12	16:N:109:ILE:N	2.21	0.56
2:01:231:PHE:CE2	2:02:39:LEU:HD11	2.40	0.56
2:02:183:ILE:N	2:02:183:ILE:HD12	2.20	0.56
3:03:519:ASN:HD21	3:03:521:LEU:HB3	1.69	0.56
16:N:81:LEU:HD23	16:N:81:LEU:H	1.71	0.56
2:02:56:VAL:HA	2:02:146:VAL:HA	1.88	0.56
3:03:1221:PHE:HB3	4:04:636:GLY:HA2	1.88	0.56
4:04:1327:GLU:HB3	4:04:1330:ARG:CG	2.34	0.56
7:E:87:CYS:HB2	7:E:89:GLN:NE2	2.12	0.56
9:G:118:SER:HA	9:G:130:ASN:HB2	1.88	0.56
15:M:80:THR:HG22	15:M:81:GLU:H	1.70	0.56
25:W:8:LYS:HB3	25:W:8:LYS:HZ2	1.68	0.56
25:W:56:ILE:HD12	25:W:56:ILE:N	2.21	0.56
3:03:127:ILE:O	3:03:127:ILE:HG13	2.06	0.56
4:04:547:ARG:HH11	4:04:547:ARG:HG3	1.70	0.56
4:04:1304:ARG:HH11	4:04:1304:ARG:HG3	1.71	0.56
3:03:255:ILE:HB	3:03:263:VAL:HB	1.87	0.56
3:03:476:LYS:HA	3:03:479:LEU:HD12	1.88	0.56
3:03:490:GLN:H	3:03:493:ILE:HG22	1.71	0.56
3:03:1150:ASP:O	3:03:1152:GLY:N	2.34	0.56
4:04:37:GLU:HG3	4:04:105:ILE:HA	1.88	0.56
4:04:417:ARG:HG2	4:04:417:ARG:HH11	1.71	0.56
4:04:579:LEU:O	4:04:583:VAL:HG23	2.06	0.56
7:E:39:HIS:O	7:E:40:ILE:CG2	2.47	0.56
7:E:209:ALA:HB1	7:E:213:TYR:CE2	2.41	0.56
19:Q:53:ASP:HA	19:Q:58:ARG:HD3	1.88	0.56
26:X:17:ARG:HB2	26:X:20:LYS:HD2	1.88	0.56
1:A:219:U:H2'	1:A:220:G:H5''	1.86	0.55
3:03:414:ILE:HD12	3:03:415:GLU:N	2.21	0.55
9:G:7:LYS:HB3	9:G:20:LEU:HD13	1.88	0.55
14:L:43:ALA:HB1	14:L:46:VAL:HG21	1.87	0.55
15:M:10:LEU:HD23	15:M:98:VAL:HA	1.88	0.55
26:X:35:ARG:HD3	26:X:37:PHE:CE2	2.41	0.55
3:03:30:ILE:H	3:03:30:ILE:CD1	2.20	0.55
3:03:896:THR:O	3:03:900:LYS:HG3	2.06	0.55
4:04:431:ARG:HD3	4:04:432:LEU:N	2.21	0.55
1:A:39:G:H3'	1:A:40:C:H5''	1.88	0.55
1:A:440:C:C2'	1:A:441:A:H5''	2.35	0.55
4:04:187:ALA:HA	4:04:190:LYS:HZ2	1.71	0.55
4:04:205:LEU:HD13	4:04:205:LEU:O	2.07	0.55
9:G:100:VAL:HG21	9:G:136:VAL:HG21	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1299:A:H2'	1:A:1300:G:H4'	1.87	0.55
3:03:97:ARG:NH1	3:03:123:TYR:HB2	2.21	0.55
3:03:560:PRO:HD3	4:04:773:PHE:HE1	1.70	0.55
4:04:66:LYS:HD3	4:04:67:ASP:N	2.22	0.55
4:04:306:LEU:O	4:04:327:LEU:HD12	2.06	0.55
4:04:797:THR:HA	4:04:800:LEU:HB2	1.88	0.55
5:05:28:ARG:HA	5:05:31:GLN:HG3	1.87	0.55
13:K:10:LEU:HD22	13:K:74:ILE:HD11	1.89	0.55
16:N:86:LYS:HA	16:N:113:THR:HA	1.88	0.55
3:03:454:ARG:HH21	3:03:535:PRO:HG2	1.70	0.55
4:04:1227:HIS:HA	4:04:1230:THR:HG22	1.88	0.55
9:G:71:PHE:HE1	9:G:93:LEU:HD11	1.72	0.55
25:W:8:LYS:HB3	25:W:8:LYS:HZ3	1.71	0.55
3:03:22:LEU:HB2	3:03:655:VAL:HG11	1.89	0.55
3:03:150:HIS:NE2	3:03:454:ARG:HG3	2.22	0.55
3:03:943:LYS:HA	3:03:946:LEU:HD12	1.88	0.55
4:04:77:ARG:HG2	7:E:20:THR:HG23	1.88	0.55
7:E:23:TRP:CE3	7:E:25:PRO:HB3	2.41	0.55
10:H:133:ILE:HD12	10:H:133:ILE:N	2.18	0.55
1:A:1210:C:H2'	1:A:1211:U:H5'	1.87	0.55
2:01:143:ARG:HD3	2:01:143:ARG:N	2.22	0.55
3:03:499:SER:O	3:03:503:LYS:HB2	2.06	0.55
4:04:202:ARG:HA	4:04:205:LEU:HB2	1.89	0.55
4:04:572:THR:OG1	4:04:576:ARG:HB2	2.05	0.55
4:04:746:LEU:HG	4:04:758:PRO:HG3	1.89	0.55
4:04:850:LYS:HB3	4:04:851:PRO:HD2	1.88	0.55
7:E:47:VAL:HB	7:E:48:PRO:CD	2.30	0.55
14:L:20:ILE:HD12	14:L:85:ALA:HB3	1.88	0.55
3:03:796:LEU:HD12	3:03:796:LEU:N	2.22	0.55
3:03:1150:ASP:O	3:03:1151:LEU:HG	2.07	0.55
4:04:116:PHE:HB3	4:04:123:ARG:HB2	1.89	0.55
4:04:800:LEU:O	4:04:803:VAL:HG12	2.06	0.55
19:Q:68:ARG:HH22	19:Q:80:ARG:NH2	2.05	0.55
20:R:2:LEU:HG	20:R:7:THR:OG1	2.07	0.55
1:A:18:C:H4'	1:A:1078:U:O2	2.07	0.55
1:A:765:G:H21	1:A:816:A:H61	1.54	0.55
1:A:1496:C:H1'	1:A:1517:G:H1	1.71	0.55
2:01:9:LEU:HD23	2:01:9:LEU:H	1.71	0.55
3:03:980:VAL:HA	3:03:984:VAL:HA	1.88	0.55
3:03:1285:TYR:O	3:03:1288:GLN:HB3	2.07	0.55
4:04:186:GLN:HB2	4:04:238:ILE:HG13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:294:ASN:O	4:04:298:MET:HG3	2.07	0.55
7:E:42:ASN:HD22	7:E:189:THR:HG23	1.70	0.55
7:E:121:SER:HA	7:E:126:PHE:HB3	1.89	0.55
19:Q:26:LEU:HD22	19:Q:43:ALA:HA	1.88	0.55
1:A:1395:C:O2'	1:A:1396:A:H5'	2.07	0.55
2:01:64:VAL:HG13	2:01:69:SER:OG	2.07	0.55
2:02:57:THR:HG22	2:02:58:GLU:HG3	1.89	0.55
15:M:80:THR:HG22	15:M:81:GLU:N	2.22	0.55
18:P:76:ILE:O	18:P:80:MET:HG3	2.07	0.55
3:03:1146:GLN:OE1	3:03:1146:GLN:HA	2.08	0.54
4:04:255:LEU:HD23	4:04:261:ALA:HB2	1.88	0.54
4:04:473:THR:HG23	4:04:476:ALA:H	1.72	0.54
7:E:213:TYR:O	7:E:217:VAL:HG23	2.07	0.54
9:G:97:LEU:HB2	9:G:134:TYR:HB3	1.88	0.54
21:S:43:ALA:HA	21:S:46:LYS:HZ3	1.70	0.54
21:S:57:ILE:O	21:S:61:VAL:HG23	2.06	0.54
23:U:50:LYS:O	23:U:54:GLN:HG2	2.07	0.54
2:02:118:ASP:HB2	2:02:121:VAL:H	1.72	0.54
3:03:1062:PRO:HG3	3:03:1079:ILE:HG22	1.89	0.54
4:04:485:MET:HB3	4:04:488:ASN:ND2	2.22	0.54
10:H:132:PRO:HA	10:H:135:VAL:HG22	1.89	0.54
17:O:29:LYS:NZ	17:O:58:ASN:ND2	2.55	0.54
13:K:50:VAL:O	13:K:50:VAL:HG22	2.07	0.54
23:U:36:SER:HB3	23:U:38:LYS:HE3	1.88	0.54
2:01:82:LEU:HD23	2:01:85:LEU:HD12	1.89	0.54
3:03:817:LEU:HD21	3:03:1080:ASN:ND2	2.23	0.54
4:04:289:ASP:HA	4:04:292:VAL:HG22	1.88	0.54
4:04:422:LEU:C	4:04:423:LEU:HD12	2.27	0.54
4:04:1218:HIS:O	4:04:1221:LEU:HB3	2.07	0.54
4:04:1320:ILE:HD12	4:04:1349:GLU:HG3	1.88	0.54
21:S:8:ARG:HH11	21:S:8:ARG:HG3	1.72	0.54
1:A:78:A:H2'	1:A:79:G:H4'	1.89	0.54
3:03:840:SER:HA	3:03:886:LYS:NZ	2.23	0.54
4:04:320:ASN:HD22	4:04:321:LYS:H	1.55	0.54
4:04:662:ALA:O	4:04:666:GLU:HG3	2.08	0.54
15:M:77:VAL:HG12	15:M:78:GLU:H	1.71	0.54
17:O:17:LYS:HB2	17:O:17:LYS:NZ	2.22	0.54
22:T:30:HIS:HB3	22:T:34:GLY:H	1.72	0.54
3:03:966:ILE:HD12	3:03:966:ILE:N	2.22	0.54
3:03:1106:ARG:N	3:03:1106:ARG:HD2	2.23	0.54
4:04:71:LEU:O	4:04:71:LEU:HD13	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:680:ASN:HA	4:04:683:ILE:HD12	1.89	0.54
7:E:25:PRO:C	7:E:28:LYS:H	2.11	0.54
24:V:4:LEU:HG	24:V:6:LYS:H	1.72	0.54
1:A:1329:A:H5'	18:P:25:GLY:N	2.19	0.54
3:03:886:LYS:H	3:03:917:SER:HA	1.72	0.54
4:04:1282:TYR:O	4:04:1285:VAL:HG12	2.06	0.54
1:A:744:C:H2'	1:A:745:G:H8	1.73	0.54
1:A:1253:G:OP1	15:M:46:LYS:HB2	2.07	0.54
2:01:102:LEU:HD23	2:01:115:ILE:HG12	1.90	0.54
4:04:76:LYS:HD3	4:04:76:LYS:N	2.23	0.54
4:04:132:LEU:O	4:04:132:LEU:HD13	2.08	0.54
4:04:532:GLU:O	4:04:536:LEU:HD23	2.07	0.54
4:04:1273:ASP:CG	4:04:1274:PHE:H	2.10	0.54
24:V:40:PHE:HB2	24:V:43:MET:HG3	1.89	0.54
3:03:222:ASP:OD1	3:03:227:LYS:HE2	2.08	0.54
3:03:445:ILE:HG12	3:03:451:ARG:HH21	1.72	0.54
4:04:1238:GLN:O	4:04:1242:ARG:HG2	2.08	0.54
5:05:37:PRO:HG3	5:05:41:GLU:OE1	2.08	0.54
1:A:1502:A:H5'	1:A:1504:G:N7	2.23	0.54
3:03:454:ARG:HG2	3:03:458:GLU:OE2	2.08	0.54
3:03:1255:THR:HB	3:03:1257:GLN:HG2	1.89	0.54
4:04:1163:VAL:HG13	4:04:1200:GLU:HA	1.90	0.54
16:N:85:VAL:HG11	16:N:92:ARG:HG2	1.90	0.54
21:S:61:VAL:HG21	21:S:67:ILE:HD11	1.89	0.54
25:W:54:GLN:N	25:W:55:PRO:CD	2.71	0.54
1:A:675:A:H2'	1:A:676:A:H8	1.72	0.53
1:A:1148:U:H5'	14:L:6:TYR:OH	2.08	0.53
4:04:317:THR:HG23	4:04:320:ASN:HB3	1.90	0.53
4:04:418:GLU:O	4:04:420:PRO:HD3	2.08	0.53
4:04:473:THR:O	4:04:477:GLN:HG3	2.07	0.53
4:04:826:ILE:HG12	4:04:831:VAL:HB	1.88	0.53
18:P:17:ALA:HB1	18:P:44:ILE:HD12	1.90	0.53
1:A:309:A:H2'	1:A:310:G:H8	1.72	0.53
1:A:626:G:H2'	1:A:627:G:H8	1.73	0.53
1:A:1297:G:N2	12:J:113:LYS:HB3	2.23	0.53
2:01:56:VAL:HA	2:01:146:VAL:HG22	1.89	0.53
3:03:34:SER:HA	3:03:37:LYS:HZ1	1.73	0.53
3:03:39:ILE:HA	3:03:49:LEU:HD12	1.90	0.53
3:03:1328:LYS:NZ	4:04:245:LEU:HA	2.24	0.53
4:04:619:ILE:O	4:04:623:GLN:HG2	2.08	0.53
7:E:164:ILE:O	7:E:186:ILE:HG23	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:9:LYS:O	9:G:13:ARG:HG2	2.07	0.53
13:K:116:ARG:HB2	13:K:116:ARG:NH1	2.23	0.53
16:N:33:ILE:HG13	16:N:41:LEU:HB2	1.91	0.53
1:A:1268:G:H1'	1:A:1327:C:H5'	1.91	0.53
1:A:1346:A:H2'	1:A:1346:A:N3	2.23	0.53
2:02:65:LEU:HD22	2:02:65:LEU:N	2.24	0.53
3:03:91:THR:HA	3:03:138:ILE:HA	1.89	0.53
3:03:138:ILE:HB	3:03:143:ARG:CZ	2.38	0.53
3:03:386:GLU:O	3:03:390:PHE:HB2	2.08	0.53
4:04:210:SER:O	4:04:214:ARG:HG2	2.08	0.53
4:04:345:LYS:O	4:04:346:ARG:HB2	2.07	0.53
4:04:374:LEU:HD23	4:04:375:GLU:N	2.23	0.53
7:E:21:ARG:HD3	7:E:22:TYR:H	1.72	0.53
7:E:21:ARG:HB3	7:E:38:VAL:HA	1.91	0.53
10:H:133:ILE:H	10:H:133:ILE:CD1	2.16	0.53
10:H:136:VAL:O	10:H:140:ILE:HG12	2.08	0.53
3:03:144:VAL:HG23	3:03:515:MET:HB2	1.90	0.53
3:03:213:LEU:HD22	3:03:215:TYR:CZ	2.43	0.53
3:03:479:LEU:HD23	3:03:487:LEU:CD1	2.37	0.53
3:03:818:VAL:HG23	3:03:1076:ILE:HD13	1.91	0.53
4:04:41:PRO:HB2	4:04:270:ARG:HG3	1.89	0.53
7:E:99:GLY:HA3	7:E:103:ASN:HD22	1.72	0.53
10:H:13:LYS:HG2	10:H:112:ALA:HB1	1.90	0.53
10:H:107:GLY:N	10:H:110:MET:HE2	2.23	0.53
11:I:51:ILE:HD12	11:I:86:ARG:HH21	1.72	0.53
1:A:440:C:H3'	1:A:441:A:H5''	1.90	0.53
8:F:112:ALA:HB1	8:F:199:VAL:HG13	1.90	0.53
10:H:56:PRO:HA	10:H:59:ILE:HG12	1.91	0.53
12:J:24:LYS:HB2	12:J:24:LYS:NZ	2.23	0.53
23:U:61:ARG:O	23:U:65:LEU:HD13	2.09	0.53
1:A:427:U:H1'	1:A:541:G:C5'	2.30	0.53
1:A:570:G:H2'	1:A:571:U:C6	2.44	0.53
1:A:584:G:H22	1:A:879:C:H4'	1.74	0.53
1:A:1271:A:H5'	1:A:1314:C:H5''	1.91	0.53
2:02:151:GLY:O	2:02:177:TYR:HB2	2.09	0.53
3:03:1272:GLU:HA	3:03:1275:VAL:CG2	2.39	0.53
4:04:659:ALA:O	4:04:663:GLU:HG2	2.08	0.53
4:04:746:LEU:N	4:04:746:LEU:HD12	2.23	0.53
22:T:70:LYS:HB2	22:T:70:LYS:HZ2	1.73	0.53
1:A:260:G:H2'	1:A:261:U:C6	2.44	0.53
1:A:1157:A:H61	1:A:1178:G:H1'	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:45:ARG:HH22	3:03:1216:ARG:HA	1.74	0.53
2:01:77:ASP:O	2:01:81:ILE:HG13	2.09	0.53
2:02:83:LEU:HA	2:02:86:LYS:NZ	2.24	0.53
3:03:682:GLY:O	3:03:686:GLN:HG3	2.09	0.53
4:04:71:LEU:H	4:04:90:VAL:HG11	1.74	0.53
4:04:612:LEU:HG	4:04:616:PRO:HG2	1.91	0.53
4:04:646:ILE:HG12	4:04:764:ARG:HH21	1.74	0.53
9:G:149:LYS:HB3	9:G:149:LYS:NZ	2.24	0.53
12:J:55:LYS:HD2	12:J:59:GLU:OE2	2.09	0.53
1:A:1118:U:OP1	14:L:105:ARG:HG3	2.09	0.53
1:A:1315:U:H1'	1:A:1361:G:H4'	1.91	0.53
3:03:243:PRO:HA	3:03:246:LEU:HD12	1.91	0.53
3:03:263:VAL:HG22	3:03:273:HIS:HB3	1.90	0.53
4:04:504:GLN:NE2	4:04:731:ARG:HD2	2.23	0.53
1:A:686:U:O2'	1:A:687:A:H5'	2.09	0.53
1:A:1369:C:H2'	1:A:1370:G:C8	2.44	0.53
3:03:81:ASP:OD2	3:03:83:GLN:HB2	2.09	0.53
3:03:399:ALA:O	3:03:403:MET:HB2	2.09	0.53
4:04:583:VAL:HG13	4:04:587:LEU:HD23	1.90	0.53
4:04:705:THR:CG2	4:04:719:PHE:H	2.14	0.53
19:Q:8:ARG:HB3	19:Q:12:ARG:NH1	2.22	0.53
24:V:40:PHE:H	24:V:43:MET:HE3	1.72	0.53
1:A:29:U:O2'	1:A:30:U:H5'	2.08	0.53
2:01:155:ALA:HA	2:01:158:ARG:HE	1.74	0.53
3:03:4:SER:H	3:03:7:GLU:HB2	1.74	0.53
7:E:27:MET:HE2	7:E:189:THR:HA	1.90	0.53
15:M:5:ARG:HH12	15:M:102:LEU:HB2	1.73	0.53
24:V:4:LEU:HD23	24:V:4:LEU:N	2.24	0.53
1:A:1315:U:H2'	1:A:1316:G:O4'	2.10	0.52
2:02:48:LEU:HD22	4:04:535:ARG:HA	1.91	0.52
3:03:363:LEU:HD23	3:03:366:ILE:HD12	1.91	0.52
4:04:130:MET:HB2	4:04:157:GLN:OE1	2.09	0.52
4:04:141:PHE:CE1	4:04:181:GLY:HA3	2.44	0.52
4:04:279:LEU:HD23	4:04:279:LEU:O	2.09	0.52
4:04:487:THR:HG21	5:05:4:VAL:HG22	1.91	0.52
4:04:902:ASP:HB3	4:04:1251:LYS:HZ1	1.74	0.52
7:E:140:GLU:O	7:E:144:LEU:HD23	2.09	0.52
10:H:10:LEU:HD21	10:H:67:ARG:HE	1.74	0.52
25:W:15:LYS:O	25:W:19:HIS:HB3	2.09	0.52
25:W:79:THR:HG23	25:W:82:ILE:HD11	1.90	0.52
1:A:946:A:H1'	1:A:1333:A:C2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:53:ARG:O	4:04:53:ARG:HD3	2.10	0.52
4:04:368:LEU:HD12	4:04:439:PRO:HB3	1.90	0.52
12:J:40:SER:HA	12:J:43:TYR:CD2	2.42	0.52
12:J:115:MET:SD	12:J:118:ARG:HD2	2.50	0.52
18:P:44:ILE:HA	18:P:47:LEU:HG	1.89	0.52
20:R:81:ILE:HG22	20:R:86:LEU:HD12	1.91	0.52
1:A:511:C:O2'	1:A:512:U:H5'	2.09	0.52
2:01:167:PRO:HG2	2:01:170:ARG:HE	1.73	0.52
3:03:22:LEU:HB2	3:03:655:VAL:CG1	2.39	0.52
3:03:838:CYS:HB2	3:03:918:LEU:HD22	1.91	0.52
3:03:1308:ILE:HG22	3:03:1308:ILE:O	2.09	0.52
4:04:531:LYS:O	4:04:534:GLU:HB3	2.10	0.52
4:04:798:ARG:O	4:04:801:VAL:HG22	2.10	0.52
1:A:414:A:H2'	1:A:414:A:N3	2.24	0.52
1:A:1369:C:H2'	1:A:1370:G:H8	1.73	0.52
3:03:89:GLY:HA2	3:03:140:GLY:H	1.75	0.52
3:03:1132:LEU:HD22	3:03:1177:ARG:NH1	2.25	0.52
4:04:706:VAL:HG23	4:04:706:VAL:O	2.10	0.52
4:04:767:LEU:HB2	4:04:771:GLN:OE1	2.10	0.52
7:E:21:ARG:C	7:E:23:TRP:HD1	2.13	0.52
7:E:47:VAL:CB	7:E:48:PRO:HD3	2.32	0.52
10:H:68:ARG:O	10:H:68:ARG:HD2	2.10	0.52
18:P:48:SER:O	18:P:52:ILE:HG13	2.10	0.52
25:W:53:MET:HE2	25:W:75:LYS:HD3	1.91	0.52
2:01:82:LEU:HB3	2:01:173:VAL:HG11	1.92	0.52
4:04:107:LEU:HD22	4:04:299:LEU:HD21	1.92	0.52
4:04:820:ILE:HG12	4:04:884:SER:HB2	1.92	0.52
11:I:47:LEU:HD21	11:I:57:ALA:CB	2.39	0.52
12:J:22:LEU:O	12:J:26:VAL:HG23	2.10	0.52
13:K:5:PRO:HB2	13:K:32:LYS:HE3	1.90	0.52
14:L:117:LEU:HD21	14:L:123:ARG:HE	1.75	0.52
22:T:30:HIS:HD2	22:T:33:TYR:H	1.58	0.52
1:A:637:C:H5''	22:T:3:LYS:HG3	1.92	0.52
3:03:80:PHE:HB3	3:03:84:GLU:HB2	1.91	0.52
3:03:502:VAL:CG1	3:03:503:LYS:HD2	2.35	0.52
4:04:154:LEU:N	4:04:154:LEU:HD12	2.25	0.52
9:G:184:LYS:HD3	9:G:185:PRO:HD2	1.91	0.52
4:04:600:ALA:HA	4:04:603:LYS:HZ1	1.74	0.52
5:05:28:ARG:HG2	5:05:31:GLN:OE1	2.10	0.52
14:L:62:LEU:HD12	14:L:62:LEU:O	2.10	0.52
18:P:82:LEU:HD11	24:V:65:MET:HG3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:92:ILE:HD13	19:Q:95:LEU:HD22	1.91	0.52
20:R:57:ARG:O	20:R:61:GLN:HG2	2.10	0.52
22:T:35:LYS:HB3	22:T:35:LYS:HZ3	1.75	0.52
1:A:328:C:H4'	1:A:329:A:H5'	1.91	0.52
1:A:454:G:H22	1:A:478:A:H2	1.57	0.52
1:A:1252:A:H61	1:A:1285:A:N6	2.07	0.52
2:02:102:LEU:C	2:02:102:LEU:HD13	2.30	0.52
3:03:42:ASP:HB3	3:03:44:GLU:HG2	1.91	0.52
3:03:1278:LEU:HD13	3:03:1287:LEU:HD13	1.91	0.52
4:04:79:LYS:HD2	7:E:20:THR:OG1	2.09	0.52
4:04:165:TYR:O	4:04:169:LEU:HG	2.09	0.52
8:F:138:GLN:O	8:F:142:ARG:HG2	2.10	0.52
20:R:27:GLN:O	20:R:31:LEU:HG	2.10	0.52
3:03:212:ALA:HA	3:03:359:ARG:HG3	1.92	0.52
3:03:525:THR:O	3:03:529:ARG:HB2	2.10	0.52
3:03:540:ARG:HB2	3:03:548:ARG:NH2	2.25	0.52
3:03:690:VAL:CG1	3:03:1234:LYS:HB3	2.40	0.52
3:03:724:VAL:HG22	3:03:775:GLU:H	1.75	0.52
3:03:890:LYS:HE3	3:03:914:LYS:HB3	1.91	0.52
4:04:362:ARG:HB2	4:04:365:GLN:HG2	1.92	0.52
4:04:437:PHE:CE2	4:04:449:LEU:HD11	2.45	0.52
7:E:44:GLU:C	7:E:46:THR:N	2.63	0.52
15:M:89:ARG:C	15:M:90:LEU:HD12	2.30	0.52
1:A:109:A:H62	1:A:324:G:H21	1.57	0.52
1:A:427:U:C1'	1:A:541:G:H5''	2.33	0.52
3:03:119:GLU:HB2	3:03:489:PRO:HG2	1.92	0.52
3:03:233:ARG:O	3:03:236:LYS:HG2	2.10	0.52
3:03:753:LEU:N	3:03:753:LEU:HD12	2.23	0.52
8:F:9:ILE:HG23	8:F:10:ARG:HG3	1.92	0.52
10:H:51:LYS:H	10:H:61:LYS:HD3	1.73	0.52
17:O:22:ALA:HB2	17:O:94:TYR:OH	2.10	0.52
19:Q:13:VAL:HA	19:Q:59:GLN:HE22	1.75	0.52
1:A:403:C:H5'	9:G:114:ARG:HH21	1.75	0.51
1:A:1099:G:H5''	26:X:67:ARG:CD	2.40	0.51
2:02:181:GLU:HB3	4:04:531:LYS:HD3	1.91	0.51
3:03:814:ASP:O	3:03:1074:GLY:HA2	2.10	0.51
3:03:882:ILE:HD12	3:03:882:ILE:N	2.25	0.51
3:03:1079:ILE:HG23	3:03:1079:ILE:O	2.10	0.51
4:04:107:LEU:CD1	4:04:239:LEU:HD12	2.40	0.51
4:04:249:LEU:C	4:04:251:PRO:HD3	2.31	0.51
10:H:107:GLY:H	10:H:110:MET:HE2	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:40:ARG:HD2	19:Q:40:ARG:O	2.10	0.51
1:A:418:C:H2'	1:A:419:C:C6	2.45	0.51
1:A:718:A:H5'	16:N:118:ASN:CB	2.40	0.51
1:A:1099:G:H5''	26:X:67:ARG:HD3	1.92	0.51
1:A:1259:C:H3'	1:A:1260:G:C5'	2.38	0.51
2:01:27:THR:C	2:01:28:LEU:HD12	2.31	0.51
2:02:78:ILE:HA	2:02:81:ILE:HD12	1.93	0.51
3:03:241:LEU:CD1	3:03:246:LEU:HD11	2.37	0.51
3:03:1100:PRO:HG2	4:04:638:SER:HB3	1.92	0.51
4:04:264:ASP:O	4:04:268:LEU:HG	2.10	0.51
4:04:305:ALA:HA	4:04:309:ASN:HA	1.92	0.51
4:04:858:VAL:HG13	4:04:858:VAL:O	2.10	0.51
7:E:31:ILE:O	7:E:32:PHE:HB3	2.11	0.51
25:W:60:GLN:HB3	25:W:66:ILE:HG12	1.91	0.51
1:A:193:C:H2'	1:A:194:C:C6	2.45	0.51
2:01:28:LEU:HD12	2:01:28:LEU:N	2.25	0.51
3:03:145:ILE:HG12	3:03:512:SER:HB2	1.91	0.51
3:03:1235:LEU:HD12	3:03:1235:LEU:N	2.24	0.51
4:04:66:LYS:HZ3	4:04:78:LEU:HD11	1.75	0.51
9:G:71:PHE:HA	9:G:74:TYR:HD2	1.75	0.51
14:L:105:ARG:HH11	14:L:107:ALA:HA	1.75	0.51
3:03:146:VAL:CG1	3:03:531:SER:HB2	2.41	0.51
3:03:672:GLU:HB2	4:04:766:GLY:CA	2.40	0.51
3:03:734:ILE:HB	3:03:749:ASP:HB2	1.91	0.51
4:04:127:LEU:HG	4:04:192:MET:HE1	1.93	0.51
4:04:688:ALA:O	4:04:692:ARG:HG3	2.10	0.51
1:A:817:C:H5'	1:A:820:U:OP1	2.10	0.51
1:A:1314:C:H2'	1:A:1315:U:C6	2.46	0.51
2:02:191:ARG:NH1	2:02:191:ARG:HB3	2.26	0.51
3:03:159:SER:O	3:03:160:ASP:HB2	2.11	0.51
7:E:67:ILE:HB	7:E:89:GLN:HG2	1.92	0.51
14:L:66:VAL:HG21	14:L:74:GLN:HB3	1.92	0.51
20:R:16:ARG:HD3	20:R:16:ARG:N	2.26	0.51
1:A:102:G:O2'	1:A:151:A:H1'	2.11	0.51
2:01:134:THR:OG1	3:03:773:LEU:HD22	2.11	0.51
2:02:83:LEU:HA	2:02:86:LYS:HZ1	1.76	0.51
4:04:108:ALA:HB2	4:04:280:LYS:HG2	1.91	0.51
4:04:278:ARG:HG3	4:04:281:ARG:HH21	1.76	0.51
9:G:37:PRO:HD2	9:G:41:GLY:HA2	1.92	0.51
11:I:40:GLU:OE1	11:I:61:LEU:HD22	2.10	0.51
15:M:8:ILE:HD12	15:M:74:VAL:HB	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:57:VAL:HG22	15:M:58:ASN:N	2.24	0.51
20:R:28:VAL:CG2	20:R:65:LEU:HD23	2.38	0.51
24:V:10:ILE:HG21	24:V:40:PHE:CZ	2.45	0.51
1:A:392:C:H2'	1:A:393:A:C8	2.45	0.51
2:02:52:PRO:HD2	2:02:223:ILE:HD13	1.93	0.51
3:03:798:GLN:NE2	3:03:827:ARG:HE	2.08	0.51
3:03:983:GLY:O	3:03:985:GLU:HG3	2.10	0.51
4:04:499:ILE:HG23	4:04:500:ILE:HG12	1.91	0.51
12:J:55:LYS:NZ	12:J:63:VAL:HG21	2.26	0.51
4:04:623:GLN:O	4:04:627:THR:HG22	2.11	0.51
4:04:1029:THR:HG23	4:04:1121:LEU:HD21	1.93	0.51
2:01:67:GLU:N	2:01:171:LEU:HD11	2.26	0.51
3:03:514:PHE:HB3	3:03:760:ASN:HD22	1.76	0.51
4:04:308:ASP:O	4:04:309:ASN:HB2	2.11	0.51
4:04:483:LEU:HA	5:05:16:ARG:NH2	2.25	0.51
4:04:1075:ARG:HG2	4:04:1075:ARG:HH11	1.75	0.51
7:E:13:GLY:C	7:E:14:VAL:HG22	2.31	0.51
7:E:46:THR:HG23	7:E:201:PRO:O	2.11	0.51
7:E:74:ARG:HH21	7:E:77:SER:CB	2.24	0.51
7:E:141:LEU:O	7:E:145:GLU:HG3	2.11	0.51
20:R:6:ALA:O	20:R:10:ILE:HG13	2.10	0.51
1:A:981:U:C4'	19:Q:62:ARG:HH22	2.23	0.51
1:A:1014:A:H5''	24:V:13:HIS:HB2	1.93	0.51
4:04:189:LEU:HD13	4:04:234:PRO:O	2.10	0.51
4:04:660:GLU:O	4:04:664:ILE:HG12	2.10	0.51
17:O:29:LYS:HE2	17:O:57:THR:HB	1.93	0.51
1:A:774:G:H2'	1:A:775:G:H5'	1.93	0.50
1:A:1371:G:H4'	14:L:70:GLY:HA3	1.93	0.50
2:02:172:LEU:H	2:02:172:LEU:CD2	2.24	0.50
4:04:27:PRO:HB2	4:04:31:ARG:HH12	1.75	0.50
4:04:428:THR:HG21	4:04:433:GLY:HA3	1.92	0.50
4:04:678:ARG:HA	4:04:681:LYS:HB3	1.92	0.50
7:E:16:PHE:CD2	7:E:41:ILE:HD12	2.46	0.50
7:E:44:GLU:C	7:E:46:THR:H	2.14	0.50
11:I:5:GLU:HB2	11:I:90:MET:HB2	1.92	0.50
1:A:105:G:N7	25:W:8:LYS:HE3	2.26	0.50
1:A:762:U:H2'	1:A:763:G:C8	2.46	0.50
1:A:1030:U:H3'	1:A:1031:C:H5'	1.94	0.50
2:01:65:LEU:HD12	2:01:168:ILE:HG13	1.92	0.50
3:03:678:ARG:HH21	3:03:1106:ARG:HG2	1.72	0.50
3:03:1013:GLN:O	3:03:1016:GLU:HB2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:110:ARG:O	9:G:114:ARG:HG3	2.11	0.50
10:H:59:ILE:O	10:H:63:MET:HG2	2.11	0.50
10:H:156:ARG:HG2	13:K:44:PHE:CE1	2.46	0.50
12:J:99:ALA:O	12:J:103:ILE:HG13	2.11	0.50
19:Q:5:MET:HG2	19:Q:62:ARG:NH1	2.26	0.50
1:A:516:U:H5	1:A:533:A:N6	2.10	0.50
1:A:517:G:H4'	1:A:519:C:C2	2.47	0.50
1:A:658:C:H1'	20:R:21:THR:HG21	1.91	0.50
1:A:1123:U:O2'	1:A:1124:G:H5'	2.11	0.50
3:03:12:ARG:HH22	3:03:705:GLU:HB2	1.75	0.50
3:03:471:VAL:O	3:03:475:VAL:HG23	2.11	0.50
4:04:749:LYS:HB3	4:04:755:ILE:HG13	1.93	0.50
4:04:865:HIS:CE1	4:04:867:GLN:HB2	2.46	0.50
4:04:1327:GLU:O	4:04:1330:ARG:HB2	2.11	0.50
11:I:18:VAL:N	11:I:19:PRO:CD	2.75	0.50
14:L:18:VAL:HG13	14:L:64:ILE:CD1	2.40	0.50
1:A:879:C:H2'	1:A:880:C:C6	2.47	0.50
7:E:222:ARG:HA	7:E:225:ARG:HG2	1.94	0.50
19:Q:22:LYS:C	19:Q:24:ALA:H	2.15	0.50
1:A:219:U:H2'	1:A:220:G:C4'	2.41	0.50
1:A:1273:C:H2'	1:A:1274:A:H5'	1.93	0.50
1:A:1527:U:O2'	1:A:1528:U:H5'	2.12	0.50
3:03:725:GLN:HB2	3:03:735:LYS:HB2	1.94	0.50
4:04:77:ARG:HB3	4:04:79:LYS:HG2	1.94	0.50
4:04:311:ARG:NH2	4:04:1329:THR:HB	2.25	0.50
4:04:1159:ILE:HG13	4:04:1160:SER:N	2.26	0.50
4:04:1230:THR:O	4:04:1234:VAL:HG13	2.11	0.50
8:F:19:SER:O	19:Q:93:PRO:HG3	2.12	0.50
11:I:90:MET:SD	23:U:61:ARG:HD3	2.52	0.50
1:A:613:C:P	9:G:80:ARG:HD3	2.52	0.50
1:A:1148:U:H5'	14:L:6:TYR:HH	1.76	0.50
4:04:179:LYS:HD2	4:04:293:ARG:HH22	1.77	0.50
4:04:204:GLU:HA	4:04:207:GLU:HB2	1.92	0.50
4:04:1221:LEU:HD23	4:04:1229:VAL:HG11	1.93	0.50
4:04:1266:ILE:HG21	4:04:1300:ALA:HB1	1.93	0.50
11:I:3:HIS:HB3	11:I:95:ALA:HB2	1.94	0.50
22:T:10:ARG:HH11	22:T:10:ARG:HG3	1.75	0.50
2:02:54:CYS:SG	2:02:92:VAL:HG22	2.52	0.50
2:02:213:PRO:O	2:02:217:ILE:HG13	2.10	0.50
3:03:615:VAL:HG12	3:03:651:ASP:OD2	2.11	0.50
3:03:960:LEU:HG	3:03:1029:LEU:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:1263:ALA:HB1	3:03:1264:GLN:OE1	2.12	0.50
3:03:1335:ILE:HD12	3:03:1335:ILE:H	1.75	0.50
7:E:23:TRP:CA	7:E:190:ASN:HB3	2.41	0.50
24:V:8:PRO:HB2	24:V:38:THR:HG21	1.94	0.50
24:V:30:LEU:HD12	24:V:30:LEU:H	1.76	0.50
1:A:577:G:H1'	1:A:816:A:H2'	1.92	0.50
1:A:1270:G:H2'	1:A:1271:A:C8	2.47	0.50
1:A:1395:C:H2'	1:A:1396:A:C8	2.46	0.50
2:01:82:LEU:HA	2:01:85:LEU:HD12	1.94	0.50
3:03:139:ASN:HB2	3:03:143:ARG:NH2	2.26	0.50
4:04:512:TYR:CD2	4:04:635:SER:HA	2.47	0.50
4:04:1370:MET:O	4:04:1370:MET:HE3	2.11	0.50
7:E:21:ARG:H	7:E:38:VAL:HB	1.76	0.50
7:E:27:MET:SD	7:E:191:SER:HB2	2.52	0.50
7:E:36:ASN:HB2	7:E:40:ILE:CD1	2.41	0.50
10:H:87:VAL:HB	10:H:92:ARG:NH1	2.27	0.50
18:P:86:ARG:O	18:P:96:VAL:HG12	2.11	0.50
25:W:27:MET:HG2	25:W:31:ILE:HD11	1.94	0.50
1:A:443:C:H2'	1:A:444:G:C8	2.47	0.50
1:A:1366:C:H2'	1:A:1367:C:C6	2.46	0.50
2:01:58:GLU:HB2	2:01:145:LYS:HB3	1.93	0.50
3:03:1267:GLY:H	4:04:346:ARG:NH2	1.95	0.50
4:04:70:CYS:SG	4:04:85:CYS:HB2	2.51	0.50
4:04:429:LEU:HD12	4:04:430:HIS:N	2.26	0.50
4:04:478:LEU:HD23	4:04:478:LEU:C	2.32	0.50
4:04:1271:SER:HB2	4:04:1299:GLY:HA2	1.93	0.50
19:Q:92:ILE:HD12	19:Q:92:ILE:N	2.27	0.50
1:A:219:U:H2'	1:A:220:G:C5'	2.42	0.49
3:03:97:ARG:HB3	3:03:121:GLU:HB2	1.94	0.49
3:03:144:VAL:HG11	3:03:527:LYS:HA	1.94	0.49
4:04:355:ILE:HG23	4:04:464:ASP:O	2.12	0.49
4:04:930:LEU:HD23	4:04:1244:GLN:HG3	1.94	0.49
10:H:91:SER:OG	10:H:134:ASN:HB3	2.12	0.49
12:J:24:LYS:HA	12:J:27:ASN:ND2	2.21	0.49
18:P:2:ARG:H	18:P:8:ILE:HG12	1.77	0.49
3:03:362:ALA:O	3:03:366:ILE:HG13	2.11	0.49
3:03:936:ARG:HA	3:03:1047:LEU:HB3	1.94	0.49
12:J:52:ARG:HH22	12:J:117:LEU:HD11	1.77	0.49
14:L:18:VAL:HG13	14:L:64:ILE:HD11	1.94	0.49
19:Q:84:ARG:C	19:Q:84:ARG:HD3	2.32	0.49
1:A:508:U:H4'	9:G:50:TYR:CD2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:35:PHE:HA	2:01:38:THR:HB	1.95	0.49
3:03:137:VAL:HG22	3:03:142:GLU:CG	2.37	0.49
3:03:414:ILE:HD12	3:03:414:ILE:C	2.32	0.49
3:03:974:ARG:HH21	3:03:977:ALA:HB3	1.77	0.49
3:03:1172:LEU:HA	3:03:1175:ASN:HD22	1.77	0.49
3:03:1253:LEU:O	3:03:1253:LEU:HD13	2.12	0.49
4:04:290:ILE:HD12	4:04:290:ILE:N	2.17	0.49
4:04:588:PRO:O	4:04:591:ILE:HG22	2.13	0.49
4:04:1173:ARG:NH2	4:04:1196:LEU:HD23	2.23	0.49
4:04:1221:LEU:HD13	4:04:1221:LEU:C	2.33	0.49
10:H:104:ILE:HG23	10:H:104:ILE:O	2.11	0.49
15:M:57:VAL:O	15:M:58:ASN:HB2	2.12	0.49
17:O:98:ARG:HB2	17:O:116:TYR:HA	1.95	0.49
1:A:118:U:H2'	1:A:119:A:H5'	1.95	0.49
1:A:675:A:H2'	1:A:676:A:C8	2.47	0.49
2:01:69:SER:O	2:01:78:ILE:HG12	2.11	0.49
3:03:498:ILE:H	3:03:498:ILE:CD1	2.24	0.49
3:03:704:MET:HA	3:03:707:ALA:HB3	1.94	0.49
3:03:820:GLU:HB3	3:03:1082:ILE:HD12	1.95	0.49
4:04:137:ARG:HB3	4:04:143:SER:OG	2.12	0.49
4:04:327:LEU:C	4:04:330:MET:HB2	2.33	0.49
4:04:615:LYS:HB2	4:04:615:LYS:NZ	2.26	0.49
4:04:821:MET:HG3	4:04:823:THR:HG23	1.93	0.49
7:E:57:LEU:HD13	7:E:217:VAL:HG13	1.93	0.49
14:L:35:GLU:HA	14:L:39:GLY:HA3	1.94	0.49
19:Q:48:GLN:HB2	24:V:12:LEU:HD22	1.95	0.49
1:A:664:G:H1	1:A:741:G:H1	1.60	0.49
1:A:1304:G:H21	1:A:1333:A:N6	1.92	0.49
3:03:1100:PRO:CG	4:04:638:SER:HB3	2.43	0.49
4:04:199:GLU:O	4:04:203:GLU:HG3	2.13	0.49
4:04:223:LEU:O	4:04:226:ALA:HB3	2.12	0.49
7:E:126:PHE:HD1	7:E:126:PHE:H	1.59	0.49
8:F:111:ASP:OD2	8:F:113:LYS:HB3	2.12	0.49
15:M:47:GLU:HB2	15:M:67:ILE:HB	1.92	0.49
24:V:10:ILE:C	24:V:10:ILE:HD12	2.32	0.49
24:V:60:PHE:O	24:V:65:MET:HE1	2.12	0.49
25:W:34:VAL:O	25:W:38:ILE:HG13	2.12	0.49
4:04:83:VAL:HB	7:E:75:ALA:HB2	1.92	0.49
18:P:18:LEU:HD12	18:P:29:SER:OG	2.12	0.49
20:R:9:LYS:NZ	20:R:9:LYS:HB3	2.27	0.49
26:X:10:GLU:H	26:X:11:PRO:CD	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1024:G:O2'	1:A:1025:U:H5'	2.12	0.49
1:A:1285:A:H4'	1:A:1286:U:C5'	2.43	0.49
3:03:971:LEU:O	3:03:974:ARG:HB3	2.11	0.49
3:03:1099:ASN:ND2	3:03:1101:LEU:HB2	2.27	0.49
4:04:131:PRO:O	4:04:135:ILE:HG13	2.12	0.49
4:04:141:PHE:HD2	4:04:297:ARG:HH11	1.61	0.49
7:E:217:VAL:O	7:E:221:VAL:HG23	2.12	0.49
8:F:42:LEU:O	8:F:42:LEU:HD23	2.12	0.49
17:O:109:ARG:CB	17:O:118:VAL:HG21	2.43	0.49
19:Q:5:MET:HG2	19:Q:62:ARG:HH11	1.78	0.49
19:Q:56:PRO:HA	19:Q:59:GLN:HG2	1.95	0.49
26:X:10:GLU:N	26:X:11:PRO:CD	2.75	0.49
1:A:419:C:C5'	1:A:513:C:H4'	2.40	0.49
2:01:67:GLU:H	2:01:171:LEU:HD11	1.78	0.49
3:03:816:ILE:HG13	3:03:1074:GLY:HA3	1.93	0.49
3:03:1235:LEU:H	3:03:1235:LEU:CD1	2.26	0.49
7:E:21:ARG:HB3	7:E:38:VAL:HG12	1.94	0.49
9:G:45:PRO:HB2	9:G:47:LEU:HD12	1.95	0.49
26:X:29:LEU:HG	26:X:33:ARG:HD3	1.95	0.49
1:A:834:U:OP1	23:U:49:ALA:HB2	2.13	0.49
3:03:208:ILE:HG13	3:03:354:ASP:OD1	2.13	0.49
3:03:798:GLN:HE22	3:03:827:ARG:HE	1.59	0.49
3:03:801:ARG:HG3	3:03:1094:VAL:HG23	1.95	0.49
3:03:1319:MET:HG3	3:03:1323:PHE:CD2	2.45	0.49
3:03:1338:GLU:HB2	4:04:21:LYS:NZ	2.27	0.49
4:04:430:HIS:HD2	4:04:432:LEU:HB2	1.76	0.49
4:04:643:ASP:HB3	4:04:720:ASN:HD22	1.77	0.49
4:04:1172:LYS:HD3	4:04:1189:MET:HB3	1.94	0.49
10:H:15:ILE:HG23	10:H:109:ALA:HA	1.93	0.49
10:H:111:ARG:O	10:H:115:GLU:HG3	2.13	0.49
19:Q:16:ALA:HA	19:Q:55:SER:HB2	1.95	0.49
25:W:28:ARG:HA	25:W:31:ILE:HD12	1.95	0.49
1:A:751:U:H2'	1:A:752:G:H5'	1.95	0.49
1:A:979:C:N3	19:Q:58:ARG:HG2	2.28	0.49
3:03:302:ILE:HG21	3:03:309:LEU:HD12	1.95	0.49
3:03:1285:TYR:HB2	4:04:1356:LEU:HD21	1.94	0.49
4:04:88:CYS:O	4:04:90:VAL:HG23	2.13	0.49
4:04:263:SER:C	4:04:265:LEU:H	2.16	0.49
4:04:689:ALA:O	4:04:693:VAL:HG23	2.13	0.49
4:04:795:TYR:O	4:04:798:ARG:HB3	2.12	0.49
4:04:896:ALA:HA	4:04:909:ILE:CG2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:29:ILE:HD11	11:I:62:MET:CE	2.43	0.49
24:V:16:LYS:O	24:V:20:LYS:HG3	2.12	0.49
3:03:99:LYS:HA	3:03:120:GLN:HA	1.95	0.48
3:03:721:GLY:HA2	3:03:777:VAL:HG23	1.95	0.48
3:03:723:VAL:HA	3:03:776:PRO:HA	1.95	0.48
3:03:1285:TYR:HE2	4:04:473:THR:HG21	1.78	0.48
4:04:514:THR:HG21	4:04:596:LEU:HB2	1.94	0.48
7:E:45:LYS:O	7:E:49:MET:HB2	2.13	0.48
1:A:361:G:H2'	1:A:362:G:O4'	2.13	0.48
1:A:1319:A:H61	1:A:1361:G:H1'	1.78	0.48
2:01:224:LEU:HD13	2:02:228:LEU:HD12	1.95	0.48
2:02:179:PRO:HA	2:02:208:ASN:HD21	1.77	0.48
3:03:8:LYS:HG3	3:03:1168:GLU:HG3	1.94	0.48
3:03:809:GLY:N	4:04:629:PHE:HB3	2.28	0.48
3:03:886:LYS:N	3:03:917:SER:HA	2.28	0.48
4:04:239:LEU:HD13	4:04:240:THR:N	2.28	0.48
4:04:1255:VAL:O	4:04:1259:GLN:HG2	2.13	0.48
7:E:87:CYS:SG	7:E:222:ARG:HD2	2.53	0.48
8:F:21:TRP:HB3	8:F:58:ARG:HB3	1.94	0.48
13:K:119:GLY:C	13:K:120:LEU:HD12	2.33	0.48
18:P:1:ALA:N	18:P:44:ILE:HD11	2.28	0.48
1:A:346:G:H2'	1:A:347:G:H5'	1.95	0.48
1:A:663:A:H61	1:A:742:G:H1	1.61	0.48
1:A:912:C:O2'	1:A:913:A:H5'	2.14	0.48
3:03:589:THR:HG23	3:03:591:TYR:CE2	2.49	0.48
4:04:365:GLN:HA	4:04:438:GLU:H	1.79	0.48
4:04:369:PRO:HB3	4:04:444:GLY:O	2.13	0.48
7:E:23:TRP:HB2	7:E:189:THR:OG1	2.13	0.48
9:G:82:LYS:HB2	9:G:82:LYS:HZ2	1.78	0.48
12:J:25:PHE:HD1	12:J:100:MET:HB3	1.78	0.48
26:X:43:THR:HA	26:X:46:LYS:HZ1	1.78	0.48
1:A:105:G:OP1	25:W:12:GLN:HG3	2.13	0.48
1:A:762:U:H2'	1:A:763:G:H8	1.77	0.48
1:A:946:A:H2'	1:A:947:G:H8	1.78	0.48
1:A:1379:G:O2'	1:A:1380:U:H5'	2.12	0.48
3:03:103:VAL:C	3:03:104:ILE:HD12	2.33	0.48
4:04:245:LEU:HD23	4:04:250:ARG:HD2	1.94	0.48
4:04:848:VAL:HB	4:04:858:VAL:CG1	2.44	0.48
4:04:850:LYS:HG2	4:04:857:LEU:HD23	1.95	0.48
7:E:19:GLN:HG3	7:E:42:ASN:ND2	2.28	0.48
7:E:35:ARG:HH11	7:E:35:ARG:HG3	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:132:LYS:O	7:E:136:MET:HG3	2.13	0.48
1:A:178:C:C2	1:A:179:A:H1'	2.48	0.48
1:A:179:A:H3'	1:A:180:U:C5	2.49	0.48
1:A:376:G:H2'	1:A:377:G:H5'	1.95	0.48
2:01:12:ARG:H	2:01:30:PRO:HD2	1.78	0.48
3:03:1059:ARG:HH11	3:03:1059:ARG:HG3	1.78	0.48
