



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:10 AM UTC

PDB ID : 4Y7N / pdb_00004y7n
Title : The Structure Insight into 5-Carboxycytosine Recognition by RNA Polymerase II during Transcription Elongation.
Authors : Wang, L.; Chong, J.; Wang, D.
Deposited on : 2015-02-15
Resolution : 3.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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A user guide is available at

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

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:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

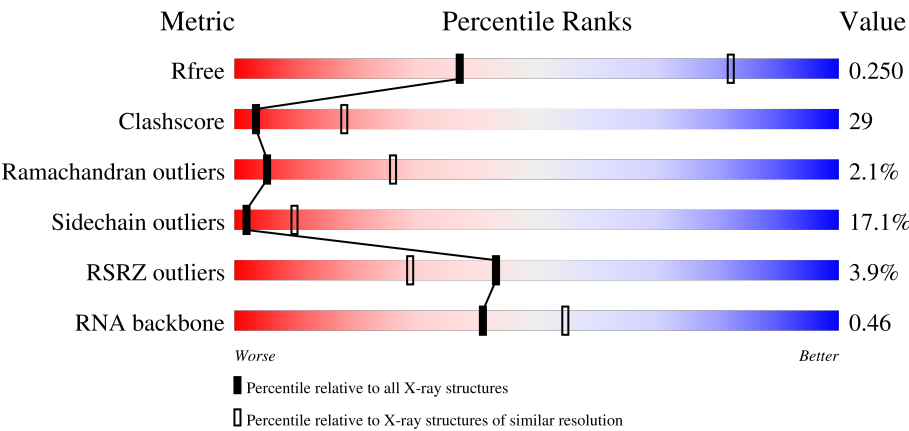
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)
RNA backbone	3983	1048 (3.60-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1733	3% 41% 31% 8% 20%
2	B	1224	4% 46% 35% 8% 10%
3	C	318	% 42% 34% 7% 16%
4	E	215	2% 56% 37% 7%

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Mol	Chain	Length	Quality of chain
5	F	155	
6	H	146	
7	I	122	
8	J	70	
9	K	120	
10	L	70	
11	T	29	
12	N	14	
13	R	9	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 29193 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 protein called DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1393	Total	C	N	O	S	0	0	0
			10953	6908	1921	2063	61			

- Molecule 2 is a protein called DNA-directed RNA polymerase II subunit RPB2,DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1103	Total	C	N	O	S	0	0	0
			8762	5549	1532	1626	55			

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	266	Total	C	N	O	S	0	0	0
			2095	1317	348	417	13			

- Molecule 4 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	214	Total	C	N	O	S	0	0	0
			1752	1111	309	321	11			

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	84	Total	C	N	O	S	0	0	0
			679	434	115	127	3			

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	H	133	Total	C	N	O	S	0	0	0
			1068	673	180	211	4			

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	I	119	Total	C	N	O	S	0	0	0
			971	596	179	186	10			

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	J	65	Total	C	N	O	S	0	0	0
			532	339	93	94	6			

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	K	114	Total	C	N	O	S	0	0	0
			919	590	156	171	2			

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	L	44	Total	C	N	O	S	0	0	0
			351	217	70	60	4			

- Molecule 11 is a DNA chain called DNA (29-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	T	29	Total	C	N	O	P	0	0	0
			587	280	108	171	28			

- Molecule 12 is a DNA chain called DNA (5'-D(*CP*TP*GP*CP*TP*TP*AP*TP*CP*GP*GP*TP*AP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	N	14	Total	C	N	O	P	0	0	0
			284	137	49	85	13			

- Molecule 13 is a RNA chain called RNA (5'-D(*AP*UP*GP*GP*AP*GP*AP*GP*G)-3').

- Molecule 14 is ZINC ION (CCD ID: ZN) (formula: Zn).

- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

- Molecule 16 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: G2P) (formula: $C_{11}H_{18}N_5O_{13}P_3$).