4:04:86:GLU:CG	26:X:67:ARG:HH22	2.26	0.48
4:04:1242:ARG:NH1	4:04:1247:LYS:HG2	2.22	0.48
5:05:32:VAL:O	5:05:34:GLY:N	2.46	0.48
7:E:43:LEU:CD1	7:E:44:GLU:N	2.76	0.48
12:J:65:LEU:HD21	12:J:96:ASN:ND2	2.28	0.48
15:M:8:ILE:HB	15:M:74:VAL:HB	1.96	0.48
15:M:36:VAL:HG23	15:M:76:ILE:HG12	1.93	0.48
1:A:229:U:H2'	1:A:230:G:C8	2.48	0.48
1:A:443:C:H2'	1:A:444:G:H8	1.78	0.48
1:A:523:A:C2'	1:A:524:G:H5''	2.44	0.48
3:03:885:GLY:HA2	3:03:917:SER:HB3	1.94	0.48
3:03:1107:MET:HB3	4:04:740:LEU:HD13	1.96	0.48
4:04:64:PRO:CG	4:04:93:THR:H	2.26	0.48
4:04:115:TRP:CZ3	4:04:307:LEU:HD13	2.49	0.48
4:04:378:LYS:HA	4:04:381:ILE:HD12	1.94	0.48
4:04:396:ALA:O	4:04:400:MET:HG3	2.13	0.48
4:04:399:LYS:HB3	4:04:403:ARG:HH12	1.79	0.48
5:05:54:ILE:HD13	5:05:59:ILE:O	2.14	0.48
7:E:18:HIS:HA	7:E:40:ILE:CA	2.44	0.48
11:I:62:MET:HG2	11:I:64:VAL:HB	1.94	0.48
1:A:946:A:H2'	1:A:947:G:C8	2.47	0.48
1:A:1261:A:H2'	1:A:1262:C:H5'	1.94	0.48
2:01:81:ILE:HA	2:01:84:ASN:HD22	1.78	0.48
3:03:605:TYR:C	3:03:606:LEU:HD12	2.33	0.48
3:03:816:ILE:HD12	3:03:1066:MET:HB3	1.94	0.48
3:03:1281:TYR:HE2	4:04:434:ILE:HB	1.78	0.48
4:04:200:GLN:HA	4:04:203:GLU:OE1	2.13	0.48
4:04:632:ALA:O	4:04:635:SER:HB3	2.14	0.48
4:04:958:ILE:HD12	4:04:982:LEU:CD1	2.38	0.48
8:F:152:VAL:HG23	8:F:165:GLU:HB3	1.95	0.48
12:J:56:SER:OG	12:J:59:GLU:HG2	2.13	0.48
14:L:104:THR:HG22	14:L:106:ASP:H	1.79	0.48
19:Q:60:ARG:HG2	19:Q:62:ARG:NH2	2.19	0.48
1:A:219:U:C3'	1:A:220:G:H5''	2.44	0.48
3:03:815:SER:HA	3:03:1075:VAL:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:87:VAL:O	10:H:87:VAL:HG13	2.12	0.48
15:M:9:ARG:HA	15:M:72:ARG:O	2.13	0.48
16:N:44:ALA:HB1	16:N:68:ARG:HB3	1.95	0.48
17:O:29:LYS:HZ1	17:O:58:ASN:ND2	2.10	0.48
17:O:43:LYS:CG	17:O:44:PRO:HD3	2.37	0.48
26:X:10:GLU:HA	26:X:12:PHE:CE1	2.49	0.48
2:01:26:VAL:CG2	2:01:203:ILE:HB	2.44	0.48
3:03:39:ILE:HG23	3:03:39:ILE:O	2.14	0.48
3:03:109:ALA:C	3:03:111:GLU:H	2.17	0.48
3:03:455:SER:O	3:03:459:MET:HG3	2.14	0.48
3:03:960:LEU:HD11	3:03:1028:LYS:CB	2.43	0.48
4:04:385:LEU:HD11	4:04:408:VAL:HG12	1.95	0.48
4:04:1306:LEU:HD23	4:04:1307:LEU:N	2.29	0.48
6:B:171:UNK:O	6:B:172:UNK:C	2.61	0.48
7:E:16:PHE:CD1	7:E:16:PHE:N	2.79	0.48
7:E:18:HIS:HA	7:E:40:ILE:HA	1.96	0.48
11:I:60:VAL:C	11:I:61:LEU:HD12	2.34	0.48
14:L:49:GLN:HA	14:L:52:GLU:OE1	2.12	0.48
16:N:113:THR:O	16:N:115:ILE:HG13	2.14	0.48
18:P:9:PRO:HG3	18:P:17:ALA:O	2.14	0.48
23:U:49:ALA:HA	23:U:52:GLN:HB3	1.96	0.48
1:A:66:A:H1'	1:A:173:U:H2'	1.95	0.48
1:A:105:G:H22	1:A:379:C:H4'	1.78	0.48
1:A:557:G:H2'	1:A:558:G:O4'	2.13	0.48
1:A:865:A:O2'	1:A:866:C:H5'	2.12	0.48
1:A:1373:G:H5''	12:J:35:LYS:HD2	1.95	0.48
3:03:678:ARG:NH2	3:03:1106:ARG:NH1	2.62	0.48
4:04:1046:ILE:HD12	4:04:1059:LEU:HB3	1.94	0.48
4:04:1358:PRO:HB3	4:04:1366:HIS:CD2	2.49	0.48
5:05:38:LEU:N	5:05:38:LEU:HD12	2.28	0.48
9:G:167:PRO:HB2	9:G:170:LEU:HB2	1.95	0.48
11:I:40:GLU:HB3	11:I:61:LEU:HB2	1.95	0.48
17:O:113:ARG:HH12	17:O:120:ARG:HH11	1.61	0.48
25:W:35:TYR:CZ	25:W:78:LEU:HD13	2.49	0.48
1:A:176:C:H5'	25:W:19:HIS:NE2	2.29	0.47
1:A:571:U:H2'	1:A:572:A:H5''	1.96	0.47
1:A:1356:G:H2'	1:A:1357:A:C8	2.49	0.47
3:03:135:THR:HB	3:03:142:GLU:HB3	1.96	0.47
3:03:557:ARG:HD2	3:03:557:ARG:N	2.29	0.47
4:04:66:LYS:HB3	4:04:69:GLU:HB2	1.94	0.47
4:04:153:ASN:HB3	4:04:154:LEU:HD12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:1253:ILE:O	4:04:1257:VAL:HG23	2.14	0.47
7:E:183:VAL:HB	7:E:196:VAL:HA	1.95	0.47
14:L:29:ILE:HG12	14:L:78:ILE:HD11	1.95	0.47
25:W:54:GLN:C	25:W:56:ILE:H	2.16	0.47
1:A:1318:A:H2'	1:A:1319:A:H5'	1.96	0.47
3:03:1258:PRO:HG3	4:04:346:ARG:HG2	1.96	0.47
4:04:796:LEU:HD22	4:04:1138:LEU:HD11	1.96	0.47
5:05:29:GLN:O	5:05:32:VAL:O	2.32	0.47
7:E:73:LYS:HE3	26:X:67:ARG:HH11	1.79	0.47
7:E:135:LEU:O	7:E:139:ARG:HG2	2.14	0.47
9:G:37:PRO:HD2	9:G:41:GLY:CA	2.44	0.47
10:H:40:ASP:OD1	10:H:44:ARG:HB3	2.14	0.47
12:J:59:GLU:O	12:J:63:VAL:HG23	2.13	0.47
15:M:6:ILE:HD13	15:M:87:LEU:HD11	1.96	0.47
25:W:68:LYS:HB2	25:W:68:LYS:HZ2	1.77	0.47
2:02:79:LEU:HD11	4:04:526:VAL:HG11	1.96	0.47
3:03:103:VAL:HG12	3:03:116:ASP:HA	1.96	0.47
3:03:1053:TYR:C	3:03:1054:LEU:HD12	2.35	0.47
3:03:1323:PHE:O	3:03:1327:LEU:HD13	2.14	0.47
4:04:168:ALA:O	4:04:172:PHE:HB2	2.15	0.47
4:04:315:ALA:O	4:04:324:LEU:HG	2.14	0.47
4:04:423:LEU:HD12	4:04:423:LEU:N	2.29	0.47
4:04:857:LEU:HD12	4:04:858:VAL:HG12	1.96	0.47
9:G:142:VAL:O	9:G:142:VAL:HG13	2.14	0.47
14:L:117:LEU:HD13	14:L:120:ALA:O	2.14	0.47
24:V:40:PHE:H	24:V:43:MET:HE2	1.79	0.47
1:A:161:A:N6	1:A:347:G:H21	2.08	0.47
1:A:837:U:H2'	1:A:838:G:H8	1.78	0.47
1:A:1395:C:H2'	1:A:1396:A:H8	1.80	0.47
2:01:215:GLU:O	2:01:219:ARG:HG3	2.13	0.47
3:03:109:ALA:O	3:03:111:GLU:N	2.44	0.47
3:03:811:ASN:HA	3:03:815:SER:O	2.14	0.47
3:03:1273:MET:HA	3:03:1276:TRP:CE3	2.49	0.47
4:04:47:ARG:HA	4:04:47:ARG:HE	1.78	0.47
4:04:537:TYR:CD2	4:04:544:LEU:HD13	2.48	0.47
7:E:108:ARG:HA	7:E:111:ILE:HB	1.97	0.47
11:I:61:LEU:HD12	11:I:61:LEU:N	2.30	0.47
19:Q:11:LYS:O	19:Q:15:LEU:HD13	2.15	0.47
20:R:30:LEU:O	20:R:34:GLN:HB2	2.15	0.47
1:A:577:G:C1'	1:A:816:A:H2'	2.45	0.47
1:A:626:G:H2'	1:A:627:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:826:C:H2'	1:A:827:U:C6	2.49	0.47
1:A:1066:C:H2'	1:A:1067:A:O4'	2.15	0.47
2:01:234:LEU:HD22	2:01:234:LEU:N	2.30	0.47
3:03:414:ILE:HD12	3:03:415:GLU:HB3	1.95	0.47
3:03:463:GLN:HG3	3:03:505:PHE:CD1	2.49	0.47
3:03:671:LEU:O	3:03:672:GLU:C	2.52	0.47
3:03:1194:GLU:O	3:03:1198:LEU:HD23	2.15	0.47
4:04:563:LEU:HD12	4:04:563:LEU:N	2.29	0.47
4:04:721:SER:HA	4:04:724:MET:CE	2.45	0.47
4:04:1306:LEU:C	4:04:1307:LEU:HD12	2.35	0.47
7:E:56:GLU:O	7:E:60:ILE:HG12	2.15	0.47
13:K:13:ILE:O	13:K:17:GLN:HG2	2.14	0.47
14:L:43:ALA:HB1	14:L:46:VAL:CG2	2.44	0.47
1:A:187:G:H1'	25:W:79:THR:HG21	1.95	0.47
2:01:218:ARG:NH1	2:02:231:PHE:HA	2.28	0.47
3:03:138:ILE:HG22	3:03:139:ASN:ND2	2.28	0.47
3:03:398:SER:C	3:03:400:VAL:H	2.18	0.47
4:04:147:ILE:HG22	4:04:188:LEU:HG	1.97	0.47
4:04:680:ASN:O	4:04:683:ILE:HB	2.15	0.47
7:E:41:ILE:HG21	7:E:43:LEU:HD23	1.96	0.47
7:E:170:HIS:HA	7:E:173:ILE:HD12	1.96	0.47
8:F:111:ASP:O	8:F:115:VAL:HG23	2.14	0.47
17:O:63:THR:HG23	17:O:92:VAL:HA	1.96	0.47
1:A:320:A:H2'	1:A:321:A:C8	2.50	0.47
1:A:909:A:H2'	1:A:910:C:O4'	2.14	0.47
1:A:1323:G:H2'	1:A:1324:A:C8	2.50	0.47
1:A:1513:A:H2'	1:A:1514:G:C8	2.50	0.47
2:01:54:CYS:SG	2:01:92:VAL:HG22	2.55	0.47
3:03:145:ILE:HG12	3:03:512:SER:CB	2.44	0.47
3:03:530:ILE:HD11	3:03:575:LEU:HD13	1.96	0.47
3:03:1106:ARG:HD2	3:03:1106:ARG:H	1.78	0.47
4:04:490:ILE:O	4:04:498:PRO:HA	2.13	0.47
4:04:514:THR:HG23	4:04:514:THR:O	2.14	0.47
4:04:859:PRO:HG2	4:04:862:THR:OG1	2.15	0.47
5:05:26:ARG:O	5:05:30:MET:HG3	2.14	0.47
5:05:50:ALA:O	5:05:54:ILE:HG12	2.15	0.47
7:E:44:GLU:O	7:E:48:PRO:CD	2.62	0.47
8:F:20:THR:HG22	15:M:95:GLY:HA3	1.96	0.47
18:P:14:ALA:HB2	18:P:47:LEU:HD21	1.97	0.47
19:Q:26:LEU:HD13	19:Q:43:ALA:O	2.14	0.47
21:S:5:ARG:HD3	21:S:5:ARG:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:39:G:C2'	1:A:40:C:H5''	2.44	0.47
1:A:168:G:O2'	1:A:169:C:H5'	2.14	0.47
1:A:545:C:O2'	1:A:546:A:H5'	2.15	0.47
1:A:1128:C:O2'	1:A:1129:C:H5'	2.15	0.47
2:01:150:ARG:HH11	2:01:150:ARG:HG3	1.79	0.47
2:01:207:THR:HG22	2:01:208:ASN:N	2.29	0.47
2:02:86:LYS:HG2	2:02:173:VAL:HB	1.97	0.47
2:02:163:GLU:HA	2:02:167:PRO:HD2	1.97	0.47
3:03:433:ILE:O	3:03:437:ASN:ND2	2.47	0.47
3:03:619:ALA:HB2	3:03:654:ASP:HB3	1.96	0.47
4:04:1179:PRO:HG2	4:04:1183:SER:O	2.14	0.47
7:E:71:GLY:HA2	7:E:164:ILE:HB	1.96	0.47
12:J:30:MET:HA	12:J:38:ALA:CB	2.45	0.47
12:J:113:LYS:HD2	12:J:117:LEU:HD23	1.97	0.47
19:Q:12:ARG:HH11	19:Q:12:ARG:HG3	1.80	0.47
1:A:614:C:H3'	1:A:615:G:H5''	1.96	0.47
3:03:4:SER:HB2	3:03:7:GLU:HG2	1.96	0.47
3:03:670:PHE:HB3	3:03:673:HIS:CD2	2.48	0.47
4:04:409:TRP:O	4:04:412:LEU:HB3	2.15	0.47
4:04:733:SER:O	4:04:737:ILE:HG12	2.14	0.47
6:B:3:GLU:O	6:B:7:GLN:HG3	2.15	0.47
7:E:74:ARG:HA	7:E:74:ARG:HE	1.80	0.47
3:03:1064:ASP:OD1	3:03:1234:LYS:HE3	2.15	0.47
4:04:449:LEU:HG	4:04:450:HIS:N	2.30	0.47
4:04:504:GLN:O	4:04:507:VAL:HG22	2.14	0.47
4:04:631:TYR:HA	4:04:634:ARG:HB2	1.97	0.47
7:E:145:GLU:O	7:E:149:GLY:HA3	2.14	0.47
8:F:32:LEU:O	8:F:32:LEU:HD23	2.14	0.47
12:J:72:VAL:HG21	12:J:144:ALA:HB2	1.97	0.47
2:01:79:LEU:HD13	2:01:79:LEU:C	2.35	0.46
2:01:102:LEU:HD21	2:01:110:VAL:HG11	1.97	0.46
2:02:98:VAL:HG13	2:02:100:LEU:HD11	1.96	0.46
3:03:30:ILE:HA	3:03:581:THR:OG1	2.15	0.46
3:03:719:LYS:HD2	3:03:719:LYS:N	2.31	0.46
3:03:1308:ILE:C	3:03:1310:ASP:H	2.18	0.46
4:04:92:VAL:O	4:04:92:VAL:HG23	2.15	0.46
4:04:506:VAL:HG13	4:04:507:VAL:N	2.29	0.46
7:E:27:MET:HG3	7:E:191:SER:H	1.80	0.46
7:E:44:GLU:O	7:E:46:THR:N	2.48	0.46
8:F:21:TRP:CB	8:F:58:ARG:HB3	2.45	0.46
9:G:130:ASN:O	9:G:131:ILE:HD13	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:93:VAL:HG22	10:H:126:ALA:HA	1.97	0.46
16:N:63:GLN:O	16:N:67:GLU:HG2	2.14	0.46
1:A:505:G:H2'	1:A:506:G:H8	1.81	0.46
1:A:618:C:H5''	1:A:620:C:OP2	2.14	0.46
1:A:1218:C:H2'	1:A:1219:A:C8	2.50	0.46
2:02:92:VAL:HA	2:02:120:ASP:O	2.15	0.46
2:02:182:ARG:HH11	2:02:182:ARG:HG3	1.81	0.46
3:03:101:ARG:HG2	3:03:103:VAL:HG13	1.96	0.46
4:04:502:PRO:HG2	4:04:601:ILE:CD1	2.45	0.46
4:04:865:HIS:HA	4:04:901:ARG:HH21	1.80	0.46
4:04:1184:ASP:N	4:04:1185:PRO:HD2	2.30	0.46
9:G:120:LYS:O	9:G:147:LYS:HD3	2.15	0.46
13:K:124:ILE:HG13	13:K:124:ILE:O	2.15	0.46
15:M:70:HIS:HB3	15:M:72:ARG:HH12	1.78	0.46
23:U:38:LYS:HB2	23:U:38:LYS:NZ	2.31	0.46
25:W:38:ILE:HG21	25:W:81:GLN:NE2	2.12	0.46
1:A:10:A:H2'	1:A:11:G:C8	2.50	0.46
1:A:1210:C:C2'	1:A:1211:U:H5'	2.45	0.46
1:A:1355:G:H2'	1:A:1356:G:H8	1.78	0.46
1:A:1393:U:H2'	1:A:1395:C:C5	2.45	0.46
1:A:1520:C:H2'	1:A:1521:C:C6	2.50	0.46
3:03:712:SER:HB3	3:03:714:VAL:HG22	1.97	0.46
3:03:855:PRO:HD2	3:03:915:ASP:HB2	1.96	0.46
3:03:1328:LYS:NZ	4:04:246:PRO:HD3	2.30	0.46
7:E:188:ASP:O	7:E:190:ASN:N	2.48	0.46
9:G:8:LEU:O	9:G:12:ARG:HG3	2.15	0.46
9:G:148:ALA:O	9:G:154:VAL:HG21	2.15	0.46
10:H:37:VAL:HG11	10:H:113:VAL:HG13	1.96	0.46
13:K:107:LYS:NZ	13:K:107:LYS:HB3	2.29	0.46
14:L:114:LYS:HE3	14:L:117:LEU:CD1	2.46	0.46
17:O:85:ARG:HA	17:O:93:ARG:HA	1.97	0.46
1:A:348:G:H2'	1:A:349:A:H8	1.79	0.46
1:A:1258:G:H2'	1:A:1259:C:C6	2.51	0.46
2:01:156:SER:O	2:01:159:ILE:HG22	2.15	0.46
2:02:10:LYS:N	2:02:10:LYS:HD2	2.30	0.46
3:03:29:SER:HB3	3:03:33:ASP:HB2	1.96	0.46
3:03:720:ARG:HD2	3:03:736:VAL:HG11	1.97	0.46
4:04:196:GLN:OE1	4:04:196:GLN:HA	2.15	0.46
4:04:370:LYS:HD3	4:04:443:GLU:HG2	1.98	0.46
4:04:1223:LEU:O	4:04:1223:LEU:HD13	2.14	0.46
7:E:16:PHE:HD2	7:E:41:ILE:HD12	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:101:LEU:HD23	7:E:175:GLU:O	2.14	0.46
8:F:11:LEU:HB3	8:F:17:TRP:NE1	2.30	0.46
1:A:147:G:H2'	1:A:148:G:C8	2.50	0.46
1:A:523:A:O2'	1:A:524:G:H5''	2.16	0.46
1:A:879:C:H2'	1:A:880:C:H6	1.81	0.46
2:01:11:PRO:HG3	2:02:227:GLN:HA	1.97	0.46
2:01:195:ARG:HE	2:01:196:THR:H	1.63	0.46
2:02:65:LEU:HD22	2:02:65:LEU:H	1.80	0.46
3:03:468:LEU:O	3:03:472:GLU:HB2	2.16	0.46
3:03:926:GLY:HA2	3:03:1056:VAL:HG22	1.97	0.46
3:03:934:PHE:O	3:03:1048:LYS:HA	2.15	0.46
3:03:956:ALA:O	3:03:960:LEU:HD23	2.15	0.46
3:03:1032:LYS:O	3:03:1036:ILE:HG13	2.16	0.46
3:03:1196:LYS:HB3	3:03:1200:LYS:HZ3	1.80	0.46
3:03:1286:THR:O	3:03:1290:MET:HB2	2.15	0.46
7:E:40:ILE:HG13	7:E:41:ILE:HG12	1.97	0.46
8:F:37:LYS:HD3	8:F:40:GLN:NE2	2.31	0.46
8:F:82:ASP:O	8:F:86:LEU:HG	2.16	0.46
21:S:36:VAL:HG13	21:S:36:VAL:O	2.15	0.46
1:A:302:G:H2'	1:A:303:A:C8	2.51	0.46
1:A:662:U:H2'	1:A:663:A:C8	2.50	0.46
2:02:80:GLU:HG2	4:04:569:LEU:HD21	1.96	0.46
2:02:172:LEU:HD23	2:02:172:LEU:N	2.30	0.46
3:03:498:ILE:O	3:03:502:VAL:HG12	2.15	0.46
3:03:593:LYS:HB3	3:03:602:GLU:HB2	1.98	0.46
3:03:675:ASP:HB2	3:03:1107:MET:HB2	1.98	0.46
4:04:195:GLU:HA	4:04:198:CYS:SG	2.55	0.46
4:04:395:LYS:HA	4:04:398:LYS:CE	2.45	0.46
4:04:909:ILE:CD1	4:04:913:GLU:HG2	2.39	0.46
15:M:102:LEU:HD23	15:M:102:LEU:N	2.25	0.46
16:N:122:PRO:HB3	26:X:32:VAL:HA	1.96	0.46
1:A:252:U:O2	1:A:252:U:C2'	2.64	0.46
1:A:346:G:C2'	1:A:347:G:H5'	2.46	0.46
2:01:89:ALA:HB1	2:01:208:ASN:ND2	2.31	0.46
3:03:392:GLU:OE1	3:03:419:ILE:HG23	2.16	0.46
3:03:702:THR:HA	3:03:1184:THR:H	1.81	0.46
4:04:255:LEU:HD13	4:04:256:ASP:N	2.31	0.46
4:04:863:LEU:HD21	4:04:901:ARG:HD3	1.96	0.46
8:F:57:GLU:HB2	8:F:64:ARG:HB3	1.97	0.46
3:03:320:ASP:O	3:03:324:LYS:HG3	2.15	0.46
3:03:360:LEU:O	3:03:364:VAL:HG23	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:1087:TYR:HB2	3:03:1091:GLY:HA2	1.97	0.46
3:03:1104:PRO:HB3	4:04:722:ILE:HG13	1.97	0.46
4:04:220:ARG:HG2	4:04:220:ARG:HH11	1.80	0.46
4:04:472:LEU:H	4:04:472:LEU:CD2	2.25	0.46
4:04:1233:ILE:O	4:04:1237:VAL:HG12	2.15	0.46
4:04:1314:LEU:HD11	4:04:1330:ARG:HH12	1.81	0.46
7:E:31:ILE:HG21	7:E:189:THR:HG22	1.98	0.46
26:X:17:ARG:HE	26:X:21:ARG:HH22	1.64	0.46
1:A:247:G:H2'	1:A:248:C:C6	2.51	0.46
1:A:285:C:H2'	1:A:286:C:C6	2.51	0.46
1:A:977:A:H4'	1:A:981:U:H3	1.81	0.46
3:03:241:LEU:O	3:03:243:PRO:HD3	2.16	0.46
3:03:696:ASP:HB3	3:03:798:GLN:HA	1.98	0.46
4:04:134:ASP:O	4:04:138:VAL:HG23	2.15	0.46
4:04:290:ILE:H	4:04:290:ILE:CD1	2.14	0.46
4:04:1323:ALA:N	4:04:1331:VAL:HG21	2.31	0.46
9:G:36:ALA:HA	9:G:41:GLY:HA3	1.98	0.46
13:K:76:ARG:HA	13:K:126:CYS:HB3	1.97	0.46
25:W:24:ARG:CB	25:W:28:ARG:HH22	2.27	0.46
1:A:39:G:H2'	1:A:40:C:C5'	2.46	0.46
1:A:751:U:C2'	1:A:752:G:H5'	2.46	0.46
1:A:824:G:H1'	13:K:1:S:SER:HA	1.97	0.46
1:A:1157:A:N6	1:A:1178:G:H1'	2.31	0.46
2:01:124:VAL:HG13	2:01:125:LYS:HG2	1.98	0.46
3:03:7:GLU:OE1	3:03:11:ILE:HD12	2.16	0.46
3:03:434:ASP:HA	3:03:437:ASN:ND2	2.27	0.46
3:03:880:GLY:HA2	3:03:920:VAL:O	2.16	0.46
3:03:1105:SER:HB2	4:04:731:ARG:O	2.17	0.46
4:04:555:TYR:HD2	4:04:585:LYS:HB3	1.81	0.46
7:E:27:MET:C	7:E:29:PRO:HD2	2.36	0.46
7:E:54:LEU:CD2	7:E:220:THR:HG21	2.39	0.46
8:F:23:ALA:HB3	8:F:28:PHE:HD1	1.81	0.46
10:H:104:ILE:HA	10:H:122:VAL:O	2.16	0.46
13:K:54:THR:HG23	13:K:55:LYS:HG3	1.98	0.46
21:S:32:PHE:H	21:S:32:PHE:HD1	1.64	0.46
1:A:1368:A:O2'	1:A:1369:C:H5'	2.15	0.45
2:01:45:ARG:HD3	3:03:1083:GLU:HB3	1.97	0.45
3:03:124:MET:HG2	3:03:493:ILE:HG12	1.97	0.45
3:03:533:LEU:HD11	3:03:571:LEU:HD13	1.97	0.45
4:04:382:TYR:O	4:04:386:GLU:HG2	2.16	0.45
4:04:1223:LEU:HD13	4:04:1223:LEU:C	2.36	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:52:LEU:HD21	15:M:59:LYS:HE2	1.98	0.45
21:S:70:ARG:HG2	21:S:70:ARG:HH11	1.80	0.45
23:U:40:VAL:HA	23:U:41:PRO:HD3	1.77	0.45
26:X:10:GLU:HA	26:X:12:PHE:HE1	1.81	0.45
1:A:648:A:H2'	1:A:649:A:C8	2.52	0.45
1:A:750:C:O2	20:R:22:GLY:HA3	2.16	0.45
1:A:770:C:H2'	1:A:771:G:H8	1.81	0.45
1:A:1372:U:OP1	14:L:73:GLY:N	2.49	0.45
2:01:145:LYS:NZ	2:01:147:GLN:HB3	2.31	0.45
2:01:166:ARG:N	2:01:167:PRO:CD	2.79	0.45
2:02:111:THR:HA	2:02:129:VAL:HA	1.97	0.45
3:03:33:ASP:HA	3:03:36:GLN:CB	2.46	0.45
3:03:213:LEU:O	3:03:213:LEU:HD23	2.16	0.45
3:03:515:MET:HA	3:03:526:HIS:ND1	2.32	0.45
3:03:582:ASN:HB2	3:03:588:GLU:HG2	1.97	0.45
3:03:753:LEU:HB3	3:03:767:GLN:HB2	1.97	0.45
3:03:1025:PHE:O	3:03:1029:LEU:HD13	2.16	0.45
4:04:399:LYS:O	4:04:402:GLU:HB3	2.16	0.45
4:04:547:ARG:HG3	4:04:547:ARG:NH1	2.31	0.45
4:04:661:VAL:HG12	4:04:685:ILE:HD11	1.99	0.45
4:04:796:LEU:O	4:04:800:LEU:HD13	2.16	0.45
4:04:1304:ARG:HG3	4:04:1304:ARG:NH1	2.30	0.45
4:04:1353:VAL:HG22	4:04:1353:VAL:O	2.16	0.45
7:E:28:LYS:O	7:E:29:PRO:C	2.53	0.45
12:J:78:ARG:HH11	12:J:78:ARG:HG3	1.81	0.45
26:X:42:THR:HG22	26:X:46:LYS:HZ3	1.81	0.45
1:A:194:C:O2	25:W:62:ALA:HB3	2.16	0.45
1:A:376:G:H2'	1:A:377:G:H5''	1.98	0.45
1:A:782:A:H62	1:A:800:G:H21	1.64	0.45
1:A:789:U:HO2'	1:A:790:A:H8	1.63	0.45
1:A:981:U:H4'	19:Q:62:ARG:NH2	2.31	0.45
2:02:158:ARG:HA	2:02:158:ARG:HE	1.80	0.45
2:02:192:VAL:O	2:02:192:VAL:HG12	2.16	0.45
3:03:589:THR:HA	3:03:590:PRO:HD3	1.82	0.45
3:03:738:GLU:HA	3:03:741:MET:CB	2.46	0.45
3:03:817:LEU:HD21	3:03:1080:ASN:HD22	1.81	0.45
4:04:86:GLU:HG2	26:X:67:ARG:NH2	2.31	0.45
4:04:309:ASN:HB3	4:04:314:ARG:HA	1.98	0.45
4:04:767:LEU:HD23	4:04:767:LEU:N	2.32	0.45
4:04:1040:MET:C	4:04:1041:ILE:HD12	2.37	0.45
7:E:20:THR:O	7:E:23:TRP:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:130:THR:HG22	7:E:132:LYS:H	1.81	0.45
9:G:58:GLN:O	9:G:62:ARG:HG2	2.16	0.45
10:H:87:VAL:HA	10:H:91:SER:O	2.15	0.45
12:J:30:MET:HG3	12:J:30:MET:O	2.17	0.45
1:A:242:G:H2'	1:A:243:A:H5'	1.98	0.45
1:A:881:G:O2'	1:A:882:C:H5'	2.17	0.45
1:A:1092:A:OP2	12:J:3:ARG:HD3	2.15	0.45
3:03:182:SER:HB2	3:03:389:PHE:HE1	1.82	0.45
3:03:367:TYR:HB3	3:03:376:PRO:HB3	1.97	0.45
4:04:320:ASN:ND2	4:04:321:LYS:N	2.65	0.45
4:04:769:VAL:O	4:04:772:TYR:HB3	2.17	0.45
7:E:20:THR:O	7:E:21:ARG:C	2.55	0.45
7:E:114:LEU:HD13	7:E:144:LEU:HB3	1.98	0.45
10:H:151:MET:O	10:H:155:LYS:HG3	2.15	0.45
14:L:83:THR:HG22	14:L:94:ARG:HH22	1.82	0.45
19:Q:77:GLY:O	19:Q:78:LEU:HD23	2.16	0.45
1:A:961:U:H2'	1:A:962:C:O4'	2.17	0.45
1:A:1066:C:H42	1:A:1191:A:H62	1.63	0.45
3:03:402:ARG:HG3	3:03:406:ASN:HD21	1.81	0.45
4:04:53:ARG:O	4:04:54:ASP:HB2	2.16	0.45
4:04:405:GLU:O	4:04:408:VAL:HG22	2.17	0.45
4:04:1196:LEU:HD12	4:04:1210:ILE:HG22	1.98	0.45
5:05:27:ALA:O	5:05:31:GLN:HG3	2.16	0.45
11:I:45:ARG:HG2	11:I:45:ARG:HH11	1.81	0.45
20:R:61:GLN:O	20:R:65:LEU:HB2	2.16	0.45
21:S:47:GLU:OE1	21:S:47:GLU:N	2.49	0.45
23:U:12:ARG:HH21	23:U:12:ARG:HG2	1.81	0.45
1:A:128:G:O2'	1:A:129:A:H5'	2.16	0.45
1:A:594:U:O2'	1:A:595:A:H5'	2.17	0.45
1:A:686:U:H1'	16:N:43:TRP:HE1	1.82	0.45
1:A:770:C:H1'	1:A:900:A:C2	2.46	0.45
2:01:99:ILE:HA	2:01:144:ILE:O	2.17	0.45
3:03:54:ARG:HH11	3:03:54:ARG:CB	2.30	0.45
3:03:699:LEU:HG	3:03:799:ASN:ND2	2.32	0.45
4:04:75:TYR:HB3	4:04:80:HIS:CG	2.52	0.45
9:G:23:GLY:HA2	9:G:160:LEU:HD11	1.99	0.45
9:G:98:ASP:OD1	9:G:132:ALA:HB1	2.16	0.45
17:O:88:ASP:C	17:O:89:LEU:HD12	2.37	0.45
23:U:26:ILE:O	23:U:30:LYS:HG3	2.16	0.45
24:V:18:VAL:O	24:V:21:ALA:HB3	2.16	0.45
26:X:47:ARG:HH11	26:X:47:ARG:HG3	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:C:H2'	1:A:137:U:H5''	1.97	0.45
1:A:337:G:H2'	1:A:338:A:C8	2.52	0.45
1:A:1250:A:H2'	1:A:1251:A:C8	2.52	0.45
1:A:1514:G:H2'	1:A:1515:G:C8	2.52	0.45
2:02:35:PHE:HA	2:02:38:THR:CG2	2.35	0.45
3:03:232:ILE:HG12	3:03:237:LEU:HD23	1.98	0.45
3:03:521:LEU:C	3:03:521:LEU:HD13	2.37	0.45
4:04:106:GLU:O	4:04:280:LYS:HD3	2.17	0.45
4:04:926:PRO:HG2	4:04:1248:ILE:CD1	2.46	0.45
11:I:18:VAL:HG12	11:I:19:PRO:HD3	1.98	0.45
11:I:47:LEU:H	11:I:56:LYS:H	1.65	0.45
13:K:31:LEU:N	13:K:31:LEU:HD12	2.32	0.45
14:L:34:LEU:C	14:L:34:LEU:HD23	2.36	0.45
16:N:72:ALA:H	16:N:74:LYS:NZ	2.14	0.45
18:P:3:ILE:HG22	18:P:56:ARG:HB2	1.97	0.45
18:P:15:VAL:O	18:P:19:THR:HG23	2.16	0.45
1:A:586:C:H2'	1:A:587:G:O4'	2.16	0.45
1:A:1238:A:C2'	1:A:1239:A:H5'	2.46	0.45
3:03:207:THR:HG22	3:03:210:LEU:HD12	1.98	0.45
3:03:421:SER:O	3:03:425:ILE:HG13	2.17	0.45
3:03:551:HIS:HA	3:03:552:PRO:HD3	1.85	0.45
3:03:642:SER:HB3	4:04:770:LEU:HD23	1.99	0.45
3:03:1184:THR:HA	3:03:1185:PRO:HD3	1.87	0.45
4:04:337:ARG:HD2	4:04:337:ARG:N	2.26	0.45
4:04:647:PRO:C	4:04:649:LYS:H	2.19	0.45
4:04:1219:ASP:O	4:04:1223:LEU:HB3	2.17	0.45
7:E:104:TRP:O	7:E:108:ARG:HG3	2.16	0.45
9:G:13:ARG:CZ	9:G:37:PRO:HB2	2.46	0.45
9:G:196:GLU:N	9:G:196:GLU:OE1	2.49	0.45
14:L:53:LEU:HD13	14:L:96:GLU:O	2.17	0.45
1:A:107:G:O6	25:W:6:ALA:HB1	2.16	0.45
1:A:173:U:H3	1:A:198:G:H21	1.65	0.45
1:A:1270:G:H2'	1:A:1271:A:H8	1.80	0.45
2:01:140:ILE:O	2:01:140:ILE:HG13	2.17	0.45
2:02:64:VAL:HG23	2:02:71:LYS:HD3	1.99	0.45
3:03:75:LEU:N	3:03:75:LEU:HD22	2.31	0.45
3:03:75:LEU:HD11	3:03:127:ILE:HD11	1.98	0.45
3:03:273:HIS:O	3:03:277:LEU:HG	2.17	0.45
3:03:903:ARG:NH2	3:03:908:GLU:HG3	2.32	0.45
4:04:769:VAL:HG12	4:04:773:PHE:CE2	2.52	0.45
4:04:848:VAL:HB	4:04:858:VAL:HG12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:25:PRO:HB2	7:E:28:LYS:CB	2.22	0.45
10:H:159:SER:HB3	10:H:162:GLU:CB	2.47	0.45
19:Q:23:ARG:HH11	19:Q:23:ARG:HG3	1.82	0.45
24:V:10:ILE:HG21	24:V:40:PHE:CE1	2.51	0.45
25:W:76:ALA:C	25:W:78:LEU:N	2.70	0.45
1:A:242:G:C2'	1:A:243:A:H5'	2.47	0.45
1:A:917:G:H2'	1:A:918:A:H8	1.82	0.45
2:O2:17:GLU:OE1	2:O2:25:LYS:HD3	2.15	0.45
3:O3:637:ARG:HA	3:O3:641:GLU:O	2.17	0.45
4:O4:45:ASN:HB2	4:O4:48:THR:O	2.17	0.45
4:O4:287:ALA:HB1	4:O4:288:PRO:HD2	1.99	0.45
4:O4:968:ASN:ND2	4:O4:974:VAL:HG13	2.31	0.45
10:H:9:GLU:OE1	10:H:9:GLU:N	2.50	0.45
18:P:22:TYR:HB3	18:P:65:GLU:HG2	1.99	0.45
1:A:219:U:C2'	1:A:220:G:H5''	2.47	0.44
2:O2:51:MET:H	2:O2:151:GLY:HA2	1.81	0.44
3:O3:451:ARG:HG3	3:O3:451:ARG:HH11	1.82	0.44
3:O3:1023:HIS:O	3:O3:1027:LYS:HG2	2.18	0.44
4:O4:378:LYS:HB2	4:O4:379:PRO:HD3	1.97	0.44
4:O4:620:PHE:O	4:O4:624:ILE:HG13	2.17	0.44
4:O4:1151:LYS:O	4:O4:1153:PRO:HD3	2.17	0.44
7:E:74:ARG:HH21	7:E:77:SER:HB3	1.82	0.44
12:J:70:PRO:HG3	12:J:102:TRP:HZ3	1.82	0.44
17:O:43:LYS:HG3	17:O:44:PRO:CD	2.41	0.44
1:A:7:A:O2'	10:H:125:LYS:HB2	2.17	0.44
1:A:932:C:OP2	12:J:2:ARG:HB3	2.17	0.44
3:O3:26:TYR:CE2	3:O3:32:LEU:HD13	2.50	0.44
3:O3:636:CYS:HB2	3:O3:645:PHE:CD2	2.52	0.44
4:O4:122:SER:OG	4:O4:125:GLY:HA3	2.18	0.44
4:O4:242:LEU:HD23	4:O4:242:LEU:C	2.37	0.44
4:O4:1350:ASN:HB2	4:O4:1357:ILE:HG22	1.98	0.44
7:E:24:ASN:HA	7:E:25:PRO:HD2	1.61	0.44
7:E:34:ALA:O	7:E:40:ILE:HG13	2.17	0.44
8:F:41:TYR:CE2	8:F:89:VAL:HG11	2.51	0.44
8:F:86:LEU:O	8:F:90:VAL:HG23	2.16	0.44
8:F:156:LEU:HD12	8:F:156:LEU:O	2.17	0.44
16:N:21:HIS:HA	16:N:84:MET:O	2.17	0.44
19:Q:12:ARG:O	19:Q:16:ALA:HB2	2.18	0.44
22:T:44:HIS:HB2	22:T:69:THR:O	2.17	0.44
1:A:200:G:H2'	1:A:201:G:H8	1.81	0.44
1:A:744:C:H2'	1:A:745:G:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1073:U:OP1	10:H:61:LYS:HG3	2.16	0.44
2:01:125:LYS:NZ	2:01:128:HIS:HB2	2.32	0.44
2:02:83:LEU:CB	4:04:528:THR:HB	2.40	0.44
4:04:85:CYS:H	4:04:90:VAL:H	1.62	0.44
4:04:418:GLU:HB3	5:05:45:LYS:HZ2	1.82	0.44
4:04:894:VAL:HG12	4:04:895:CYS:N	2.32	0.44
8:F:42:LEU:HD22	8:F:54:ILE:HD13	1.99	0.44
10:H:10:LEU:HD11	10:H:67:ARG:NH2	2.32	0.44
13:K:100:ILE:HD12	13:K:111:THR:CG2	2.47	0.44
18:P:18:LEU:HD21	18:P:55:LEU:HD13	1.97	0.44
1:A:309:A:H2'	1:A:310:G:C8	2.52	0.44
1:A:1239:A:H5''	1:A:1240:U:C5	2.51	0.44
2:01:79:LEU:HD13	2:01:79:LEU:O	2.17	0.44
2:01:224:LEU:HD13	2:02:228:LEU:CD1	2.47	0.44
3:03:828:PHE:CE2	3:03:1234:LYS:HD2	2.52	0.44
4:04:98:ARG:O	4:04:98:ARG:HG2	2.17	0.44
4:04:293:ARG:HA	4:04:296:LYS:HG3	2.00	0.44
4:04:510:LEU:HD13	4:04:628:GLY:HA2	1.98	0.44
4:04:757:THR:HA	4:04:758:PRO:HD3	1.79	0.44
4:04:1323:ALA:CA	4:04:1331:VAL:HG21	2.47	0.44
7:E:35:ARG:HG3	7:E:35:ARG:NH1	2.31	0.44
8:F:37:LYS:HA	8:F:40:GLN:HE21	1.83	0.44
14:L:121:ARG:HG3	14:L:121:ARG:HH11	1.82	0.44
21:S:14:ARG:HH11	21:S:14:ARG:HG3	1.82	0.44
1:A:244:U:H3	1:A:893:C:H42	1.66	0.44
1:A:358:U:H2'	1:A:359:G:H8	1.82	0.44
1:A:404:G:H1	1:A:499:A:H62	1.65	0.44
1:A:668:G:H21	20:R:45:HIS:CE1	2.35	0.44
1:A:692:U:H2'	1:A:694:A:OP2	2.17	0.44
1:A:903:G:H2'	1:A:904:U:C6	2.53	0.44
1:A:1066:C:O2'	1:A:1067:A:H5'	2.16	0.44
3:03:347:ILE:O	3:03:351:LEU:HG	2.18	0.44
3:03:673:HIS:HB3	3:03:1109:ILE:HG23	1.99	0.44
3:03:952:GLN:HB2	3:03:1036:ILE:HD13	1.98	0.44
4:04:109:SER:OG	4:04:296:LYS:HA	2.17	0.44
4:04:193:ASP:OD2	4:04:196:GLN:HG2	2.17	0.44
4:04:250:ARG:HD3	4:04:250:ARG:N	2.32	0.44
4:04:328:ALA:HA	4:04:331:ILE:HG13	1.98	0.44
4:04:956:GLY:HA2	4:04:986:ASP:HA	1.98	0.44
4:04:1123:ARG:O	4:04:1125:PRO:HD3	2.18	0.44
7:E:38:VAL:O	7:E:39:HIS:CB	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:126:ARG:HD3	8:F:126:ARG:N	2.32	0.44
12:J:65:LEU:HD21	12:J:96:ASN:HD22	1.83	0.44
15:M:10:LEU:HB2	15:M:72:ARG:HB2	1.99	0.44
18:P:44:ILE:HG13	18:P:47:LEU:HD12	2.00	0.44
24:V:55:GLN:HG3	24:V:56:HIS:N	2.33	0.44
1:A:192:A:O2'	25:W:55:PRO:HG3	2.18	0.44
1:A:1071:C:H2'	1:A:1072:G:H8	1.81	0.44
2:02:100:LEU:N	2:02:100:LEU:HD12	2.32	0.44
3:03:183:TRP:HB2	3:03:199:ASP:HA	2.00	0.44
3:03:448:LEU:HA	3:03:451:ARG:HB2	1.99	0.44
3:03:522:SER:HA	3:03:525:THR:HG22	1.99	0.44
3:03:618:GLN:HG3	3:03:620:ASN:H	1.82	0.44
3:03:834:GLN:O	3:03:1053:TYR:HA	2.17	0.44
3:03:1238:LEU:HB2	3:03:1241:ASP:OD2	2.18	0.44
4:04:47:ARG:HA	4:04:47:ARG:NE	2.32	0.44
4:04:1249:ASN:OD1	4:04:1251:LYS:HG3	2.18	0.44
7:E:57:LEU:CD1	7:E:217:VAL:HG13	2.47	0.44
8:F:12:GLY:HA3	19:Q:96:LYS:HG3	1.99	0.44
8:F:129:PHE:HD1	8:F:129:PHE:H	1.65	0.44
9:G:190:LEU:HD12	9:G:192:ALA:N	2.29	0.44
18:P:95:PRO:HA	18:P:108:ARG:HG2	2.00	0.44
21:S:25:ARG:HD3	21:S:25:ARG:H	1.82	0.44
1:A:171:A:O2'	1:A:172:A:H5'	2.17	0.44
1:A:631:C:H3'	1:A:632:U:H5'	2.00	0.44
2:01:89:ALA:CB	2:01:208:ASN:HD22	2.28	0.44
2:02:224:LEU:HD23	2:02:224:LEU:O	2.17	0.44
3:03:616:ILE:N	3:03:616:ILE:CD1	2.79	0.44
3:03:974:ARG:NE	3:03:974:ARG:HA	2.32	0.44
3:03:1119:MET:HG3	3:03:1204:LEU:HD11	2.00	0.44
3:03:1304:MET:O	3:03:1308:ILE:HG12	2.18	0.44
4:04:230:SER:OG	4:04:232:ASN:ND2	2.51	0.44
4:04:615:LYS:HG2	5:05:5:THR:OG1	2.18	0.44
4:04:997:VAL:HA	4:04:998:PRO:HD3	1.88	0.44
4:04:1346:GLY:O	4:04:1350:ASN:ND2	2.51	0.44
7:E:188:ASP:OD1	7:E:188:ASP:N	2.51	0.44
13:K:54:THR:C	13:K:56:PRO:HD3	2.37	0.44
16:N:60:PHE:O	16:N:64:VAL:HG23	2.18	0.44
17:O:3:VAL:HA	17:O:6:LEU:HD12	1.99	0.44
18:P:32:ILE:HG13	18:P:59:VAL:HG12	1.99	0.44
18:P:78:ARG:HH21	24:V:64:GLU:HB3	1.83	0.44
19:Q:61:ASN:HB3	19:Q:72:PHE:CZ	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:54:GLN:C	25:W:56:ILE:N	2.71	0.44
26:X:55:ARG:O	26:X:59:LYS:HG2	2.17	0.44
1:A:352:C:H4'	1:A:354:G:OP1	2.17	0.44
1:A:372:C:H41	1:A:387:U:H2'	1.83	0.44
1:A:521:G:OP1	17:O:69:GLU:HG3	2.18	0.44
1:A:831:A:H2'	1:A:832:G:H5''	2.00	0.44
1:A:1119:C:H5'	14:L:84:ARG:HH22	1.82	0.44
1:A:1238:A:H2'	1:A:1239:A:H5'	2.00	0.44
2:02:31:LEU:HD22	2:02:31:LEU:N	2.33	0.44
4:04:242:LEU:HA	4:04:243:PRO:HD3	1.78	0.44
4:04:614:LEU:O	4:04:618:VAL:HG23	2.18	0.44
4:04:697:MET:O	4:04:701:LEU:HD23	2.17	0.44
4:04:1046:ILE:HG22	4:04:1061:VAL:HA	1.99	0.44
4:04:1273:ASP:CG	4:04:1274:PHE:N	2.71	0.44
4:04:1286:LYS:O	4:04:1290:ARG:HB2	2.17	0.44
7:E:31:ILE:O	7:E:32:PHE:CB	2.66	0.44
11:I:47:LEU:HD21	11:I:57:ALA:HB3	2.00	0.44
12:J:13:PRO:HB3	12:J:20:GLU:HG2	2.00	0.44
12:J:134:VAL:O	12:J:138:GLU:HG2	2.17	0.44
22:T:11:VAL:HG23	22:T:56:ASP:O	2.17	0.44
25:W:27:MET:SD	25:W:66:ILE:HG13	2.58	0.44
2:02:50:SER:HA	2:02:151:GLY:HA3	2.00	0.44
3:03:552:PRO:HB3	4:04:770:LEU:HD11	2.00	0.44
3:03:1305:TYR:O	3:03:1309:VAL:HG13	2.18	0.44
4:04:222:LYS:HD3	4:04:222:LYS:C	2.39	0.44
4:04:285:LEU:N	4:04:285:LEU:HD12	2.33	0.44
4:04:844:THR:HG21	4:04:858:VAL:HG11	2.00	0.44
5:05:10:VAL:O	5:05:14:GLY:HA2	2.18	0.44
7:E:9:MET:SD	7:E:10:LEU:N	2.91	0.44
10:H:131:ASN:HB2	10:H:134:ASN:HD22	1.82	0.44
13:K:5:PRO:HB2	13:K:32:LYS:CE	2.48	0.44
13:K:104:SER:HB2	13:K:125:ILE:HD11	1.99	0.44
16:N:12:ARG:NE	16:N:12:ARG:HA	2.33	0.44
17:O:109:ARG:HB2	17:O:118:VAL:HG21	1.99	0.44
1:A:548:G:O2'	1:A:549:C:H5'	2.18	0.43
3:03:33:ASP:HA	3:03:36:GLN:HB2	1.99	0.43
3:03:1289:GLU:HA	3:03:1293:VAL:HB	2.00	0.43
4:04:62:PHE:HD1	4:04:101:ARG:HB3	1.82	0.43
4:04:894:VAL:HG22	4:04:1258:ARG:NH1	2.33	0.43
7:E:80:VAL:HA	7:E:214:LEU:HD21	2.00	0.43
7:E:104:TRP:CZ2	7:E:108:ARG:HD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:58:GLN:OE1	9:G:61:ARG:HD3	2.18	0.43
11:I:18:VAL:O	11:I:22:ILE:HG13	2.18	0.43
11:I:25:TYR:O	11:I:29:ILE:HG13	2.17	0.43
15:M:6:ILE:O	15:M:75:ASP:HA	2.18	0.43
21:S:11:ALA:HB3	21:S:14:ARG:HB2	1.99	0.43
22:T:47:ASP:HB3	22:T:74:LEU:HD21	1.99	0.43
25:W:80:ALA:O	25:W:84:LYS:HG3	2.18	0.43
26:X:17:ARG:HG2	26:X:17:ARG:HH11	1.83	0.43
1:A:156:C:O2'	1:A:157:U:H5'	2.18	0.43
1:A:253:A:H61	1:A:273:U:H3	1.64	0.43
1:A:337:G:H2'	1:A:338:A:H8	1.82	0.43
1:A:654:G:N2	1:A:755:G:H5'	2.33	0.43
3:03:974:ARG:O	3:03:978:VAL:HG23	2.18	0.43
3:03:1271:GLY:O	3:03:1274:GLU:HB2	2.17	0.43
4:04:755:ILE:HG22	4:04:757:THR:H	1.83	0.43
4:04:1041:ILE:N	4:04:1041:ILE:CD1	2.81	0.43
4:04:1323:ALA:HB1	4:04:1328:THR:HG23	2.00	0.43
7:E:162:PHE:HA	7:E:184:PHE:O	2.17	0.43
9:G:43:ARG:NH1	9:G:43:ARG:HB3	2.33	0.43
9:G:150:LYS:HA	9:G:154:VAL:HB	1.99	0.43
11:I:48:ALA:HB1	23:U:69:PRO:HB3	1.99	0.43
12:J:125:ASP:HB3	12:J:130:LYS:O	2.18	0.43
14:L:9:GLY:HA3	14:L:16:ALA:HB3	1.99	0.43
17:O:86:VAL:HG23	17:O:88:ASP:H	1.82	0.43
1:A:302:G:H2'	1:A:303:A:H8	1.82	0.43
1:A:1082:A:H2'	1:A:1083:U:O4'	2.19	0.43
1:A:1123:U:H2'	1:A:1124:G:C8	2.53	0.43
1:A:1128:C:H2'	1:A:1129:C:C6	2.53	0.43
1:A:1155:A:H2'	1:A:1156:G:O4'	2.17	0.43
1:A:1204:A:O2'	1:A:1205:U:H5'	2.18	0.43
1:A:1293:C:H2'	1:A:1294:G:C8	2.53	0.43
1:A:1371:G:OP2	14:L:12:LYS:HE2	2.18	0.43
2:01:161:SER:C	2:01:163:GLU:H	2.21	0.43
2:01:219:ARG:O	2:01:223:ILE:HG13	2.19	0.43
2:02:182:ARG:HG3	2:02:182:ARG:NH1	2.34	0.43
3:03:623:LEU:HD12	3:03:623:LEU:C	2.39	0.43
3:03:693:LEU:HG	3:03:829:THR:O	2.18	0.43
4:04:141:PHE:HB3	4:04:180:MET:HE3	2.00	0.43
4:04:1090:ILE:HD12	4:04:1095:MET:HB2	2.00	0.43
4:04:1183:SER:OG	4:04:1185:PRO:HD2	2.18	0.43
13:K:31:LEU:O	13:K:35:ILE:HG13	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:U:C2'	1:A:119:A:H5'	2.48	0.43
1:A:545:C:H5'	9:G:61:ARG:HH12	1.83	0.43
4:04:56:LEU:N	4:04:56:LEU:HD12	2.33	0.43
4:04:320:ASN:HD22	4:04:321:LYS:N	2.15	0.43
4:04:368:LEU:HA	4:04:369:PRO:HD3	1.85	0.43
4:04:767:LEU:HD23	4:04:767:LEU:H	1.83	0.43
7:E:56:GLU:OE2	7:E:60:ILE:HG23	2.18	0.43
7:E:68:LEU:HD23	7:E:161:LEU:HD11	2.00	0.43
12:J:20:GLU:O	12:J:23:ALA:HB3	2.18	0.43
25:W:34:VAL:CG1	25:W:78:LEU:HD11	2.48	0.43
1:A:730:G:H2'	1:A:731:G:O4'	2.18	0.43
1:A:1306:A:H2'	1:A:1307:U:C6	2.53	0.43
4:04:21:LYS:HD2	4:04:21:LYS:C	2.38	0.43
4:04:133:ARG:HH21	4:04:136:GLU:CD	2.22	0.43
4:04:431:ARG:HD2	4:04:493:PRO:HG3	2.01	0.43
4:04:431:ARG:HG2	4:04:431:ARG:HH11	1.84	0.43
4:04:555:TYR:CD2	4:04:585:LYS:HB3	2.54	0.43
7:E:27:MET:SD	7:E:193:PRO:HD3	2.59	0.43
8:F:91:ALA:HA	8:F:96:VAL:O	2.18	0.43
8:F:206:ILE:OXT	8:F:206:ILE:HG12	2.19	0.43
9:G:36:ALA:HA	9:G:37:PRO:HD2	1.94	0.43
10:H:82:HIS:HB3	13:K:98:LEU:HD22	1.99	0.43
13:K:6:ILE:O	13:K:10:LEU:HG	2.18	0.43
16:N:12:ARG:O	16:N:13:LYS:HB2	2.19	0.43
23:U:28:THR:HA	23:U:31:ASN:ND2	2.33	0.43
26:X:10:GLU:N	26:X:11:PRO:HD2	2.33	0.43
1:A:211:G:H3'	1:A:211:G:N3	2.33	0.43
1:A:1100:C:P	26:X:67:ARG:HD2	2.59	0.43
3:03:663:VAL:O	3:03:667:LEU:HG	2.18	0.43
3:03:1086:PRO:HD2	3:03:1094:VAL:CG1	2.48	0.43
3:03:1299:ASN:O	3:03:1303:LYS:HG2	2.18	0.43
4:04:78:LEU:HD12	4:04:78:LEU:N	2.34	0.43
4:04:94:GLN:HB2	4:04:97:VAL:CG2	2.35	0.43
4:04:184:ALA:O	4:04:187:ALA:HB3	2.18	0.43
4:04:447:ILE:HD13	4:04:468:VAL:CG1	2.49	0.43
4:04:569:LEU:HD12	4:04:569:LEU:N	2.34	0.43
7:E:18:HIS:HA	7:E:40:ILE:CG2	2.47	0.43
15:M:66:GLU:HG2	19:Q:96:LYS:O	2.19	0.43
16:N:17:ASP:HA	16:N:80:ASN:O	2.18	0.43
16:N:80:ASN:HA	16:N:105:ARG:O	2.17	0.43
19:Q:40:ARG:HD2	19:Q:40:ARG:C	2.38	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:S:31:ARG:HD3	21:S:31:ARG:C	2.39	0.43
23:U:48:ARG:H	23:U:48:ARG:HD2	1.83	0.43
24:V:48:ILE:O	24:V:48:ILE:HG13	2.19	0.43
1:A:3:A:H2	1:A:628:G:H21	1.66	0.43
1:A:9:G:O2'	1:A:10:A:H5'	2.19	0.43
3:03:104:ILE:N	3:03:104:ILE:CD1	2.82	0.43
3:03:777:VAL:HG11	3:03:783:LEU:HD11	2.00	0.43
3:03:817:LEU:HD13	3:03:818:VAL:N	2.34	0.43
3:03:1012:GLU:O	3:03:1016:GLU:HG3	2.19	0.43
3:03:1255:THR:CG2	3:03:1256:GLN:H	2.23	0.43
4:04:56:LEU:HD12	4:04:56:LEU:H	1.83	0.43
4:04:374:LEU:O	4:04:378:LYS:HG3	2.19	0.43
4:04:378:LYS:HB3	4:04:382:TYR:CE2	2.54	0.43
4:04:550:VAL:O	4:04:569:LEU:HA	2.19	0.43
4:04:690:ASN:HD21	4:04:738:ARG:HD3	1.83	0.43
4:04:1265:THR:HG23	4:04:1305:ASP:HB2	2.00	0.43
7:E:18:HIS:HA	7:E:40:ILE:CB	2.49	0.43
9:G:184:LYS:CD	9:G:185:PRO:HD2	2.49	0.43
10:H:20:VAL:HG23	10:H:31:SER:HB3	2.01	0.43
11:I:47:LEU:HD21	11:I:57:ALA:HB2	2.01	0.43
13:K:116:ARG:CB	13:K:116:ARG:HH11	2.31	0.43
16:N:22:ILE:HG12	16:N:31:VAL:HG13	2.00	0.43
1:A:10:A:H2'	1:A:11:G:H8	1.84	0.43
1:A:920:U:H2'	1:A:921:U:C5	2.54	0.43
2:02:82:LEU:HA	2:02:85:LEU:HD12	2.00	0.43
3:03:54:ARG:O	3:03:57:PHE:O	2.36	0.43
4:04:600:ALA:HA	4:04:603:LYS:HZ3	1.82	0.43
4:04:884:SER:OG	4:04:886:VAL:HG12	2.18	0.43
11:I:11:HIS:HB2	11:I:14:GLN:NE2	2.34	0.43
20:R:10:ILE:HG23	20:R:14:PHE:HE2	1.83	0.43
2:01:65:LEU:HD22	2:01:65:LEU:N	2.34	0.43
2:02:61:ILE:HG12	2:02:171:LEU:HD12	2.01	0.43
3:03:139:ASN:H	3:03:143:ARG:NH2	2.15	0.43
3:03:339:ASN:HD21	3:03:343:HIS:HB2	1.83	0.43
3:03:644:LEU:HD22	3:03:644:LEU:N	2.34	0.43
3:03:1059:ARG:HG3	3:03:1059:ARG:NH1	2.33	0.43
3:03:1063:GLY:H	3:03:1076:ILE:CG2	2.25	0.43
4:04:26:SER:O	4:04:29:MET:HB2	2.18	0.43
4:04:29:MET:O	4:04:32:SER:HB2	2.19	0.43
4:04:63:GLY:HA3	4:04:64:PRO:HD3	1.73	0.43
4:04:111:THR:HB	4:04:239:LEU:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:133:ARG:NH2	4:04:136:GLU:HB3	2.34	0.43
4:04:958:ILE:HG23	4:04:982:LEU:HD12	2.01	0.43
4:04:1089:LEU:N	4:04:1089:LEU:HD12	2.34	0.43
7:E:120:GLN:CB	7:E:137:ARG:HH22	2.31	0.43
10:H:95:MET:HG2	10:H:124:ALA:HB2	2.00	0.43
12:J:47:GLU:OE2	12:J:57:GLU:HG2	2.19	0.43
12:J:90:VAL:HG13	12:J:95:ARG:HE	1.84	0.43
13:K:49:LYS:O	13:K:58:LEU:HD12	2.19	0.43
19:Q:5:MET:CG	19:Q:62:ARG:NH1	2.81	0.43
1:A:104:G:OP2	25:W:11:ILE:HD12	2.19	0.43
1:A:880:C:H5''	17:O:8:ARG:HH12	1.84	0.43
2:01:167:PRO:HG2	2:01:170:ARG:NE	2.33	0.43
3:03:424:ASP:O	3:03:428:VAL:HG23	2.19	0.43
3:03:801:ARG:HG2	3:03:1094:VAL:HA	2.01	0.43
4:04:492:SER:HB2	4:04:499:ILE:HD13	2.01	0.43
7:E:61:ALA:HB3	7:E:224:GLY:HA3	2.00	0.43
7:E:133:GLU:O	7:E:137:ARG:HG2	2.19	0.43
8:F:16:PRO:HG2	8:F:53:ARG:HH22	1.84	0.43
8:F:56:ILE:HG23	8:F:63:ILE:HD11	2.00	0.43
10:H:131:ASN:HD22	10:H:133:ILE:HD13	1.83	0.43
12:J:49:LEU:HB3	12:J:120:ALA:HA	2.00	0.43
17:O:3:VAL:O	17:O:6:LEU:HB2	2.19	0.43
18:P:32:ILE:HG23	18:P:58:GLU:CG	2.49	0.43
25:W:27:MET:N	25:W:56:ILE:HG21	2.34	0.43
1:A:730:G:H2'	1:A:731:G:H5'	2.01	0.42
1:A:911:U:H2'	1:A:912:C:C6	2.53	0.42
1:A:1313:U:OP2	24:V:4:LEU:HB2	2.19	0.42
1:A:1328:C:OP1	18:P:27:THR:HG21	2.19	0.42
2:01:208:ASN:HD21	2:01:210:THR:CG2	2.32	0.42
3:03:448:LEU:HD12	3:03:608:ALA:HB2	2.01	0.42
3:03:578:TYR:HD2	3:03:659:GLN:HA	1.84	0.42
3:03:603:ILE:O	3:03:603:ILE:HG13	2.18	0.42
3:03:690:VAL:HG11	3:03:1234:LYS:HB3	2.01	0.42
3:03:732:ILE:CG1	3:03:753:LEU:HD11	2.45	0.42
3:03:1082:ILE:HG22	3:03:1082:ILE:O	2.19	0.42
3:03:1176:LEU:C	3:03:1178:LYS:H	2.21	0.42
4:04:70:CYS:HB2	4:04:75:TYR:HB2	2.00	0.42
4:04:293:ARG:HA	4:04:296:LYS:HD2	2.01	0.42
4:04:420:PRO:HG3	4:04:481:ARG:HH21	1.84	0.42
4:04:468:VAL:HG23	4:04:468:VAL:O	2.19	0.42
4:04:849:LEU:H	4:04:849:LEU:CD2	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:984:LEU:HB3	4:04:993:GLU:H	1.84	0.42
6:B:139:UNK:O	6:B:141:UNK:N	2.51	0.42
7:E:91:PHE:N	7:E:91:PHE:CD1	2.87	0.42
8:F:7:ASN:O	8:F:11:LEU:HG	2.19	0.42
21:S:12:LYS:O	21:S:13:LYS:HB2	2.19	0.42
22:T:12:VAL:HG13	22:T:13:SER:N	2.34	0.42
22:T:65:PRO:HA	22:T:71:SER:HA	2.01	0.42
23:U:43:ARG:HG2	23:U:43:ARG:HH11	1.84	0.42
26:X:36:GLU:C	26:X:38:TYR:H	2.22	0.42
1:A:323:U:H2'	1:A:324:G:O4'	2.19	0.42
1:A:723:U:C2	1:A:855:U:H4'	2.54	0.42
2:01:108:GLY:HA2	2:01:109:PRO:HD3	1.88	0.42
2:02:148:ARG:HH11	2:02:148:ARG:HG3	1.85	0.42
4:04:147:ILE:HA	4:04:188:LEU:HD21	2.00	0.42
4:04:190:LYS:NZ	4:04:190:LYS:HB3	2.34	0.42
4:04:195:GLU:HA	4:04:198:CYS:CB	2.46	0.42
4:04:268:LEU:HD11	4:04:325:LYS:HB2	2.00	0.42
4:04:478:LEU:HD23	4:04:478:LEU:O	2.19	0.42
4:04:870:ASP:O	4:04:874:GLU:HG2	2.19	0.42
4:04:1220:ILE:O	4:04:1224:ARG:HB3	2.20	0.42
5:05:27:ALA:HB1	5:05:46:THR:OG1	2.19	0.42
7:E:76:ALA:HB1	7:E:210:VAL:HG11	2.00	0.42
9:G:30:LYS:O	9:G:32:LYS:N	2.49	0.42
11:I:86:ARG:HD3	23:U:64:TYR:O	2.18	0.42
20:R:21:THR:OG1	20:R:30:LEU:HD22	2.18	0.42
23:U:62:ALA:HB3	23:U:68:LEU:HD12	2.00	0.42
1:A:211:G:C2'	1:A:212:G:H5'	2.49	0.42
1:A:440:C:H2'	1:A:441:A:C5'	2.47	0.42
1:A:546:A:OP2	9:G:67:LEU:HD22	2.18	0.42
1:A:867:G:H21	1:A:873:A:H2	1.66	0.42
1:A:1351:U:H2'	1:A:1352:C:C6	2.54	0.42
2:01:224:LEU:O	2:01:228:LEU:HG	2.19	0.42
3:03:194:LEU:HD11	3:03:432:LEU:HD23	2.02	0.42
3:03:364:VAL:HG13	3:03:376:PRO:CG	2.46	0.42
3:03:854:ILE:O	3:03:854:ILE:HG23	2.19	0.42
3:03:1014:LEU:HD12	3:03:1014:LEU:N	2.35	0.42
4:04:250:ARG:HH11	4:04:250:ARG:HG3	1.84	0.42
4:04:568:SER:C	4:04:569:LEU:HD12	2.40	0.42
4:04:583:VAL:HA	4:04:620:PHE:CE1	2.54	0.42
4:04:661:VAL:CG1	4:04:685:ILE:HD11	2.49	0.42
4:04:863:LEU:HD22	4:04:908:ILE:HD11	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:04:896:ALA:HA	4:04:909:ILE:HG22	2.00	0.42
4:04:1068:THR:O	4:04:1072:LYS:HG3	2.19	0.42
4:04:1327:GLU:O	4:04:1331:VAL:HG23	2.19	0.42
7:E:148:LEU:N	7:E:148:LEU:HD12	2.34	0.42
8:F:115:VAL:O	8:F:119:ILE:HG13	2.20	0.42
13:K:76:ARG:HH11	13:K:76:ARG:HG3	1.84	0.42
18:P:96:VAL:HG13	18:P:108:ARG:HH21	1.84	0.42
19:Q:44:VAL:HA	19:Q:47:LEU:HB3	2.00	0.42
22:T:25:GLU:HB3	22:T:38:LYS:HB3	2.00	0.42
22:T:58:VAL:HG21	22:T:74:LEU:HD22	2.01	0.42
1:A:406:G:H2'	1:A:407:U:C6	2.54	0.42
2:02:143:ARG:HG2	2:02:143:ARG:HH11	1.85	0.42
3:03:232:ILE:HG12	3:03:237:LEU:CD2	2.49	0.42
3:03:633:LEU:C	3:03:633:LEU:HD12	2.40	0.42
3:03:1268:GLN:HB2	4:04:467:ALA:CB	2.49	0.42
4:04:506:VAL:HG13	4:04:507:VAL:HG13	2.01	0.42
4:04:740:LEU:O	4:04:764:ARG:HB2	2.19	0.42
4:04:843:VAL:O	4:04:882:VAL:HG13	2.20	0.42
9:G:127:ARG:O	9:G:129:VAL:HG23	2.20	0.42
14:L:74:GLN:O	14:L:78:ILE:HG13	2.18	0.42
15:M:15:HIS:HA	15:M:18:ILE:HG22	2.01	0.42
18:P:73:SER:O	18:P:77:LYS:HG3	2.19	0.42
21:S:28:ARG:HG2	21:S:29:ASN:OD1	2.19	0.42
3:03:862:LEU:HD23	3:03:865:LEU:HD12	2.02	0.42
4:04:144:TYR:HA	4:04:180:MET:HB3	2.00	0.42
4:04:609:TYR:CE1	4:04:614:LEU:HB2	2.48	0.42
7:E:9:MET:C	7:E:11:LYS:N	2.71	0.42
9:G:149:LYS:HB3	9:G:149:LYS:HZ3	1.85	0.42
12:J:137:ARG:O	12:J:137:ARG:HD2	2.19	0.42
1:A:774:G:C2'	1:A:775:G:H5'	2.49	0.42
1:A:1099:G:H2'	1:A:1100:C:O4'	2.20	0.42
2:01:27:THR:HA	2:01:201:LEU:O	2.20	0.42
2:01:40:GLY:O	2:01:44:ARG:HG3	2.19	0.42
2:02:196:THR:O	2:02:198:LEU:HD22	2.20	0.42
3:03:29:SER:C	3:03:31:GLN:N	2.72	0.42
3:03:1258:PRO:HB3	4:04:346:ARG:NH1	2.26	0.42
3:03:1328:LYS:HZ2	4:04:245:LEU:HA	1.83	0.42
4:04:215:LYS:O	4:04:218:THR:HG22	2.20	0.42
4:04:1177:ILE:HB	4:04:1186:TYR:O	2.19	0.42
4:04:1307:LEU:N	4:04:1307:LEU:HD12	2.34	0.42
5:05:27:ALA:O	5:05:30:MET:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:108:ARG:HA	7:E:111:ILE:CG1	2.49	0.42
9:G:171:GLU:HB2	9:G:180:THR:HB	2.00	0.42
13:K:7:ALA:HB2	13:K:76:ARG:HD2	2.01	0.42
16:N:15:VAL:HG11	16:N:41:LEU:HD11	2.01	0.42
25:W:28:ARG:HG3	25:W:28:ARG:HH11	1.85	0.42
1:A:106:C:H2'	1:A:107:G:O4'	2.18	0.42
1:A:427:U:H5''	1:A:428:G:H2'	2.02	0.42
2:01:14:VAL:HG22	2:01:15:ASP:N	2.33	0.42
3:03:339:ASN:ND2	3:03:343:HIS:HB2	2.33	0.42
4:04:141:PHE:HB3	4:04:180:MET:CE	2.49	0.42
4:04:335:GLN:HG2	4:04:340:GLN:O	2.20	0.42
4:04:801:VAL:O	4:04:805:GLN:HG3	2.19	0.42
7:E:39:HIS:C	7:E:40:ILE:HG12	2.40	0.42
9:G:144:ILE:HD12	9:G:177:MET:HB2	2.00	0.42
19:Q:45:LEU:O	24:V:12:LEU:HD13	2.20	0.42
19:Q:59:GLN:OE1	19:Q:59:GLN:HA	2.19	0.42
21:S:78:VAL:HG13	21:S:80:LYS:H	1.85	0.42
1:A:219:U:H3'	1:A:220:G:H5''	2.02	0.42
1:A:505:G:H2'	1:A:506:G:C8	2.55	0.42
1:A:672:U:H2'	1:A:673:A:H8	1.85	0.42
1:A:831:A:C2'	1:A:832:G:H5''	2.49	0.42
1:A:981:U:C5'	19:Q:62:ARG:HH22	2.33	0.42
3:03:689:ALA:HB2	3:03:796:LEU:HD23	2.01	0.42
3:03:1022:LYS:O	3:03:1025:PHE:HB3	2.20	0.42
4:04:197:GLU:O	4:04:201:LEU:HG	2.20	0.42
4:04:279:LEU:O	4:04:283:LEU:HG	2.20	0.42
4:04:681:LYS:O	4:04:684:ASP:HB2	2.20	0.42
4:04:857:LEU:HD22	4:04:875:ASN:OD1	2.20	0.42
4:04:901:ARG:HG3	4:04:901:ARG:NH1	2.35	0.42
5:05:32:VAL:C	5:05:34:GLY:N	2.71	0.42
14:L:7:GLY:N	14:L:85:ALA:HB2	2.35	0.42
18:P:18:LEU:O	18:P:24:VAL:HG13	2.20	0.42
24:V:30:LEU:H	24:V:30:LEU:CD1	2.33	0.42
25:W:17:ARG:HD2	25:W:17:ARG:C	2.40	0.42
26:X:16:LEU:HA	26:X:18:ARG:NH1	2.33	0.42
26:X:17:ARG:HG2	26:X:17:ARG:NH1	2.34	0.42
1:A:454:G:H2'	1:A:455:G:C8	2.55	0.42
1:A:952:U:H4'	1:A:964:A:H61	1.85	0.42
1:A:1516:G:H2'	1:A:1518:A:OP2	2.19	0.42
3:03:426:ILE:O	3:03:430:LYS:HG3	2.20	0.42
3:03:575:LEU:HG	3:03:576:SER:N	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:1257:GLN:HA	3:03:1258:PRO:HD3	1.89	0.42
3:03:1294:LYS:HD3	3:03:1295:SER:HB2	2.01	0.42
4:04:356:THR:CG2	4:04:448:GLN:HG2	2.50	0.42
4:04:410:ASP:HA	4:04:413:ASP:OD2	2.20	0.42
4:04:515:ARG:HH11	4:04:515:ARG:HG2	1.85	0.42
4:04:649:LYS:O	4:04:653:ILE:HG13	2.20	0.42
7:E:23:TRP:CE3	7:E:189:THR:HB	2.43	0.42
17:O:3:VAL:O	17:O:7:VAL:HG23	2.20	0.42
1:A:176:C:C5'	25:W:19:HIS:NE2	2.83	0.42
1:A:358:U:H2'	1:A:359:G:C8	2.54	0.42
1:A:663:A:H5'	1:A:836:G:OP1	2.20	0.42
2:01:102:LEU:HD13	2:01:102:LEU:C	2.39	0.42
2:01:106:GLY:HA2	2:01:136:GLU:HA	2.02	0.42
3:03:696:ASP:O	3:03:795:ALA:HB1	2.20	0.42
3:03:1107:MET:HG2	4:04:740:LEU:HB2	2.02	0.42
3:03:1335:ILE:N	3:03:1335:ILE:CD1	2.79	0.42
4:04:203:GLU:O	4:04:207:GLU:HG2	2.19	0.42
4:04:352:ARG:HH12	4:04:465:GLN:HG2	1.85	0.42
4:04:363:LEU:HD23	4:04:618:VAL:HG13	2.02	0.42
4:04:901:ARG:HG3	4:04:901:ARG:HH11	1.85	0.42
4:04:1076:PRO:O	4:04:1100:PHE:HA	2.20	0.42
6:B:208:UNK:HA	6:B:216:UNK:O	2.20	0.42
7:E:120:GLN:HB2	7:E:137:ARG:HH22	1.85	0.42
8:F:40:GLN:O	8:F:44:LYS:HG2	2.20	0.42
8:F:55:VAL:HG22	8:F:66:THR:O	2.19	0.42
16:N:97:ARG:HH11	16:N:97:ARG:HG3	1.84	0.42
19:Q:65:GLN:HG3	19:Q:66:THR:HG23	2.02	0.42
22:T:10:ARG:HG3	22:T:10:ARG:NH1	2.35	0.42
22:T:27:PHE:CZ	22:T:38:LYS:HE2	2.54	0.42
26:X:10:GLU:H	26:X:11:PRO:HD2	1.85	0.42
1:A:701:U:H5''	1:A:703:G:H1'	2.02	0.41
1:A:779:C:O2'	1:A:780:A:H5'	2.20	0.41
2:01:39:LEU:HD11	2:02:227:GLN:HB3	2.01	0.41
3:03:178:PRO:HA	3:03:397:LEU:HD21	2.02	0.41
3:03:540:ARG:HB3	3:03:571:LEU:HD11	2.02	0.41
3:03:875:ALA:H	3:03:928:VAL:HG23	1.84	0.41
4:04:320:ASN:ND2	4:04:321:LYS:H	2.16	0.41
4:04:543:SER:O	4:04:574:VAL:HG21	2.20	0.41
4:04:620:PHE:CE2	4:04:624:ILE:HD11	2.55	0.41
4:04:850:LYS:C	4:04:852:GLY:N	2.72	0.41
8:F:59:PRO:HG2	8:F:62:SER:OG	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:9:MET:O	11:I:84:VAL:HA	2.20	0.41
12:J:12:LEU:HD12	12:J:12:LEU:N	2.35	0.41
1:A:412:A:H3'	1:A:413:G:C5'	2.50	0.41
1:A:1148:U:O2'	14:L:15:ALA:HB1	2.20	0.41
2:02:79:LEU:HD13	2:02:79:LEU:C	2.40	0.41
4:04:97:VAL:HG12	4:04:97:VAL:O	2.20	0.41
4:04:116:PHE:CE1	4:04:1333:THR:HA	2.44	0.41
4:04:181:GLY:O	4:04:185:ILE:HG12	2.19	0.41
4:04:394:ILE:O	4:04:398:LYS:HG3	2.21	0.41
4:04:478:LEU:HD22	5:05:20:VAL:HG22	2.01	0.41
4:04:1158:GLU:HA	4:04:1223:LEU:CD2	2.50	0.41
5:05:44:ASP:HB3	5:05:48:VAL:HB	2.02	0.41
10:H:44:ARG:HE	10:H:70:MET:CB	2.29	0.41
26:X:12:PHE:CD1	26:X:12:PHE:N	2.87	0.41
1:A:177:G:OP2	1:A:195:A:H5''	2.21	0.41
1:A:273:U:H2'	1:A:274:A:H5'	2.01	0.41
1:A:395:C:O2'	1:A:396:C:H5'	2.20	0.41
1:A:639:G:O2'	1:A:640:A:H5'	2.19	0.41
1:A:1134:G:H2'	1:A:1135:U:O4'	2.20	0.41
1:A:1175:G:H2'	1:A:1176:A:H8	1.85	0.41
1:A:1204:A:H2'	1:A:1205:U:O4'	2.20	0.41
2:01:118:ASP:HB3	2:01:121:VAL:HG23	2.02	0.41
3:03:816:ILE:O	3:03:1076:ILE:HD12	2.20	0.41
4:04:520:ALA:HB3	4:04:523:GLU:OE1	2.20	0.41
4:04:624:ILE:O	4:04:628:GLY:N	2.51	0.41
4:04:833:GLU:OE1	4:04:1242:ARG:NH2	2.53	0.41
4:04:982:LEU:HD21	4:04:1017:VAL:HG21	2.01	0.41
7:E:21:ARG:HA	7:E:38:VAL:O	2.20	0.41
9:G:43:ARG:HB3	9:G:43:ARG:CZ	2.50	0.41
11:I:85:ILE:HG13	11:I:86:ARG:N	2.35	0.41
13:K:46:GLU:HG3	13:K:47:ASP:OD2	2.20	0.41
16:N:30:ILE:HG13	16:N:45:THR:HG22	2.01	0.41
25:W:23:ARG:HB3	25:W:60:GLN:HE22	1.85	0.41
1:A:35:G:H4'	17:O:117:GLY:CA	2.50	0.41
1:A:273:U:C2'	1:A:274:A:H5'	2.50	0.41
1:A:1144:G:O2'	1:A:1145:A:H5'	2.20	0.41
1:A:1259:C:H2'	1:A:1260:G:H4'	2.02	0.41
2:01:19:VAL:HG13	2:01:20:SER:N	2.35	0.41
2:02:79:LEU:O	2:02:83:LEU:HD13	2.20	0.41
3:03:72:SER:OG	3:03:73:TYR:N	2.52	0.41
3:03:678:ARG:CZ	3:03:1072:ASN:HA	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:1214:ASP:HA	3:03:1221:PHE:CZ	2.56	0.41
4:04:48:THR:C	4:04:50:LYS:H	2.23	0.41
4:04:278:ARG:O	4:04:282:LEU:HG	2.20	0.41
4:04:478:LEU:HD11	5:05:51:LEU:HD21	2.03	0.41
4:04:661:VAL:HG11	4:04:686:TRP:HE1	1.85	0.41
4:04:1047:THR:CG2	4:04:1049:GLN:HE21	2.32	0.41
4:04:1287:ILE:HA	4:04:1290:ARG:HB3	2.01	0.41
5:05:26:ARG:O	5:05:30:MET:HE2	2.20	0.41
7:E:31:ILE:O	7:E:33:GLY:N	2.53	0.41
7:E:89:GLN:H	7:E:89:GLN:HE21	1.64	0.41
7:E:101:LEU:CD2	7:E:176:ALA:HA	2.51	0.41
8:F:173:PRO:HB2	8:F:176:THR:HB	2.02	0.41
11:I:7:VAL:HG22	11:I:61:LEU:HG	2.03	0.41
18:P:12:LYS:HB3	18:P:16:ILE:HB	2.01	0.41
18:P:72:ILE:HG13	18:P:73:SER:N	2.35	0.41
20:R:63:ARG:NE	20:R:63:ARG:HA	2.35	0.41
25:W:28:ARG:O	25:W:32:LYS:HG2	2.21	0.41
1:A:669:G:OP1	1:A:807:A:H5'	2.21	0.41
1:A:686:U:H2'	1:A:687:A:C8	2.55	0.41
1:A:993:G:H2'	1:A:993:G:N3	2.35	0.41
1:A:1293:C:H2'	1:A:1294:G:H8	1.84	0.41
3:03:216:THR:HG22	3:03:217:THR:N	2.35	0.41
3:03:501:ALA:O	3:03:504:GLU:HB3	2.21	0.41
3:03:851:THR:CB	3:03:885:GLY:HA3	2.50	0.41
4:04:390:LEU:N	4:04:390:LEU:HD12	2.35	0.41
4:04:417:ARG:HG2	4:04:417:ARG:NH1	2.33	0.41
4:04:1232:TYR:O	4:04:1235:ASN:HB2	2.21	0.41
7:E:43:LEU:HB3	7:E:44:GLU:H	1.54	0.41
7:E:108:ARG:HA	7:E:111:ILE:HG12	2.02	0.41
9:G:99:ASN:O	9:G:102:TYR:HB3	2.20	0.41
13:K:101:ALA:HB3	13:K:112:ASP:HB3	2.03	0.41
14:L:8:THR:O	14:L:81:GLY:HA2	2.20	0.41
15:M:66:GLU:OE1	19:Q:98:ALA:HA	2.21	0.41
18:P:12:LYS:O	18:P:43:LYS:HA	2.21	0.41
1:A:50:A:C4'	1:A:51:A:H5'	2.50	0.41
1:A:104:G:H3'	25:W:8:LYS:HD2	2.02	0.41
1:A:113:G:H1'	1:A:354:G:C5'	2.50	0.41
1:A:185:U:H2'	1:A:186:C:C6	2.55	0.41
1:A:366:A:H2	1:A:394:G:H1	1.69	0.41
1:A:803:G:O2'	1:A:804:U:H5'	2.20	0.41
1:A:1175:G:H2'	1:A:1176:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1348:U:O2'	1:A:1349:A:H5'	2.20	0.41
1:A:1353:G:H2'	1:A:1354:U:C6	2.56	0.41
2:02:31:LEU:HD12	2:02:35:PHE:HB3	2.01	0.41
3:03:184:LEU:HD12	3:03:184:LEU:HA	1.72	0.41
4:04:552:ILE:H	4:04:552:ILE:HG13	1.57	0.41
4:04:615:LYS:HB2	4:04:616:PRO:HD3	2.02	0.41
4:04:749:LYS:HE2	4:04:751:ASP:OD2	2.20	0.41
4:04:1319:PHE:H	4:04:1319:PHE:HD1	1.68	0.41
8:F:139:ASN:O	8:F:143:LEU:HB2	2.20	0.41
11:I:18:VAL:CG1	11:I:19:PRO:HD3	2.51	0.41
14:L:121:ARG:HG3	14:L:121:ARG:NH1	2.35	0.41
16:N:43:TRP:HE3	16:N:45:THR:HG23	1.86	0.41
16:N:84:MET:HB3	16:N:112:VAL:HG22	2.01	0.41
17:O:31:GLY:HA3	17:O:54:VAL:HG13	2.02	0.41
18:P:43:LYS:O	18:P:47:LEU:HG	2.20	0.41
18:P:48:SER:HB2	18:P:51:GLN:HG3	2.03	0.41
19:Q:40:ARG:HH11	19:Q:40:ARG:HG3	1.86	0.41
24:V:13:HIS:HE1	24:V:34:SER:HB2	1.86	0.41
25:W:16:ALA:HB1	25:W:20:ASN:ND2	2.35	0.41
1:A:104:G:OP2	25:W:8:LYS:HG3	2.20	0.41
1:A:227:G:O2'	1:A:228:A:H5'	2.20	0.41
1:A:521:G:O2'	1:A:536:C:H4'	2.20	0.41
1:A:872:A:H2'	1:A:872:A:N3	2.36	0.41
3:03:57:PHE:HB2	3:03:70:TYR:HB2	2.03	0.41
3:03:119:GLU:HG3	3:03:489:PRO:HD2	2.02	0.41
3:03:287:VAL:O	3:03:287:VAL:HG23	2.20	0.41
3:03:451:ARG:HG3	3:03:451:ARG:NH1	2.36	0.41
3:03:1246:ARG:C	3:03:1246:ARG:HD3	2.41	0.41
4:04:483:LEU:HG	4:04:484:MET:HG3	2.03	0.41
4:04:586:GLY:HA3	4:04:612:LEU:HD13	2.01	0.41
4:04:767:LEU:HB2	4:04:771:GLN:CD	2.41	0.41
8:F:149:LYS:HE2	8:F:168:ARG:HD3	2.03	0.41
11:I:54:LEU:HD12	11:I:54:LEU:O	2.20	0.41
15:M:9:ARG:HA	15:M:73:LEU:HD23	2.02	0.41
19:Q:12:ARG:NH1	19:Q:12:ARG:HG3	2.36	0.41
1:A:826:C:H2'	1:A:827:U:H6	1.85	0.41
1:A:1005:A:H2'	1:A:1006:G:O4'	2.21	0.41
1:A:1342:C:H2'	1:A:1343:G:C8	2.55	0.41
2:01:56:VAL:HG11	2:01:85:LEU:HB3	2.02	0.41
2:02:211:ILE:HD11	2:02:215:GLU:HB3	2.02	0.41
3:03:498:ILE:N	3:03:498:ILE:CD1	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:03:1032:LYS:HA	3:03:1035:LYS:HE2	2.03	0.41
3:03:1294:LYS:HE2	4:04:348:ASP:H	1.86	0.41
4:04:108:ALA:CB	4:04:283:LEU:HD11	2.46	0.41
4:04:339:ARG:O	4:04:344:GLY:HA3	2.20	0.41
4:04:474:LEU:H	4:04:474:LEU:HD22	1.86	0.41
4:04:1227:HIS:HA	4:04:1230:THR:CG2	2.49	0.41
4:04:1320:ILE:HD12	4:04:1349:GLU:CG	2.49	0.41
9:G:158:LEU:O	9:G:158:LEU:HD23	2.21	0.41
1:A:26:A:H61	1:A:558:G:H1'	1.85	0.41
1:A:516:U:O4	1:A:533:A:N7	2.54	0.41
1:A:658:C:C1'	20:R:21:THR:HG21	2.51	0.41
1:A:736:C:H2'	1:A:737:C:C6	2.56	0.41
1:A:739:C:H2'	1:A:740:U:O4'	2.21	0.41
1:A:1068:G:H5'	1:A:1388:C:H5'	2.03	0.41
1:A:1078:U:H2'	1:A:1079:G:H5'	2.02	0.41
1:A:1237:C:OP1	1:A:1238:A:H1'	2.21	0.41
2:02:104:LYS:HD3	2:02:114:ASP:OD2	2.20	0.41
3:03:678:ARG:NH2	3:03:1106:ARG:HH11	2.18	0.41
3:03:771:VAL:HG21	3:03:783:LEU:HD13	2.03	0.41
3:03:926:GLY:HA3	3:03:1054:LEU:HB3	2.03	0.41
3:03:1130:ALA:O	3:03:1134:GLN:HG3	2.21	0.41
4:04:77:ARG:HA	4:04:77:ARG:HD2	1.92	0.41
4:04:116:PHE:CD1	4:04:123:ARG:HG3	2.56	0.41
4:04:154:LEU:HD23	4:04:158:GLN:HE21	1.85	0.41
4:04:221:ILE:HG23	4:04:222:LYS:N	2.35	0.41
4:04:226:ALA:O	4:04:229:GLN:HB3	2.20	0.41
4:04:502:PRO:HG2	4:04:601:ILE:HD13	2.02	0.41
4:04:746:LEU:HB3	4:04:754:ILE:HD11	2.03	0.41
4:04:841:GLY:O	4:04:900:GLY:HA3	2.20	0.41
4:04:871:LEU:C	4:04:871:LEU:HD23	2.41	0.41
4:04:1047:THR:HG23	4:04:1049:GLN:HG3	2.02	0.41
4:04:1095:MET:HA	4:04:1096:PRO:HD3	1.82	0.41
7:E:44:GLU:O	7:E:48:PRO:HD2	2.20	0.41
8:F:55:VAL:CG2	8:F:66:THR:HB	2.50	0.41
9:G:3:TYR:HE2	9:G:6:PRO:HG2	1.86	0.41
9:G:44:LYS:HA	9:G:45:PRO:HD3	1.83	0.41
9:G:169:TRP:CD1	9:G:170:LEU:HG	2.55	0.41
14:L:48:ARG:HG3	14:L:48:ARG:HH11	1.86	0.41
14:L:83:THR:O	14:L:94:ARG:NH1	2.54	0.41
14:L:109:GLN:HG2	14:L:110:VAL:N	2.34	0.41
14:L:112:ARG:HD3	14:L:113:LYS:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:83:THR:O	15:M:87:LEU:HG	2.21	0.41
18:P:19:THR:HG22	18:P:25:GLY:C	2.41	0.41
18:P:85:TYR:O	18:P:89:ARG:HG2	2.21	0.41
22:T:46:HIS:HB2	22:T:70:LYS:HD3	2.03	0.41
23:U:48:ARG:HD3	23:U:51:TYR:CE2	2.56	0.41
26:X:34:ARG:HH11	26:X:34:ARG:HG3	1.86	0.41
1:A:962:C:O2'	1:A:963:G:H5'	2.21	0.41
2:02:100:LEU:HD21	2:02:121:VAL:CG1	2.50	0.41
2:02:182:ARG:HE	2:02:184:ALA:HB2	1.86	0.41
3:03:257:ALA:HB3	3:03:262:TYR:CE2	2.56	0.41
3:03:528:ARG:HH21	3:03:663:VAL:HG13	1.86	0.41
3:03:617:ALA:HB2	3:03:650:VAL:CG1	2.51	0.41
3:03:886:LYS:CB	3:03:917:SER:HA	2.49	0.41
3:03:1119:MET:HG3	3:03:1204:LEU:CD1	2.50	0.41
4:04:38:VAL:HB	4:04:105:ILE:HD11	2.03	0.41
4:04:110:PRO:HD2	4:04:296:LYS:HE3	2.01	0.41
4:04:278:ARG:HG3	4:04:281:ARG:NH2	2.35	0.41
4:04:480:ALA:HA	4:04:484:MET:HB2	2.02	0.41
4:04:603:LYS:O	4:04:607:THR:HG23	2.21	0.41
4:04:1039:ASP:OD1	4:04:1074:LEU:HD13	2.21	0.41
4:04:1242:ARG:HA	4:04:1242:ARG:HD3	1.85	0.41
4:04:1268:ASN:HB3	4:04:1301:THR:H	1.86	0.41
7:E:21:ARG:NH1	7:E:21:ARG:HB2	2.35	0.41
7:E:45:LYS:HD3	7:E:45:LYS:HA	1.89	0.41
9:G:131:ILE:HG22	9:G:133:SER:H	1.86	0.41
12:J:4:ARG:HD2	12:J:6:ILE:HD11	2.03	0.41
12:J:31:VAL:HG22	12:J:32:ASP:OD2	2.21	0.41
12:J:110:ARG:HG2	12:J:110:ARG:HH11	1.85	0.41
14:L:26:LYS:HD2	14:L:26:LYS:N	2.36	0.41
21:S:39:PHE:CD2	21:S:41:PRO:HD3	2.56	0.41
26:X:35:ARG:N	26:X:35:ARG:HD2	2.36	0.41
1:A:1014:A:H2'	1:A:1015:G:O4'	2.21	0.40
1:A:1233:G:OP1	14:L:124:PRO:HB3	2.20	0.40
1:A:1255:G:H2'	1:A:1279:G:N2	2.36	0.40
2:02:9:LEU:C	2:02:10:LYS:HD2	2.41	0.40
3:03:502:VAL:HG22	3:03:506:PHE:HD2	1.87	0.40
4:04:165:TYR:CE1	4:04:178:ALA:HB3	2.56	0.40
4:04:579:LEU:HA	4:04:582:ILE:HD12	2.03	0.40
4:04:1189:MET:N	4:04:1189:MET:SD	2.94	0.40
9:G:124:VAL:HB	9:G:142:VAL:HG23	2.03	0.40
10:H:97:PRO:HG2	10:H:98:ALA:H	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:86:ARG:HH11	11:I:86:ARG:HG2	1.85	0.40
13:K:45:ILE:HG12	13:K:60:LEU:HD22	2.03	0.40
14:L:20:ILE:HD11	14:L:82:ILE:HA	2.02	0.40
1:A:419:C:H2'	1:A:420:U:O4'	2.22	0.40
2:01:28:LEU:HD21	2:02:231:PHE:HE2	1.85	0.40
2:01:74:VAL:HG22	2:01:75:GLN:N	2.36	0.40
2:01:195:ARG:HE	2:01:195:ARG:HA	1.86	0.40
3:03:406:ASN:HA	3:03:409:LEU:HD12	2.03	0.40
3:03:487:LEU:HD23	3:03:487:LEU:H	1.86	0.40
4:04:201:LEU:O	4:04:217:LEU:HD21	2.20	0.40
4:04:797:THR:O	4:04:801:VAL:HG13	2.21	0.40
4:04:1010:GLN:CD	4:04:1010:GLN:N	2.74	0.40
6:B:4:SER:HA	6:B:7:GLN:OE1	2.22	0.40
11:I:29:ILE:HD11	11:I:62:MET:SD	2.61	0.40
20:R:35:ILE:HG22	20:R:39:GLN:HE21	1.85	0.40
22:T:58:VAL:HG23	22:T:76:ARG:O	2.21	0.40
25:W:84:LYS:HB2	25:W:84:LYS:NZ	2.37	0.40
1:A:71:A:H3'	1:A:72:A:C5'	2.48	0.40
1:A:560:A:H4'	1:A:561:U:H5'	2.03	0.40
2:01:90:VAL:HG21	2:01:121:VAL:HG13	2.03	0.40
2:01:192:VAL:HG11	2:01:195:ARG:HB3	2.02	0.40
3:03:528:ARG:HH11	3:03:575:LEU:HB3	1.87	0.40
3:03:1087:TYR:CE1	3:03:1213:TYR:HB2	2.56	0.40
3:03:1094:VAL:HG22	3:03:1095:ASP:N	2.35	0.40
4:04:37:GLU:HA	4:04:104:HIS:O	2.21	0.40
4:04:514:THR:HB	4:04:576:ARG:HG2	2.04	0.40
4:04:526:VAL:C	4:04:527:LEU:HD12	2.42	0.40
4:04:665:GLN:HA	4:04:665:GLN:OE1	2.22	0.40
4:04:726:ALA:HA	4:04:732:GLY:O	2.21	0.40
4:04:1357:ILE:HG13	4:04:1359:ALA:H	1.86	0.40
6:B:115:UNK:HA	6:B:119:UNK:O	2.20	0.40
6:B:171:UNK:O	6:B:175:UNK:N	2.54	0.40
7:E:21:ARG:C	7:E:23:TRP:H	2.24	0.40
9:G:82:LYS:HZ1	9:G:82:LYS:HA	1.86	0.40
10:H:68:ARG:HD2	10:H:68:ARG:C	2.42	0.40
14:L:53:LEU:HD12	14:L:97:LEU:HD12	2.03	0.40
20:R:31:LEU:O	20:R:35:ILE:HG12	2.22	0.40
22:T:30:HIS:HA	22:T:31:PRO:HD3	1.89	0.40
25:W:35:TYR:CE1	25:W:78:LEU:HD13	2.56	0.40
25:W:57:VAL:O	25:W:61:ALA:HB2	2.21	0.40
1:A:606:G:O5'	1:A:607:A:H5'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:748:G:O2'	1:A:749:A:H5'	2.21	0.40
1:A:1372:U:H2'	1:A:1373:G:O4'	2.21	0.40
3:03:159:SER:HA	3:03:172:TYR:HA	2.03	0.40
3:03:697:LYS:H	3:03:697:LYS:CD	2.28	0.40
3:03:1239:VAL:HG23	3:03:1240:ASP:N	2.36	0.40
3:03:1252:SER:HB3	3:03:1255:THR:O	2.22	0.40
4:04:672:LEU:N	4:04:672:LEU:HD12	2.37	0.40
4:04:1038:THR:O	4:04:1040:MET:HG3	2.21	0.40
4:04:1206:ARG:HG3	4:04:1206:ARG:O	2.21	0.40
7:E:21:ARG:HB2	7:E:21:ARG:HH11	1.87	0.40
7:E:23:TRP:CH2	7:E:25:PRO:HB3	2.52	0.40
7:E:209:ALA:HB1	7:E:213:TYR:CD2	2.57	0.40
11:I:71:ILE:HA	11:I:74:LEU:HB3	2.04	0.40
1:A:252:U:O2	1:A:253:A:C8	2.75	0.40
1:A:893:C:H2'	1:A:894:G:H8	1.87	0.40
1:A:1513:A:H2'	1:A:1514:G:H8	1.85	0.40
2:02:100:LEU:HD21	2:02:121:VAL:CG2	2.49	0.40
3:03:147:SER:HA	3:03:459:MET:HE2	2.04	0.40
3:03:272:ARG:O	3:03:276:GLN:HG3	2.22	0.40
3:03:710:VAL:HA	3:03:715:THR:HG21	2.03	0.40
4:04:58:CYS:SG	4:04:61:ILE:HG13	2.61	0.40
4:04:399:LYS:HA	4:04:402:GLU:CB	2.52	0.40
4:04:721:SER:HA	4:04:724:MET:HE3	2.02	0.40
4:04:851:PRO:HG3	4:04:876:SER:HB2	2.02	0.40
4:04:861:ASN:OD1	4:04:861:ASN:O	2.39	0.40
4:04:1231:ARG:HA	4:04:1234:VAL:HG22	2.03	0.40
7:E:26:LYS:O	7:E:28:LYS:N	2.54	0.40
11:I:38:ARG:HA	11:I:38:ARG:NE	2.37	0.40
13:K:45:ILE:CD1	13:K:60:LEU:HB3	2.52	0.40
13:K:76:ARG:HG3	13:K:76:ARG:NH1	2.37	0.40
14:L:25:GLY:C	14:L:26:LYS:HD2	2.42	0.40
14:L:29:ILE:HA	14:L:64:ILE:O	2.22	0.40
23:U:30:LYS:HA	23:U:33:ILE:CG1	2.50	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%)	192 (85%)	30 (13%)	3 (1%)	12	48
2	02	225/229 (98%)	176 (78%)	36 (16%)	13 (6%)	1	18
3	03	1323/1340 (99%)	1076 (81%)	209 (16%)	38 (3%)	4	29
4	04	1339/1369 (98%)	1128 (84%)	167 (12%)	44 (3%)	4	26
5	05	57/59 (97%)	46 (81%)	9 (16%)	2 (4%)	3	25
6	B	6/153 (4%)	6 (100%)	0	0	100	100
7	E	216/218 (99%)	159 (74%)	31 (14%)	26 (12%)	0	6
8	F	204/206 (99%)	185 (91%)	17 (8%)	2 (1%)	15	55
9	G	203/205 (99%)	166 (82%)	32 (16%)	5 (2%)	5	32
10	H	155/157 (99%)	123 (79%)	28 (18%)	4 (3%)	5	31
11	I	98/100 (98%)	82 (84%)	14 (14%)	2 (2%)	7	38
12	J	149/151 (99%)	133 (89%)	14 (9%)	2 (1%)	12	48
13	K	127/129 (98%)	105 (83%)	20 (16%)	2 (2%)	9	44
14	L	125/127 (98%)	98 (78%)	25 (20%)	2 (2%)	9	44
15	M	96/98 (98%)	72 (75%)	19 (20%)	5 (5%)	2	19
16	N	114/116 (98%)	87 (76%)	20 (18%)	7 (6%)	1	17
17	O	121/123 (98%)	92 (76%)	23 (19%)	6 (5%)	2	20
18	P	112/114 (98%)	95 (85%)	14 (12%)	3 (3%)	5	31
19	Q	98/100 (98%)	79 (81%)	14 (14%)	5 (5%)	2	19
20	R	86/88 (98%)	77 (90%)	9 (10%)	0	100	100
21	S	80/82 (98%)	66 (82%)	12 (15%)	2 (2%)	5	32
22	T	78/80 (98%)	63 (81%)	13 (17%)	2 (3%)	5	31
23	U	63/65 (97%)	51 (81%)	8 (13%)	4 (6%)	1	17
24	V	77/79 (98%)	63 (82%)	13 (17%)	1 (1%)	12	48
25	W	83/85 (98%)	66 (80%)	16 (19%)	1 (1%)	13	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	X	63/65 (97%)	47 (75%)	12 (19%)	4 (6%)	1	17
All	All	5523/5767 (96%)	4533 (82%)	805 (15%)	185 (3%)	6	26