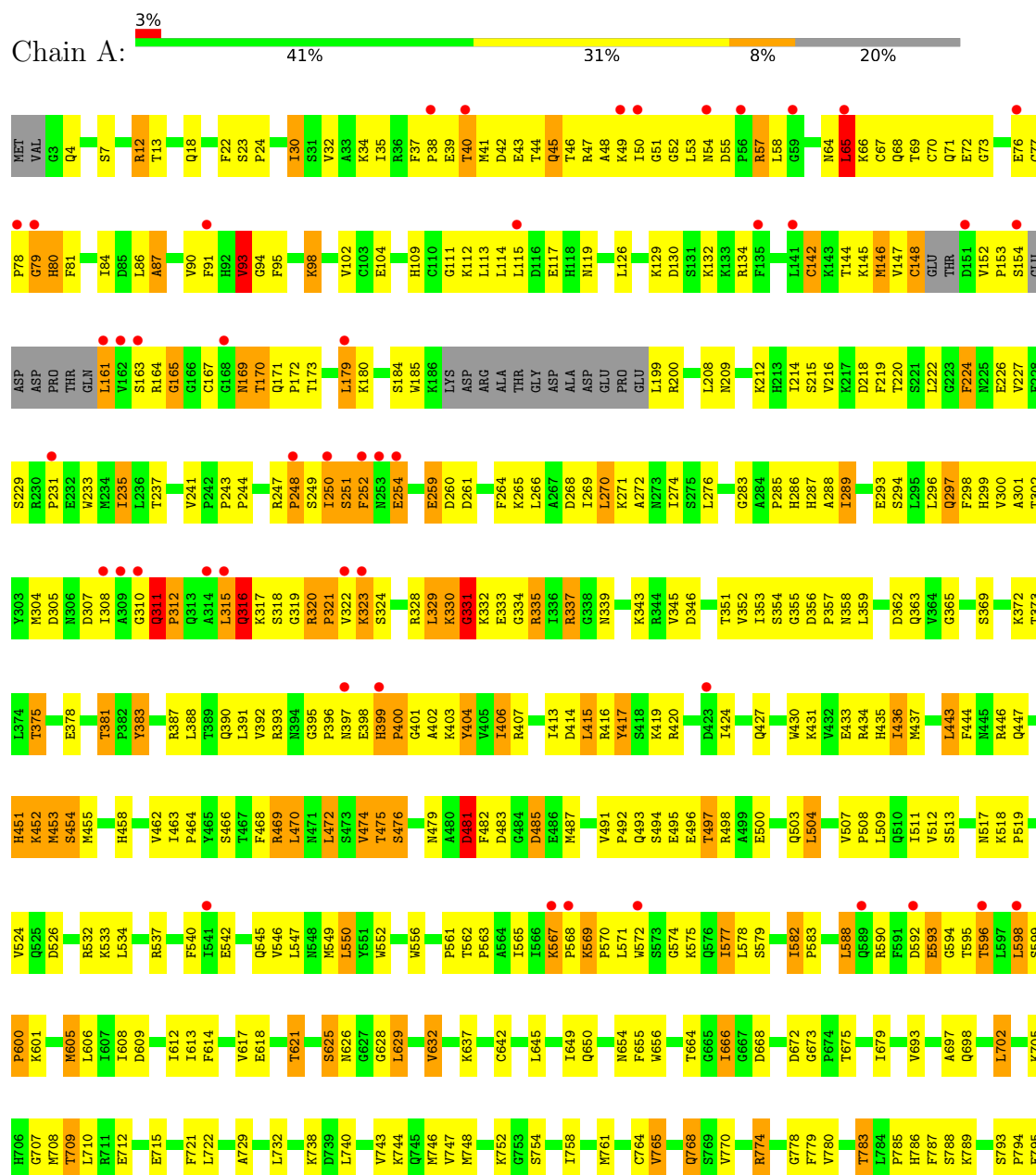


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
16	T	1	Total	C	N	O	P	0	0
			32	11	5	13	3		

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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: DNA-directed RNA polymerase II subunit RPB1