All (185) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	02	20	SER
2	02	136	GLU
2	02	137	ASN
3	03	398	SER
3	03	625	GLU
3	03	672	GLU
3	03	674	ASP
3	03	842	ASP
3	03	1321	GLU
4	04	122	SER
4	04	345	LYS
4	04	357	VAL
4	04	503	SER
4	04	1167	LYS
4	04	1343	GLU
7	E	14	VAL
7	E	25	PRO
7	E	39	HIS
7	E	40	ILE
7	E	44	GLU
7	E	189	THR
9	G	31	CYS
16	N	126	ARG
17	O	27	PRO
18	P	26	LYS
23	U	20	GLU
2	01	168	ILE
3	03	16	GLY
3	03	47	TYR
3	03	63	SER
3	03	491	ASP
3	03	566	GLY
3	03	655	VAL
3	03	673	HIS
3	03	917	SER
3	03	1224	PRO

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Mol	Chain	Res	Type
4	04	89	GLY
4	04	175	GLU
4	04	318	GLY
4	04	332	LYS
4	04	860	ARG
4	04	1084	GLN
4	04	1341	ARG
7	E	37	LYS
7	E	43	LEU
7	E	76	ALA
7	E	89	GLN
7	E	101	LEU
8	F	126	ARG
9	G	26	ALA
9	G	47	LEU
10	H	11	GLN
15	M	53	ILE
16	N	87	GLY
16	N	119	GLY
17	O	23	LEU
18	P	98	GLY
22	T	19	SER
23	U	49	ALA
26	X	38	TYR
2	01	67	GLU
2	02	13	LEU
2	02	63	GLY
3	03	596	ASP
3	03	746	ALA
3	03	1157	GLN
4	04	49	PHE
4	04	108	ALA
4	04	264	ASP
4	04	307	LEU
4	04	343	LEU
4	04	417	ARG
4	04	523	GLU
4	04	596	LEU
4	04	840	LEU
4	04	1170	LYS
7	E	18	HIS
7	E	27	MET