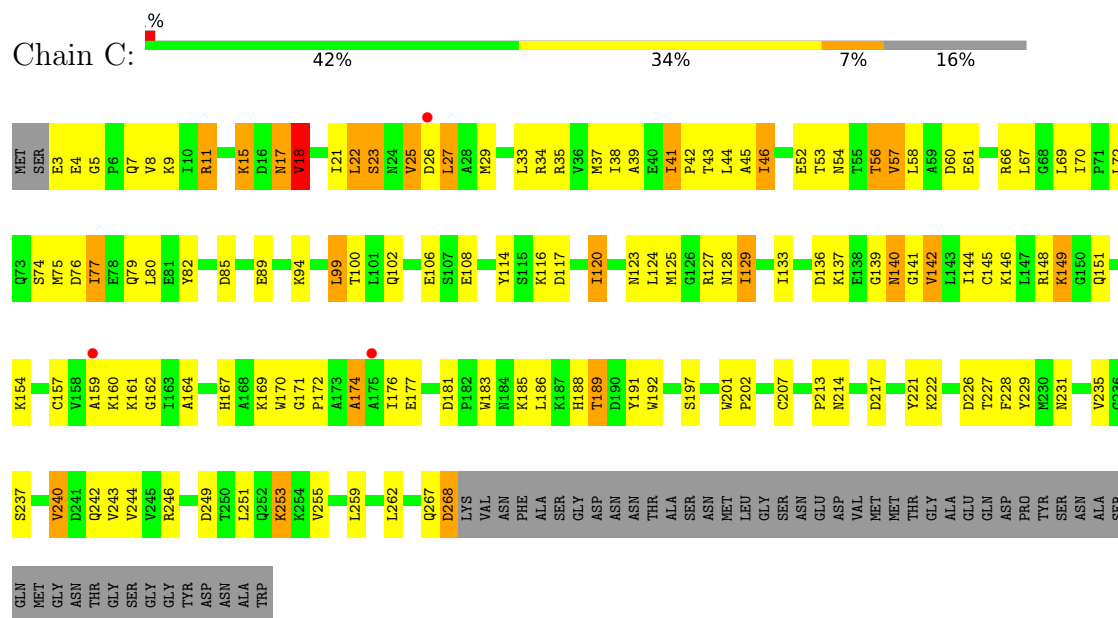




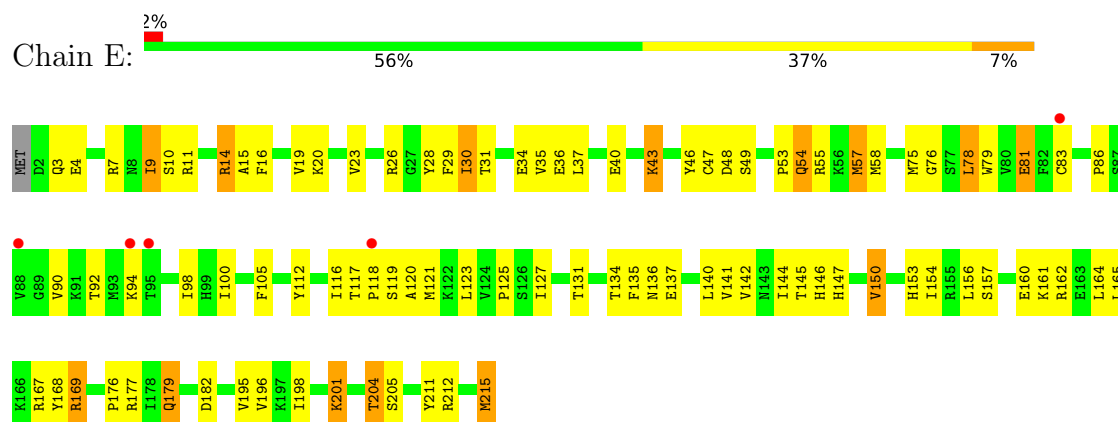
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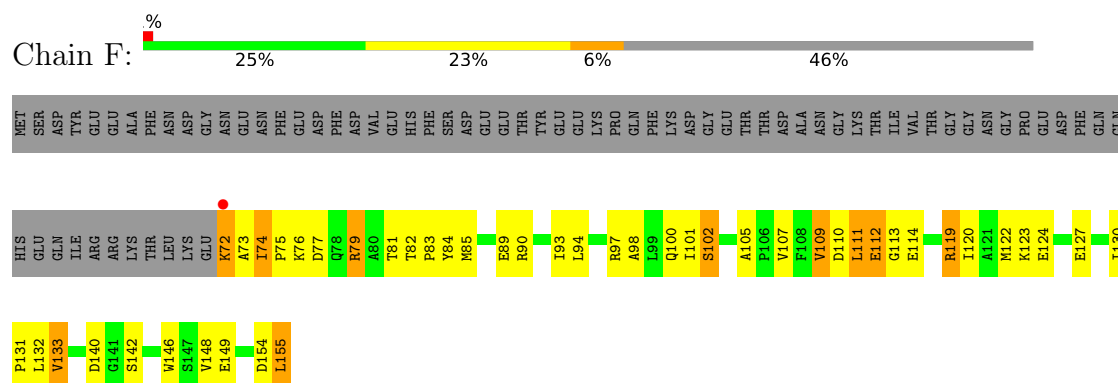
- Molecule 3: DNA-directed RNA polymerase II subunit RPB3



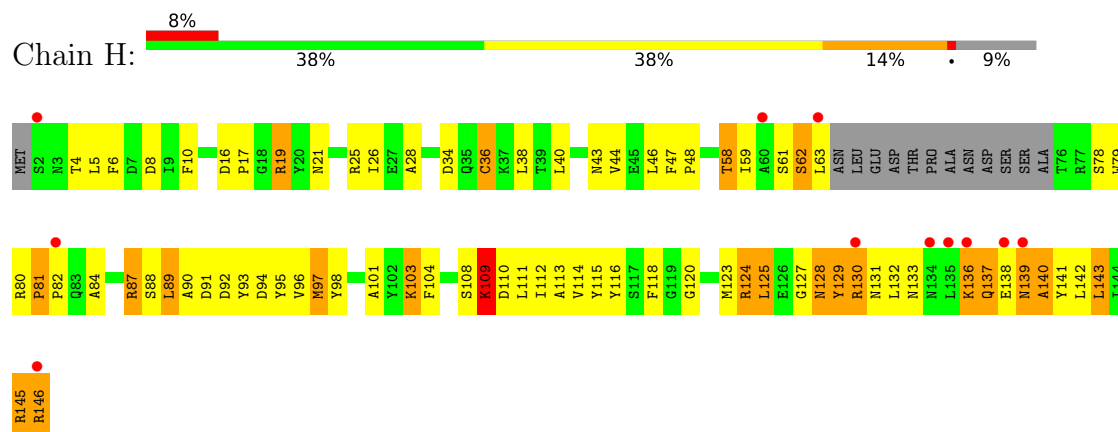
- Molecule 4: DNA-directed RNA polymerases I, II, and III subunit RPABC1



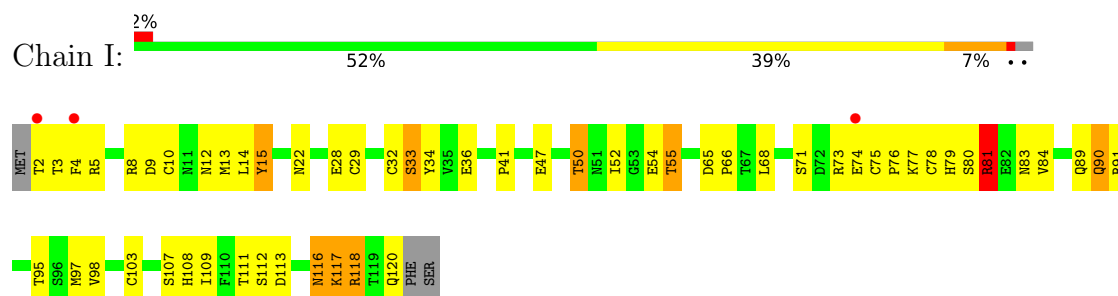
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC2



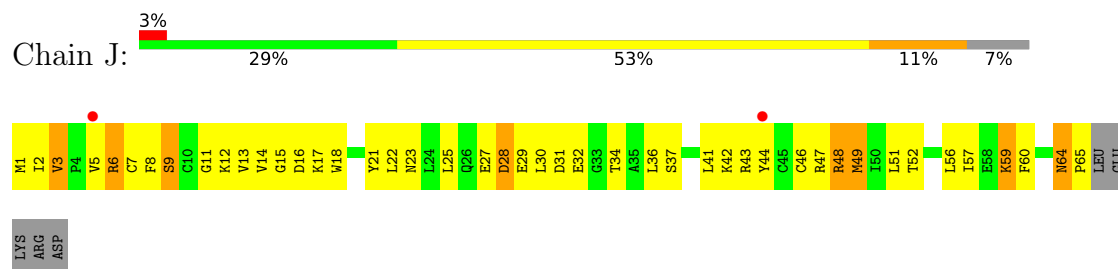
- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC3