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Mol	Chain	Res	Type
7	E	45	LYS
7	E	64	LYS
7	E	152	LYS
7	E	213	TYR
10	H	110	MET
11	I	53	LYS
13	K	47	ASP
14	L	107	ALA
15	M	43	PRO
15	M	56	HIS
15	M	75	ASP
16	N	14	GLN
17	O	108	ASP
19	Q	31	SER
19	Q	61	ASN
21	S	28	ARG
2	02	130	ILE
3	03	342	ASP
3	03	841	ARG
3	03	851	THR
3	03	879	GLY
3	03	1270	PHE
4	04	256	ASP
4	04	903	LEU
4	04	1250	ASP
4	04	1275	LEU
4	04	1334	GLU
5	05	16	ARG
7	E	77	SER
7	E	88	ASP
10	H	23	THR
14	L	124	PRO
15	M	92	LEU
16	N	91	GLY
16	N	93	GLU
17	O	35	ARG
23	U	19	GLN
23	U	44	ILE
26	X	25	LYS
2	02	52	PRO
3	03	1062	PRO
3	03	1151	LEU

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Mol	Chain	Res	Type
3	03	1249	GLY
4	04	595	ALA
4	04	761	ALA
4	04	826	ILE
4	04	1294	ALA
4	04	1332	LEU
7	E	11	LYS
7	E	29	PRO
9	G	45	PRO
10	H	77	ASN
11	I	33	GLU
12	J	57	GLU
12	J	149	ALA
13	K	53	ASP
17	O	41	PRO
19	Q	65	GLN
25	W	65	LEU
2	02	72	GLU
2	02	138	ALA
2	02	169	GLY
2	02	209	GLY
3	03	545	PHE
3	03	840	SER
3	03	853	ASP
3	03	1320	PRO
4	04	251	PRO
4	04	734	ALA
7	E	21	ARG
7	E	47	VAL
19	Q	21	ALA
22	T	50	ASN
26	X	10	GLU
3	03	1317	PRO
4	04	815	GLY
5	05	4	VAL
3	03	21	VAL
4	04	998	PRO
4	04	1000	GLY
16	N	38	GLY
17	O	62	VAL
18	P	23	GLY
2	02	166	ARG

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Mol	Chain	Res	Type
3	03	110	PRO
3	03	329	GLY
3	03	355	PRO
4	04	451	PRO
4	04	825	VAL
7	E	193	PRO
8	F	144	GLY
9	G	24	VAL
24	V	75	PRO
2	01	179	PRO
2	02	167	PRO
3	03	302	ILE
3	03	564	PRO
3	03	1155	VAL
4	04	333	GLY
4	04	1171	GLY
7	E	33	GLY
7	E	98	GLY
21	S	36	VAL
4	04	92	VAL
4	04	258	GLY
26	X	11	PRO
19	Q	56	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	01	194/197 (98%)	192 (99%)	2 (1%)	76	86
2	02	194/197 (98%)	189 (97%)	5 (3%)	46	66
3	03	1098/1155 (95%)	1081 (98%)	17 (2%)	65	80
4	04	1103/1141 (97%)	1088 (99%)	15 (1%)	67	80
5	05	49/49 (100%)	49 (100%)	0	100	100
6	B	6/7 (86%)	6 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	E	180/180 (100%)	173 (96%)	7 (4%)	32	56
8	F	170/170 (100%)	167 (98%)	3 (2%)	59	77
9	G	172/172 (100%)	165 (96%)	7 (4%)	30	55
10	H	119/119 (100%)	117 (98%)	2 (2%)	60	78
11	I	87/87 (100%)	87 (100%)	0	100	100
12	J	124/124 (100%)	122 (98%)	2 (2%)	62	79
13	K	104/104 (100%)	101 (97%)	3 (3%)	42	64
14	L	105/105 (100%)	102 (97%)	3 (3%)	42	64
15	M	86/86 (100%)	84 (98%)	2 (2%)	50	70
16	N	89/89 (100%)	87 (98%)	2 (2%)	52	71
17	O	103/103 (100%)	101 (98%)	2 (2%)	57	75
18	P	92/92 (100%)	92 (100%)	0	100	100
19	Q	83/83 (100%)	82 (99%)	1 (1%)	71	83
20	R	76/76 (100%)	75 (99%)	1 (1%)	69	81
21	S	65/65 (100%)	62 (95%)	3 (5%)	27	52
22	T	74/74 (100%)	74 (100%)	0	100	100
23	U	56/56 (100%)	55 (98%)	1 (2%)	59	77
24	V	70/70 (100%)	70 (100%)	0	100	100
25	W	65/65 (100%)	60 (92%)	5 (8%)	13	37
26	X	55/55 (100%)	51 (93%)	4 (7%)	14	39
All	All	4619/4721 (98%)	4532 (98%)	87 (2%)	59	75