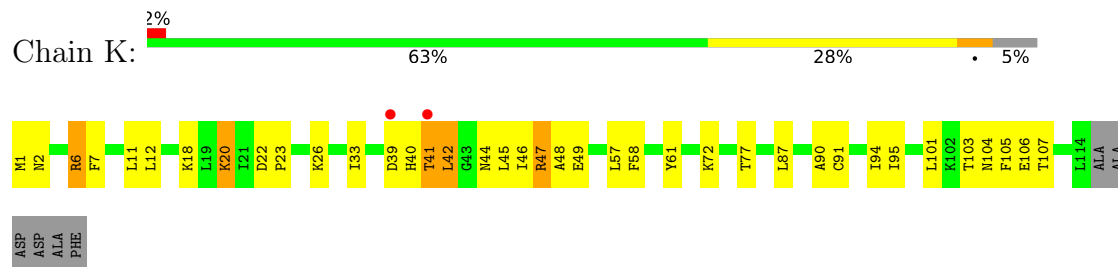
- Molecule 7: DNA-directed RNA polymerase II subunit RPB9



- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC5

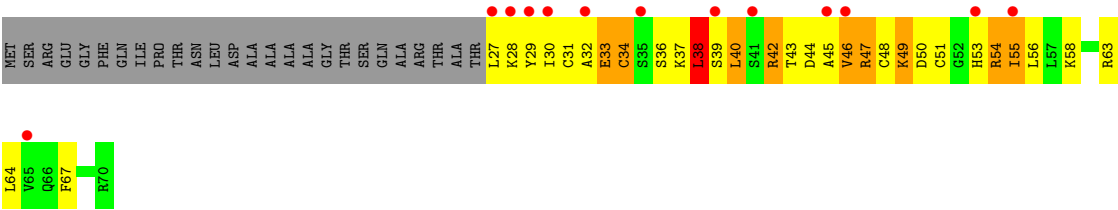


- Molecule 9: DNA-directed RNA polymerase II subunit RPB11

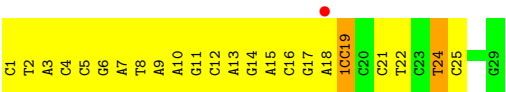


- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC4

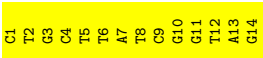
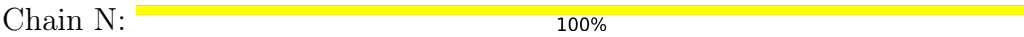




● Molecule 11: DNA (29-MER)



● Molecule 12: DNA (5'-D(*CP*TP*GP*CP*TP*TP*AP*TP*CP*GP*GP*TP*AP*G)-3')



● Molecule 13: RNA (5'-D(*AP*UP*GP*GP*AP*GP*AP*GP*G)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	168.18Å 222.61Å 192.83Å 90.00° 101.59° 90.00°	Depositor
Resolution (Å)	48.88 – 3.30 48.88 – 3.30	Depositor EDS
% Data completeness (in resolution range)	98.0 (48.88-3.30) 99.4 (48.88-3.30)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 3.25Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.207 , 0.250 0.207 , 0.250	Depositor DCC
R_{free} test set	5268 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	83.9	Xtriage
Anisotropy	0.481	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 57.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	29193	wwPDB-VP
Average B, all atoms (Å ²)	102.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.70% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG, G2P, 1CC

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	0.53	1/11146 (0.0%)	1.01	47/15066 (0.3%)
2	B	0.58	1/8932 (0.0%)	1.02	35/12045 (0.3%)
3	C	0.59	0/2133	1.07	6/2891 (0.2%)
4	E	0.49	0/1788	0.88	0/2406
5	F	0.50	0/691	0.92	1/933 (0.1%)
6	H	0.46	0/1086	0.86	4/1470 (0.3%)
7	I	0.50	0/989	0.93	3/1331 (0.2%)
8	J	0.64	0/541	0.99	1/727 (0.1%)
9	K	0.51	0/937	0.86	0/1265
10	L	0.44	0/353	0.98	2/468 (0.4%)
11	T	0.39	0/632	0.84	5/969 (0.5%)
12	N	0.28	0/317	0.47	0/488
13	R	0.35	0/223	0.58	0/348
All	All	0.54	2/29768 (0.0%)	0.98	104/40407 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	707	PRO	N-CD	5.35	1.55	1.47
1	A	400	PRO	N-CD	5.19	1.55	1.47