All (87) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	01	143	ARG
2	01	166	ARG
2	02	13	LEU
2	02	133	LEU
2	02	148	ARG
2	02	172	LEU
2	02	182	ARG
3	03	143	ARG
3	03	214	ASN
3	03	487	LEU

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Mol	Chain	Res	Type
3	03	490	GLN
3	03	557	ARG
3	03	620	ASN
3	03	697	LYS
3	03	791	LEU
3	03	800	MET
3	03	808	ASN
3	03	1111	GLN
3	03	1170	MET
3	03	1172	LEU
3	03	1224	PRO
3	03	1232	MET
3	03	1301	ARG
3	03	1324	ASN
4	04	21	LYS
4	04	53	ARG
4	04	217	LEU
4	04	239	LEU
4	04	250	ARG
4	04	320	ASN
4	04	337	ARG
4	04	429	LEU
4	04	431	ARG
4	04	514	THR
4	04	596	LEU
4	04	704	GLU
4	04	1126	GLN
4	04	1189	MET
4	04	1193	TRP
7	E	14	VAL
7	E	20	THR
7	E	21	ARG
7	E	35	ARG
7	E	42	ASN
7	E	43	LEU
7	E	89	GLN
8	F	24	ASN
8	F	156	LEU
8	F	163	ARG
9	G	20	LEU
9	G	29	THR
9	G	68	GLU

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Mol	Chain	Res	Type
9	G	80	ARG
9	G	82	LYS
9	G	99	ASN
9	G	196	GLU
10	H	75	LEU
10	H	145	ASN
12	J	9	ARG
12	J	78	ARG
13	K	37	ASN
13	K	53	ASP
13	K	113	ARG
14	L	108	ARG
14	L	112	ARG
14	L	122	ARG
15	M	43	PRO
15	M	48	ARG
16	N	74	LYS
16	N	100	ASN
17	O	72	ASN
17	O	88	ASP
19	Q	37	ASP
20	R	16	ARG
21	S	5	ARG
21	S	25	ARG
21	S	47	GLU
23	U	48	ARG
25	W	2	ASN
25	W	8	LYS
25	W	19	HIS
25	W	63	LYS
25	W	65	LEU
26	X	17	ARG
26	X	34	ARG
26	X	35	ARG
26	X	38	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (99) such sidechains are listed below:

Mol	Chain	Res	Type
2	01	84	ASN
2	01	208	ASN
2	02	37	HIS

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Mol	Chain	Res	Type
2	02	84	ASN
2	02	137	ASN
3	03	31	GLN
3	03	133	ASN
3	03	139	ASN
3	03	193	ASN
3	03	214	ASN
3	03	235	ASN
3	03	258	ASN
3	03	406	ASN
3	03	437	ASN
3	03	519	ASN
3	03	551	HIS
3	03	554	HIS
3	03	620	ASN
3	03	658	GLN
3	03	808	ASN
3	03	1070	HIS
3	03	1080	ASN
3	03	1090	ASN
3	03	1099	ASN
3	03	1111	GLN
3	03	1175	ASN
3	03	1236	ASN
3	03	1237	HIS
3	03	1307	ASN
3	03	1324	ASN
4	04	113	HIS
4	04	158	GLN
4	04	186	GLN
4	04	232	ASN
4	04	320	ASN
4	04	465	GLN
4	04	488	ASN
4	04	504	GLN
4	04	593	ASN
4	04	792	ASN
4	04	861	ASN
4	04	907	HIS
4	04	921	GLN
4	04	1049	GLN
4	04	1197	ASN

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Mol	Chain	Res	Type
4	04	1218	HIS
4	04	1235	ASN
4	04	1259	GLN
4	04	1279	GLN
4	04	1295	ASN
4	04	1326	GLN
4	04	1350	ASN
7	E	19	GLN
7	E	42	ASN
7	E	89	GLN
7	E	177	ASN
8	F	24	ASN
8	F	40	GLN
8	F	139	ASN
8	F	184	ASN
9	G	39	GLN
9	G	53	GLN
9	G	73	ASN
9	G	99	ASN
9	G	125	ASN
9	G	163	GLN
10	H	76	ASN
10	H	77	ASN
10	H	81	GLN
10	H	134	ASN
10	H	145	ASN
12	J	27	ASN
12	J	121	ASN
13	K	15	ASN
13	K	37	ASN
14	L	30	ASN
15	M	58	ASN
15	M	99	GLN
16	N	28	ASN
16	N	118	ASN
17	O	28	GLN
17	O	72	ASN
19	Q	34	ASN
19	Q	65	GLN
20	R	34	GLN
20	R	36	ASN
20	R	39	GLN

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Mol	Chain	Res	Type
20	R	50	HIS
21	S	18	GLN
21	S	26	ASN
21	S	40	ASN
22	T	30	HIS
22	T	50	ASN
23	U	31	ASN
25	W	2	ASN
25	W	12	GLN
25	W	54	GLN
25	W	74	HIS
25	W	81	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1441/1539 (93%)	164 (11%)	2 (0%)

All (164) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	40	C
1	A	48	C
1	A	51	A
1	A	60	A
1	A	61	G
1	A	66	A
1	A	68	G
1	A	70	U
1	A	71	A
1	A	72	A
1	A	83	C
1	A	85	U
1	A	86	G
1	A	89	U
1	A	90	C
1	A	94	G

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Mol	Chain	Res	Type
1	A	95	C
1	A	137	U
1	A	144	G
1	A	174	A
1	A	180	U
1	A	183	C
1	A	184	G
1	A	185	U
1	A	209	U
1	A	210	C
1	A	220	G
1	A	245	U
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C
1	A	280	C
1	A	281	G
1	A	289	G
1	A	306	A
1	A	328	C
1	A	344	A
1	A	345	C
1	A	352	C
1	A	372	C
1	A	377	G
1	A	388	G
1	A	397	A
1	A	398	U
1	A	406	G
1	A	413	G
1	A	414	A
1	A	423	G
1	A	427	U
1	A	429	U
1	A	441	A
1	A	448	A
1	A	467	U
1	A	468	A
1	A	479	U
1	A	480	U
1	A	486	U

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Mol	Chain	Res	Type
1	A	487	A
1	A	495	A
1	A	497	G
1	A	500	G
1	A	509	A
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	615	G
1	A	633	G
1	A	642	A
1	A	665	A
1	A	703	G
1	A	723	U
1	A	724	G
1	A	755	G
1	A	777	A
1	A	817	C
1	A	818	G
1	A	819	A
1	A	821	G
1	A	828	U
1	A	832	G
1	A	843	U
1	A	846	G
1	A	871	U

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Mol	Chain	Res	Type
1	A	873	A
1	A	902	G
1	A	926	G
1	A	934	C
1	A	935	A
1	A	945	G
1	A	960	U
1	A	961	U
1	A	966	G
1	A	969	A
1	A	975	A
1	A	977	A
1	A	982	U
1	A	984	C
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1004	A
1	A	1031	C
1	A	1033	G
1	A	1055	A
1	A	1068	G
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	1240	U
1	A	1241	G
1	A	1258	G
1	A	1260	G

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Mol	Chain	Res	Type
1	A	1261	A
1	A	1275	A
1	A	1280	A
1	A	1282	C
1	A	1287	A
1	A	1300	G
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	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 monosaccharides 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

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	53.99
1	B	179:UNK	C	191:UNK	N	19.24

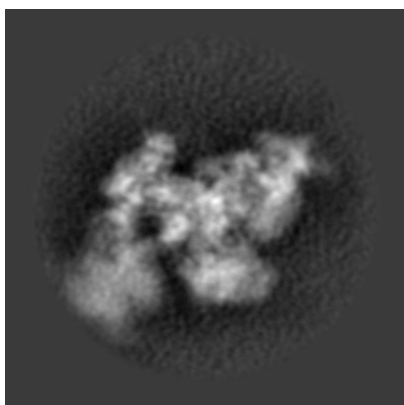
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7015. These allow visual inspection of the internal detail of the map and identification of artifacts.

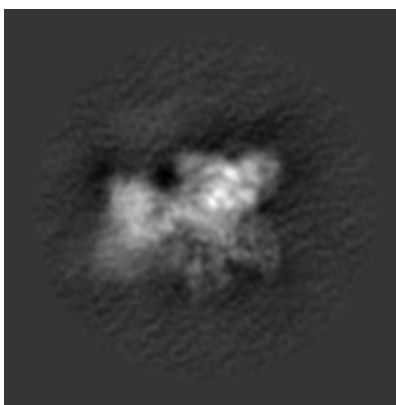
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

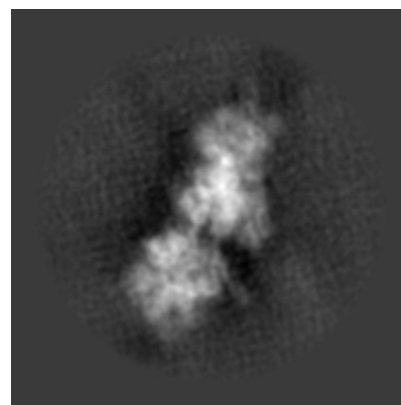
6.1.1 Primary map



X



Y

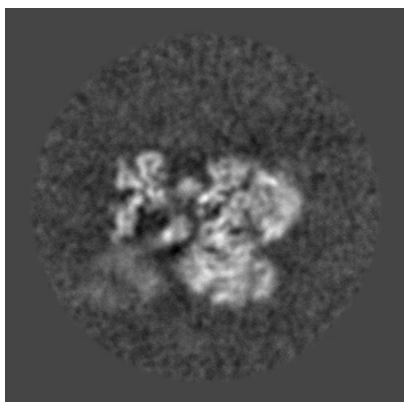


Z

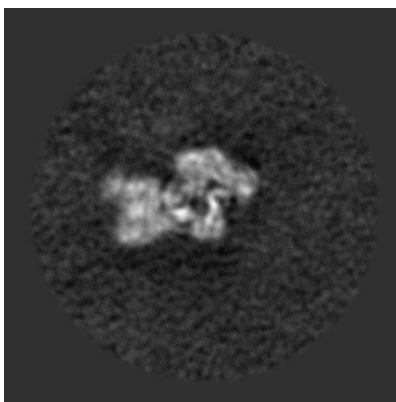
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

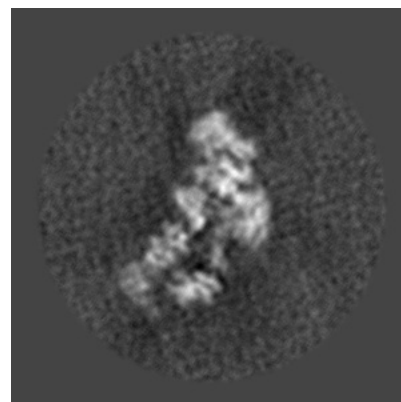
6.2.1 Primary map



X Index: 140



Y Index: 140

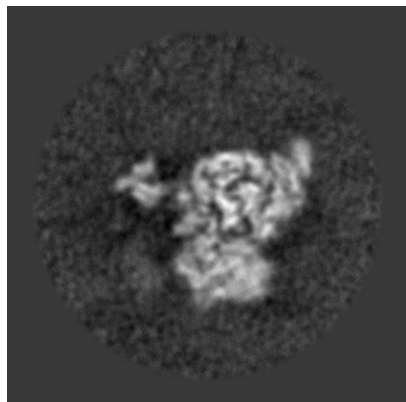


Z Index: 140

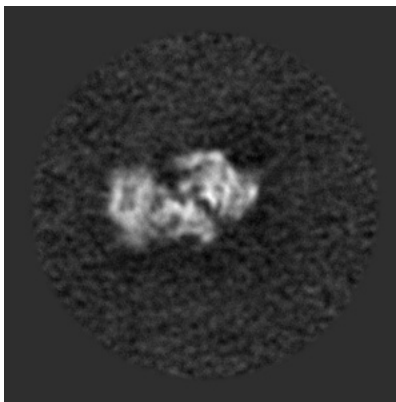
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

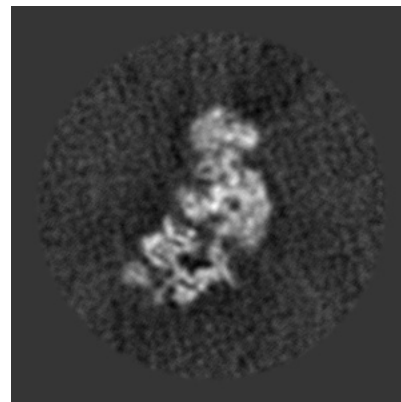
6.3.1 Primary map



X Index: 149



Y Index: 150

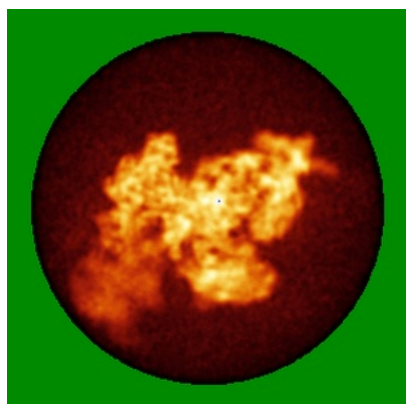


Z Index: 146

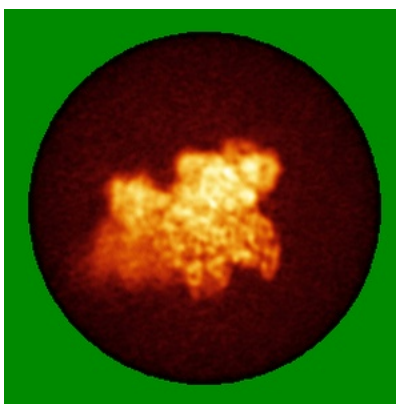
The images above show the largest variance slices of the map in three orthogonal directions.