All (104) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	734	HIS	N-CA-C	-10.18	100.94	113.97
10	L	33	GLU	N-CA-C	-9.56	101.30	113.16
6	H	139	ASN	N-CA-C	9.40	122.46	110.33
1	A	77	CYS	N-CA-C	-9.30	96.10	110.14
2	B	1007	VAL	N-CA-C	-9.27	101.59	109.19
2	B	37	PHE	N-CA-C	-8.81	99.58	110.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	331	GLY	N-CA-C	8.35	132.97	113.18
3	C	174	ALA	N-CA-C	-8.23	94.90	108.48
2	B	248	SER	N-CA-C	-8.18	95.40	108.73
1	A	919	ILE	CB-CA-C	-8.11	98.94	112.16
1	A	919	ILE	N-CA-C	7.90	122.03	111.44
2	B	1156	ASP	N-CA-C	7.47	121.79	111.55
1	A	81	PHE	N-CA-C	7.38	120.27	110.53
1	A	598	LEU	N-CA-C	-7.14	95.58	110.80
2	B	711	GLU	C-N-CD	7.02	136.04	120.60
2	B	66	ASP	N-CA-C	-7.00	104.74	113.28
1	A	316	GLN	N-CA-C	6.90	118.75	110.19
1	A	993	LEU	N-CA-C	-6.80	103.80	111.14
3	C	18	VAL	CB-CA-C	-6.78	104.38	111.23
2	B	764	SER	CA-C-N	-6.73	112.76	119.56
2	B	764	SER	C-N-CA	-6.73	112.76	119.56
1	A	617	VAL	CB-CA-C	-6.62	104.08	111.23
7	I	81	ARG	N-CA-C	6.56	120.96	113.15
1	A	399	HIS	C-N-CD	6.54	134.99	120.60
11	T	24	DT	P-O5'-C5'	-6.53	110.20	120.00
1	A	1074	GLU	CA-C-N	-6.45	113.07	120.04
1	A	1074	GLU	C-N-CA	-6.45	113.07	120.04
2	B	475	SER	N-CA-C	6.22	117.75	110.97
2	B	1108	ARG	N-CA-C	-6.21	99.29	108.79
1	A	582	ILE	CA-C-N	6.20	127.59	119.84
1	A	582	ILE	C-N-CA	6.20	127.59	119.84
6	H	128	ASN	N-CA-C	6.19	121.35	113.55
2	B	973	ILE	CA-C-N	6.15	127.52	119.84
2	B	973	ILE	C-N-CA	6.15	127.52	119.84
6	H	36	CYS	N-CA-C	6.13	118.28	107.61
2	B	1154	ALA	N-CA-C	-6.10	102.48	110.53
1	A	673	GLY	CA-C-N	6.08	127.44	119.84
1	A	673	GLY	C-N-CA	6.08	127.44	119.84
2	B	616	ILE	CB-CA-C	-5.95	104.12	111.32
1	A	1412	ALA	N-CA-C	-5.94	105.12	112.90
2	B	21	GLU	N-CA-C	5.92	120.63	113.17
1	A	170	THR	N-CA-C	-5.89	100.40	109.76
1	A	406	ILE	N-CA-C	5.88	116.07	107.37
2	B	410	GLY	CA-C-N	5.85	125.98	119.32
2	B	410	GLY	C-N-CA	5.85	125.98	119.32
1	A	886	ILE	N-CA-C	5.84	117.27	110.62
2	B	780	VAL	CB-CA-C	-5.83	101.73	111.29
1	A	1311	VAL	N-CA-C	5.82	116.45	107.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	582	ILE	CB-CA-C	-5.76	105.58	110.94
11	T	22	DT	P-O5'-C5'	-5.75	111.38	120.00
11	T	22	DT	C5'-C4'-C3'	-5.74	106.29	114.90
8	J	15	GLY	N-CA-C	5.65	120.64	113.24
10	L	40	LEU	N-CA-C	-5.64	101.08	110.17
2	B	756	ILE	CB-CA-C	-5.64	104.80	110.89
1	A	474	VAL	N-CA-C	-5.63	107.49	112.90
1	A	664	THR	CB-CA-C	-5.60	102.06	110.24
2	B	606	LYS	N-CA-C	-5.57	106.84	113.97
1	A	595	THR	N-CA-C	-5.57	101.61	109.96
1	A	58	LEU	N-CA-C	-5.56	106.33	114.39
1	A	524	VAL	N-CA-C	5.52	116.80	108.96
2	B	382	ILE	CB-CA-C	-5.52	104.69	112.14
1	A	1340	GLY	N-CA-C	5.48	118.43	112.29
3	C	17	ASN	N-CA-C	5.47	117.71	109.23
1	A	1424	VAL	N-CA-C	-5.46	105.00	110.30
3	C	27	LEU	N-CA-C	-5.46	105.22	111.07
2	B	296	GLU	N-CA-C	-5.46	105.75	112.90
3	C	46	ILE	CB-CA-C	-5.44	103.12	111.71
2	B	868	MET	N-CA-C	-5.43	107.67	114.56
2	B	273	LEU	CA-C-N	5.42	126.62	119.84
2	B	273	LEU	C-N-CA	5.42	126.62	119.84
2	B	102	VAL	CB-CA-C	-5.41	102.55	110.62
2	B	825	VAL	N-CA-C	5.40	115.89	108.12
1	A	632	VAL	CB-CA-C	-5.39	105.08	111.81
1	A	507	VAL	CA-C-N	-5.38	113.07	119.05
1	A	507	VAL	C-N-CA	-5.38	113.07	119.05
1	A	1226	VAL	N-CA-C	5.31	115.50	107.75
2	B	712	PRO	CA-N-CD	-5.31	104.07	111.50
11	T	24	DT	C5'-C4'-C3'	-5.29	106.96	114.90
2	B	570	VAL	CA-C-N	5.27	125.33	119.32
2	B	570	VAL	C-N-CA	5.27	125.33	119.32
2	B	580	VAL	N-CA-C	5.25	116.26	108.23
1	A	825	ILE	CB-CA-C	-5.25	105.06	112.14
1	A	23	SER	CA-C-N	5.24	126.39	119.84
1	A	23	SER	C-N-CA	5.24	126.39	119.84
1	A	930	ASP	N-CA-C	-5.23	105.49	111.14
2	B	1009	ASP	N-CA-C	-5.23	106.41	112.89
1	A	80	HIS	N-CA-C	-5.23	102.01	110.32
1	A	595	THR	CB-CA-C	5.22	118.25	109.89
3	C	108	GLU	N-CA-C	-5.20	105.29	111.69
1	A	311	GLN	CA-C-N	-5.20	113.34	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	311	GLN	C-N-CA	-5.20	113.34	119.84
7	I	54	GLU	N-CA-C	5.19	121.86	110.80
2	B	1066	SER	N-CA-C	5.19	119.24	113.01
1	A	1221	LYS	CB-CA-C	-5.18	110.18	117.23
7	I	90	GLN	N-CA-C	-5.17	98.60	108.17
1	A	414	ASP	N-CA-C	5.17	117.14	107.99
1	A	165	GLY	N-CA-C	5.15	121.00	112.66
6	H	129	TYR	N-CA-C	-5.12	107.03	113.28
2	B	1155	SER	CB-CA-C	-5.12	109.70	115.79
1	A	988	LEU	N-CA-C	-5.10	106.90	113.23
11	T	24	DT	N1-C1'-C2'	5.10	121.15	113.50
1	A	1028	THR	N-CA-C	5.05	117.17	111.11
1	A	481	ASP	N-CA-C	-5.02	102.45	109.69
5	F	105	ALA	N-CA-C	-5.02	102.86	110.39

There are no chirality outliers.

There are no planarity outliers.

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	10953	0	11053	704	0
2	B	8762	0	8797	472	0
3	C	2095	0	2051	106	0
4	E	1752	0	1776	65	0
5	F	679	0	701	35	0
6	H	1068	0	1040	92	0
7	I	971	0	927	39	0
8	J	532	0	542	69	0
9	K	919	0	929	30	0
10	L	351	0	374	66	0
11	T	587	0	326	123	0
12	N	284	0	161	50	0
13	R	198	0	99	9	0
14	A	2	0	0	0	0
14	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	C	1	0	0	0	0
14	I	2	0	0	0	0
14	J	1	0	0	0	0
14	L	1	0	0	0	0
15	A	2	0	0	0	0
16	T	32	0	14	2	0
All	All	29193	0	28790	1706	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 29.

All (1706) 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)
1:A:317:LYS:CG	1:A:318:SER:HB2	1.25	1.56
2:B:714:GLU:HA	2:B:715:ALA:CB	1.40	1.45
1:A:317:LYS:HG3	1:A:318:SER:CB	1.46	1.42
1:A:317:LYS:CG	1:A:318:SER:CB	1.98	1.42
10:L:38:LEU:HD12	10:L:40:LEU:CG	1.52	1.36
11:T:5:DC:C2'	11:T:6:DG:H5'	1.56	1.34
2:B:711:GLU:HB2	2:B:712:PRO:CA	1.57	1.33
1:A:1175:SER:HA	1:A:1176:LEU:C	1.37	1.31
1:A:317:LYS:CB	1:A:318:SER:HB2	1.62	1.30
1:A:43:GLU:HB2	1:A:50:ILE:CD1	1.61	1.30
1:A:43:GLU:CB	1:A:50:ILE:HD12	1.63	1.28
2:B:714:GLU:CA	2:B:715:ALA:HB2	1.62	1.28
1:A:57:ARG:HB3	1:A:68:GLN:CG	1.65	1.26
11:T:17:DG:H2''	11:T:18:DA:C5'	1.63	1.25
2:B:711:GLU:CB	2:B:712:PRO:HA	1.65	1.21
1:A:316:GLN:CB	1:A:318:SER:HA	1.72	1.18
1:A:403:LYS:HB3	1:A:404:TYR:CD1	1.80	1.17
3:C:41:ILE:HG13	3:C:172:PRO:HG3	1.26	1.16
1:A:38:PRO:HB3	1:A:270:LEU:HB3	1.19	1.15
1:A:57:ARG:HB3	1:A:68:GLN:CB	1.78	1.12
11:T:5:DC:H2''	11:T:6:DG:C5'	1.80	1.12
1:A:912:LEU:CD2	1:A:1036:ARG:HH21	1.62	1.11
6:H:137:GLN:HB2	6:H:138:GLU:HA	1.18	1.11
1:A:57:ARG:HB3	1:A:68:GLN:HG2	1.15	1.10
1:A:251:SER:HB2	1:A:252:PHE:HB3	1.33	1.09
1:A:1175:SER:CA	1:A:1176:LEU:C	2.23	1.08
6:H:62:SER:O	6:H:63:LEU:CD1	2.02	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:137:GLN:CB	6:H:138:GLU:HA	1.81	1.08
12:N:6:DT:H2''	12:N:7:DA:OP2	1.50	1.08
11:T:18:DA:H2''	11:T:19:1CC:OP2	1.49	1.07
11:T:12:DC:H1'	11:T:13:DA:N9	1.68	1.07
1:A:316:GLN:HB3	1:A:318:SER:HA	1.10	1.07
1:A:316:GLN:CB	1:A:317:LYS:HA	1.79	1.06
12:N:3:DG:H2''	12:N:4:DC:H5'	1.35	1.06
1:A:38:PRO:HB3	1:A:270:LEU:CB	1.85	1.06
1:A:57:ARG:CB	1:A:68:GLN:HG2	1.85	1.06
1:A:249:SER:HB2	1:A:250:ILE:HB	1.32	1.05
1:A:316:GLN:HB2	1:A:317:LYS:HA	1.08	1.05
5:F:74:ILE:HG13	5:F:75:PRO:HD2	1.39	1.04
1:A:399:HIS:CD2	1:A:400:PRO:HA	1.91	1.04
11:T:16:DC:H2''	11:T:17:DG:H5''	1.37	1.04
1:A:57:ARG:HB3	1:A:68:GLN:HB3	1.37	1.04
1:A:39:GLU:HA	1:A:40:THR:HB	1.37	1.03
10:L:46:VAL:HB	10:L:47:ARG:HA	1.36	1.03
11:T:8:DT:H1'	11:T:9:DA:C8	1.93	1.03
2:B:711:GLU:HB3	2:B:713:ALA:HA	1.41	1.02
10:L:47:ARG:HB3	10:L:54:ARG:HB3	1.41	1.02
1:A:38:PRO:HG2	1:A:39:GLU:OE1	1.58	1.02
10:L:38:LEU:HD12	10:L:40:LEU:HG	1.06	1.01
1:A:265:LYS:HE3	1:A:302:THR:HG23	1.40	1.01
10:L:38:LEU:CD1	10:L:40:LEU:HD21	1.91	1.01