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

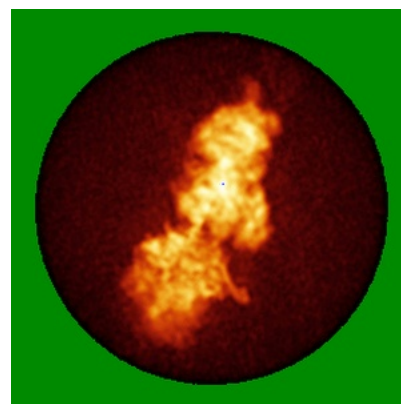
6.4.1 Primary map



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.

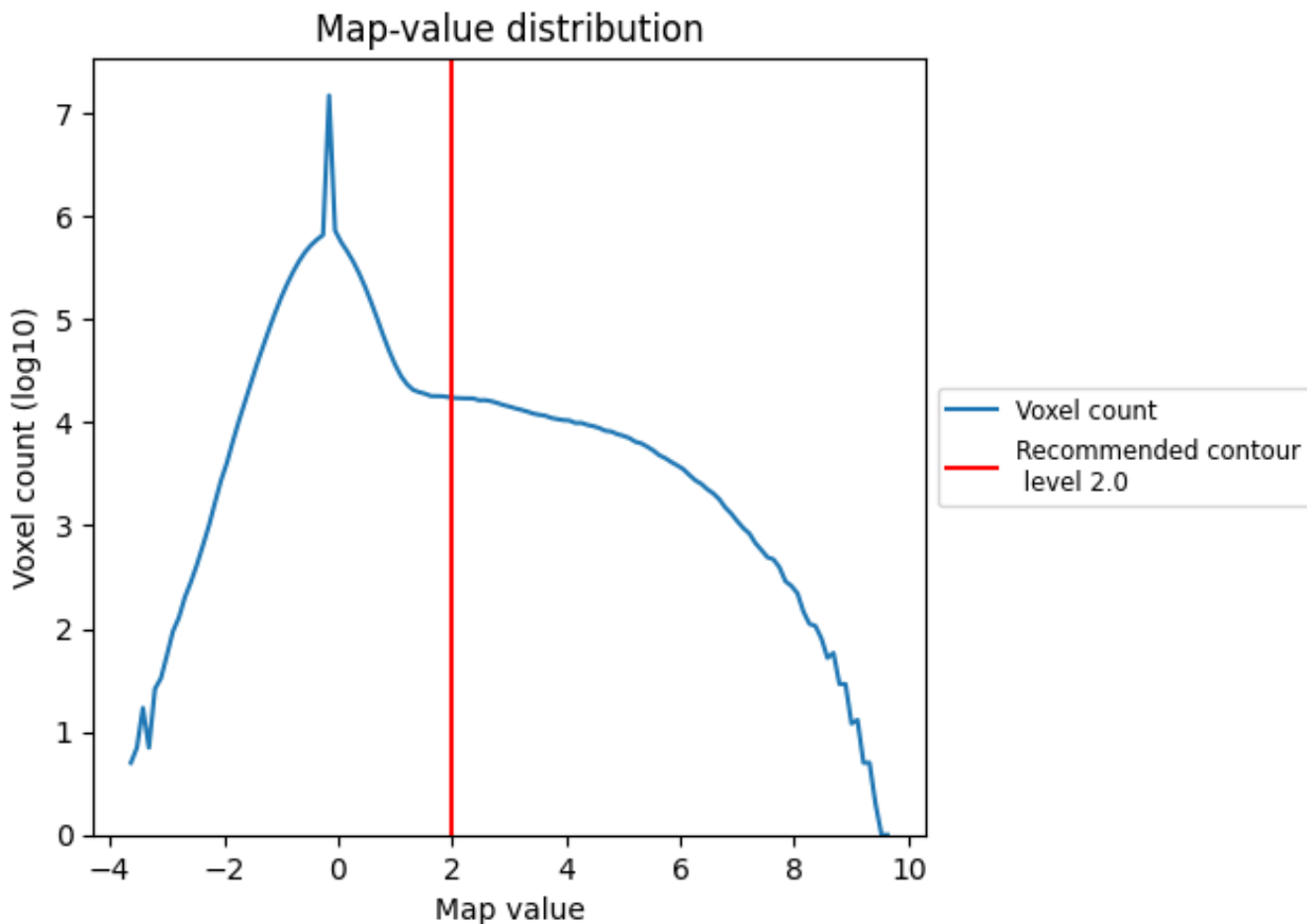
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

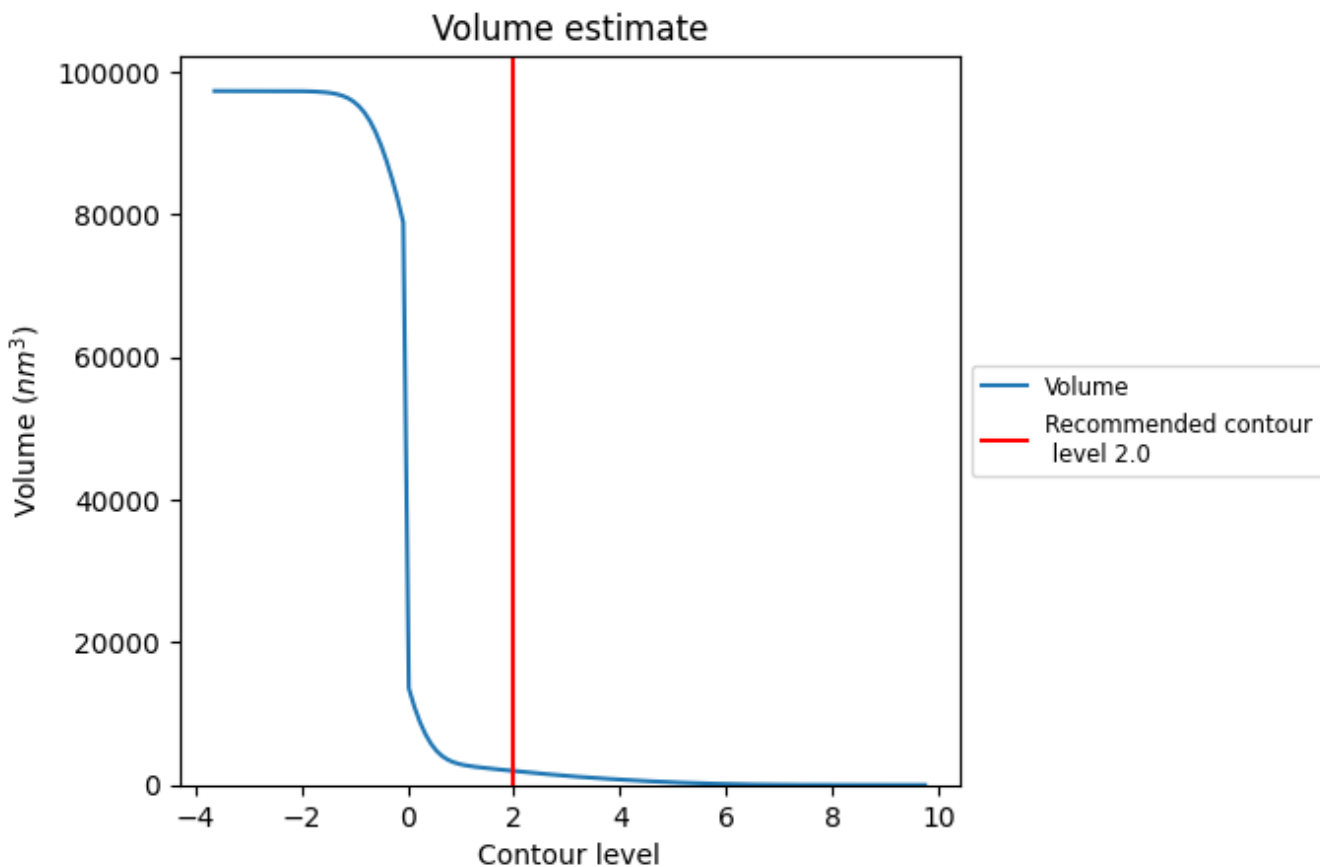
This section contains the results of statistical analysis of the map.

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.

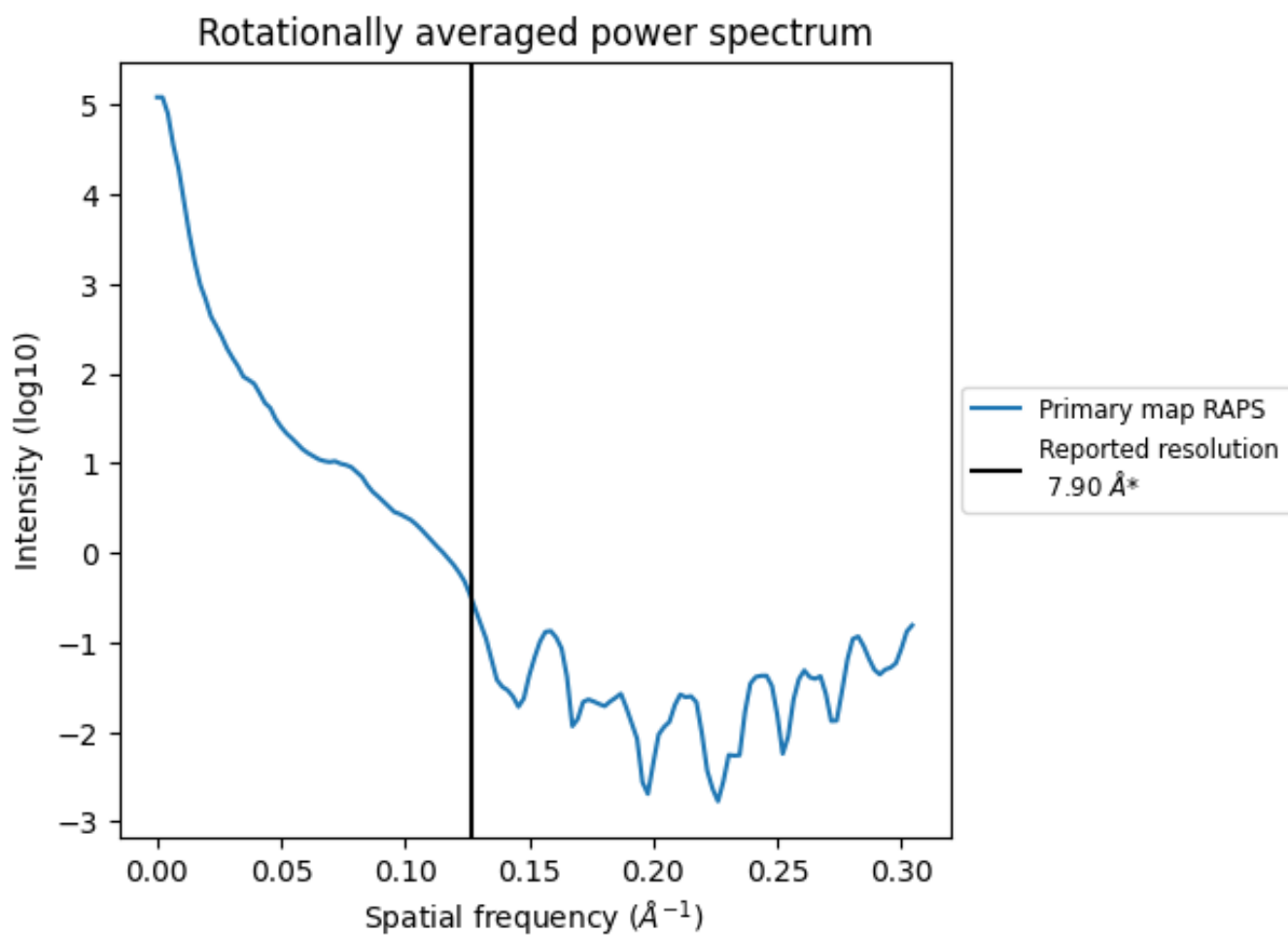
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1962 nm^3 ; this corresponds to an approximate mass of 1773 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 [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.127\AA^{-1}

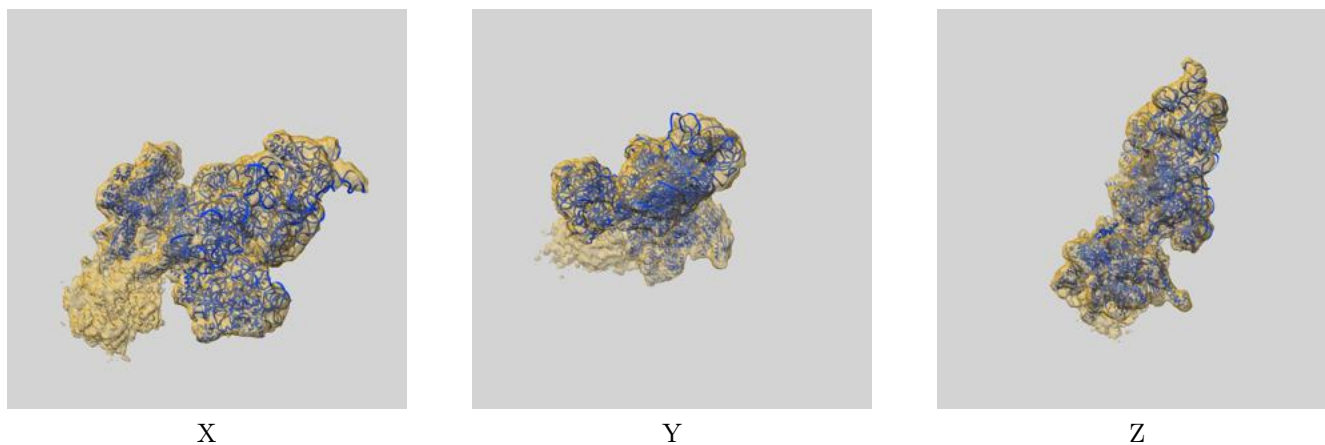
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

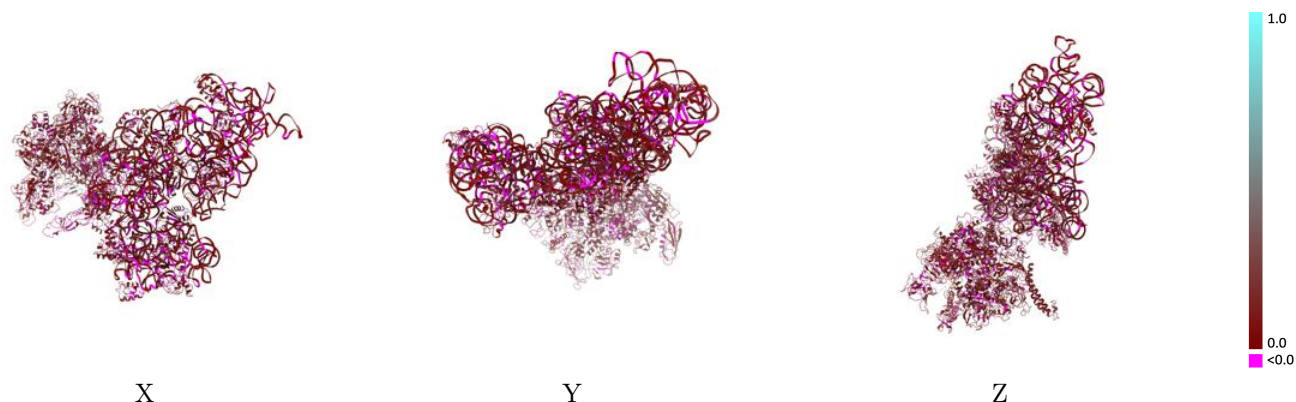
This section contains information regarding the fit between EMDB map EMD-7015 and PDB model 6AWC. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



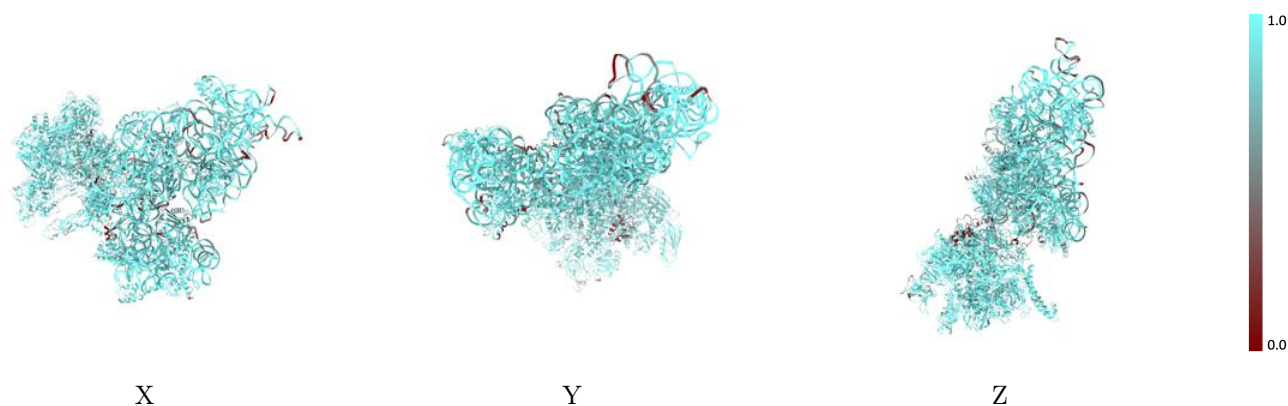
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



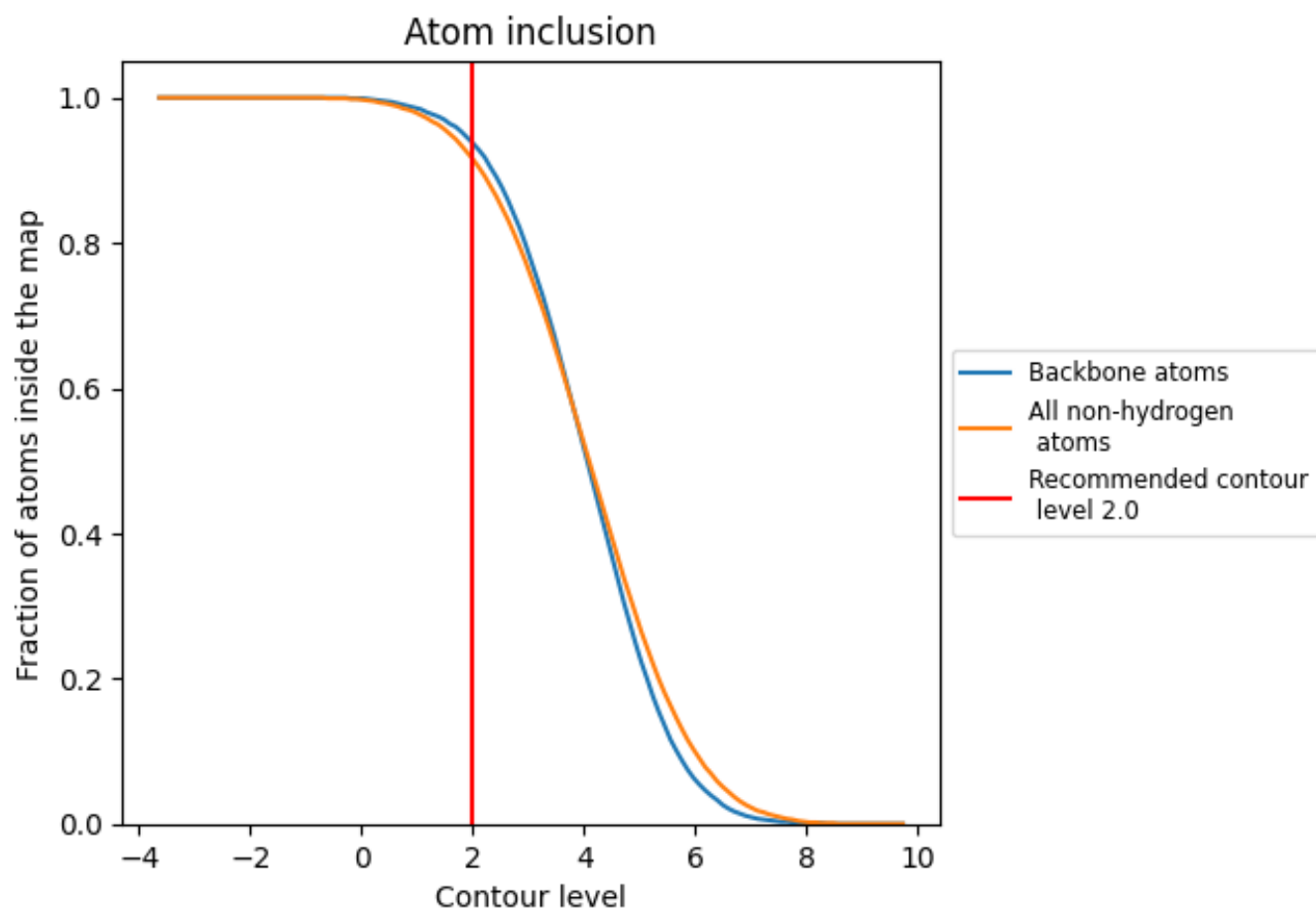
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.0).

























































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 92% 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 (2.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9160	 0.0950
01	 0.9410	 0.1410
02	 0.9460	 0.1200
03	 0.9060	 0.1110
04	 0.9140	 0.1210
05	 0.2890	 0.0470
A	 0.9260	 0.0890
B	 0.8900	 0.0700
E	 0.9680	 0.1250
F	 0.8560	 0.0970
G	 0.9270	 0.0660
H	 0.9180	 0.1200
I	 0.8470	 0.1130
J	 0.8500	 0.0660
K	 0.9290	 0.0960
L	 0.8980	 0.0530
M	 0.8910	 0.0440
N	 0.9720	 0.0530
O	 0.8790	 0.0640
P	 0.9270	 0.0590
Q	 0.9700	 0.0330
R	 0.9350	 0.0940
S	 0.9430	 0.0640
T	 0.9590	 0.0860
U	 0.9110	 0.0610
V	 0.9320	 0.0380
W	 0.9680	 0.0750
X	 0.8820	 0.1080