2:B:710:LEU:O	2:B:711:GLU:HG2	1.59	1.00
11:T:17:DG:H2''	11:T:18:DA:H5'	1.43	1.00
1:A:912:LEU:HD23	1:A:1036:ARG:HH21	1.22	1.00
6:H:62:SER:O	6:H:63:LEU:HD13	1.61	1.00
2:B:714:GLU:CA	2:B:715:ALA:CB	2.22	0.99
1:A:570:PRO:HB2	1:A:572:TRP:CZ3	1.98	0.99
2:B:711:GLU:CB	2:B:713:ALA:HA	1.92	0.99
1:A:885:THR:CG2	1:A:943:LEU:HD12	1.90	0.99
1:A:317:LYS:HG3	1:A:318:SER:HB3	1.40	0.99
1:A:316:GLN:HB3	1:A:319:GLY:HA2	1.43	0.98
12:N:3:DG:C2'	12:N:4:DC:H5'	1.93	0.98
1:A:403:LYS:HB3	1:A:404:TYR:HD1	1.24	0.98
1:A:399:HIS:HD2	1:A:400:PRO:HA	1.29	0.97
10:L:38:LEU:HD12	10:L:40:LEU:CD2	1.95	0.97
11:T:13:DA:H5'	11:T:14:DG:OP2	1.65	0.97
1:A:46:THR:HG22	1:A:47:ARG:H	1.30	0.96
11:T:9:DA:N6	12:N:6:DT:H3	1.63	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1187:ASN:HD21	2:B:1190:ASP:HB2	1.27	0.96
1:A:317:LYS:HG3	1:A:318:SER:HB2	1.09	0.95
1:A:68:GLN:NE2	1:A:80:HIS:HD2	1.64	0.95
1:A:406:ILE:HB	1:A:431:LYS:HB2	1.45	0.95
2:B:1187:ASN:HD21	2:B:1190:ASP:CB	1.80	0.95
1:A:317:LYS:HG2	1:A:318:SER:CB	1.94	0.95
13:R:1:A:H2'	13:R:2:U:H5''	1.46	0.95
1:A:563:PRO:HB3	1:A:572:TRP:CE2	2.01	0.94
10:L:38:LEU:HD11	10:L:49:LYS:CD	1.98	0.94
1:A:249:SER:CB	1:A:250:ILE:HB	1.97	0.94
10:L:38:LEU:CD1	10:L:40:LEU:CG	2.46	0.94
11:T:12:DC:H1'	11:T:13:DA:C1'	1.98	0.94
1:A:1435:PRO:C	1:A:1436:ILE:HD12	1.92	0.94
10:L:38:LEU:CD1	10:L:40:LEU:CD2	2.46	0.93
2:B:25:ILE:HD11	2:B:653:VAL:HB	1.48	0.93
1:A:38:PRO:CB	1:A:270:LEU:HB3	1.96	0.93
1:A:316:GLN:CB	1:A:319:GLY:HA2	1.98	0.93
10:L:46:VAL:CB	10:L:47:ARG:HA	1.95	0.93
2:B:708:GLU:O	2:B:712:PRO:HB3	1.70	0.92
11:T:6:DG:H1'	11:T:7:DA:C8	2.05	0.92
8:J:6:ARG:HG3	8:J:13:VAL:HA	1.52	0.92
13:R:1:A:H8	13:R:1:A:HO5'	0.98	0.92
1:A:563:PRO:HB3	1:A:572:TRP:CZ2	2.04	0.92
1:A:828:ALA:O	1:A:831:THR:HG22	1.69	0.92
1:A:317:LYS:CA	1:A:318:SER:HB2	2.00	0.92
1:A:392:VAL:HG13	1:A:415:LEU:HD11	1.50	0.91
1:A:1435:PRO:HA	1:A:1439:GLY:O	1.70	0.91
10:L:47:ARG:HG2	10:L:48:CYS:H	1.34	0.90
2:B:706:GLN:O	2:B:709:ASP:HB2	1.71	0.90
2:B:784:ASN:ND2	2:B:788:ARG:HD2	1.87	0.90
11:T:5:DC:H2''	11:T:6:DG:H5'	0.91	0.90
1:A:592:ASP:O	1:A:593:GLU:HB2	1.71	0.90
10:L:38:LEU:CD1	10:L:40:LEU:HG	2.00	0.90
2:B:884:ARG:HG3	2:B:935:ARG:HG2	1.53	0.90
2:B:1002:THR:HG23	2:B:1004:GLU:H	1.37	0.89
10:L:38:LEU:HD21	10:L:49:LYS:HB2	1.50	0.89
2:B:855:PHE:HZ	2:B:857:ARG:NH1	1.70	0.89
11:T:7:DA:H2'	11:T:8:DT:C6	2.08	0.89
1:A:912:LEU:HD23	1:A:1036:ARG:NH2	1.86	0.89
1:A:316:GLN:HB2	1:A:317:LYS:CA	2.01	0.89
11:T:5:DC:C1'	11:T:6:DG:H5'	2.02	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:323:LYS:HE2	1:A:328:ARG:HE	1.37	0.89
2:B:711:GLU:HB3	2:B:713:ALA:CA	2.03	0.89
1:A:317:LYS:HG2	1:A:318:SER:HB2	1.48	0.88
1:A:899:VAL:HB	1:A:929:LEU:HD13	1.56	0.88
1:A:57:ARG:CB	1:A:68:GLN:HB3	2.04	0.88
2:B:911:ILE:HD11	2:B:941:LEU:HD23	1.56	0.88
6:H:62:SER:O	6:H:63:LEU:HD12	1.71	0.88
1:A:50:ILE:HG23	1:A:51:GLY:H	1.39	0.88
1:A:316:GLN:HB3	1:A:319:GLY:CA	2.04	0.88
3:C:70:ILE:HD11	3:C:144:ILE:HD11	1.53	0.87
1:A:317:LYS:CG	1:A:318:SER:HB3	1.99	0.87
2:B:711:GLU:HB2	2:B:712:PRO:HA	0.87	0.87
6:H:137:GLN:HB2	6:H:138:GLU:CA	2.04	0.87
1:A:316:GLN:HG2	1:A:319:GLY:O	1.75	0.87
1:A:372:LYS:HA	1:A:435:HIS:HD1	1.40	0.87
1:A:981:LEU:HD23	1:A:981:LEU:N	1.90	0.87
1:A:42:ASP:HB2	1:A:48:ALA:O	1.74	0.86
12:N:1:DC:H4'	12:N:2:DT:OP1	1.73	0.86
1:A:1116:LEU:H	1:A:1308:THR:HB	1.40	0.86
1:A:1161:THR:HG22	1:A:1163:ILE:H	1.38	0.86
6:H:130:ARG:HH11	6:H:130:ARG:HG2	1.40	0.86
11:T:7:DA:H2''	11:T:8:DT:H5'	1.56	0.86
11:T:10:DA:H2''	11:T:11:DG:OP2	1.76	0.86
11:T:6:DG:H1'	11:T:7:DA:N7	1.90	0.86
1:A:399:HIS:CD2	1:A:400:PRO:CA	2.58	0.85
1:A:407:ARG:HD2	1:A:413:ILE:HD11	1.57	0.85
1:A:35:ILE:HG23	1:A:52:GLY:O	1.75	0.85
2:B:648:HIS:CD2	2:B:711:GLU:HG3	2.10	0.85
1:A:403:LYS:HB3	1:A:404:TYR:CE1	2.10	0.85
1:A:979:SER:HB2	1:A:981:LEU:HD21	1.56	0.85
5:F:111:LEU:O	5:F:112:GLU:HG3	1.75	0.85
5:F:74:ILE:HG13	5:F:75:PRO:CD	2.07	0.85
1:A:250:ILE:HG23	1:A:251:SER:O	1.77	0.85
1:A:68:GLN:NE2	1:A:80:HIS:CD2	2.45	0.84
1:A:709:THR:HG23	1:A:712:GLU:HB2	1.60	0.84
12:N:2:DT:O2	12:N:3:DG:C6	2.30	0.84
1:A:981:LEU:HD12	1:A:986:ILE:HD11	1.57	0.84
1:A:251:SER:HB2	1:A:252:PHE:CB	2.06	0.83
3:C:33:LEU:HG	3:C:37:MET:HE2	1.61	0.83
2:B:29:ASP:HB3	2:B:658:ILE:HG12	1.61	0.83
12:N:9:DC:O2	12:N:10:DG:C6	2.31	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:855:PHE:HZ	2:B:857:ARG:HH12	1.24	0.83
7:I:109:ILE:CG2	7:I:120:GLN:HG3	2.09	0.83
1:A:40:THR:HG23	1:A:41:MET:HG3	1.59	0.82
2:B:416:LEU:HD12	2:B:466:TRP:CZ2	2.14	0.82
2:B:710:LEU:O	2:B:712:PRO:HA	1.79	0.82
1:A:1132:LYS:HG3	1:A:1135:ARG:HH12	1.44	0.82
1:A:67:CYS:HB3	1:A:70:CYS:SG	2.19	0.82
1:A:407:ARG:CD	1:A:413:ILE:HD11	2.08	0.82
10:L:30:ILE:HA	10:L:36:SER:O	1.79	0.82
2:B:711:GLU:HB2	2:B:712:PRO:C	2.04	0.82
1:A:316:GLN:HB3	1:A:318:SER:CA	2.04	0.81
1:A:372:LYS:HA	1:A:435:HIS:ND1	1.94	0.81
2:B:108:VAL:HG12	2:B:109:THR:H	1.45	0.81
1:A:84:ILE:HD11	1:A:270:LEU:HG	1.63	0.81
1:A:912:LEU:CD2	1:A:1036:ARG:NH2	2.43	0.81
12:N:3:DG:C1'	12:N:4:DC:H5'	2.09	0.81
8:J:49:MET:HE2	8:J:49:MET:HA	1.59	0.81
12:N:2:DT:H2''	12:N:3:DG:N7	1.96	0.81
1:A:1224:LEU:HD21	1:A:1240:CYS:HB3	1.62	0.80
6:H:137:GLN:CB	6:H:138:GLU:CA	2.60	0.80
1:A:67:CYS:SG	1:A:68:GLN:OE1	2.40	0.80
3:C:66:ARG:HA	8:J:5:VAL:HG21	1.62	0.80
2:B:635:ARG:HG3	2:B:637:LEU:HD21	1.64	0.80
2:B:843:GLN:HB2	2:B:993:THR:HB	1.61	0.80
11:T:12:DC:H1'	11:T:13:DA:C8	2.16	0.80
11:T:17:DG:H2''	11:T:18:DA:H5''	1.63	0.80
1:A:1063:MET:SD	1:A:1436:ILE:HG23	2.21	0.80
2:B:711:GLU:CB	2:B:712:PRO:CA	2.38	0.80
1:A:46:THR:HG22	1:A:47:ARG:N	1.93	0.80
2:B:710:LEU:O	2:B:711:GLU:CG	2.30	0.80
10:L:31:CYS:HB3	10:L:34:CYS:SG	2.22	0.79
1:A:53:LEU:HD23	1:A:54:ASN:HB2	1.65	0.79
2:B:464:GLY:HA2	2:B:480:SER:OG	1.82	0.79
1:A:249:SER:CA	1:A:250:ILE:HB	2.13	0.79
1:A:323:LYS:CE	1:A:328:ARG:HE	1.95	0.79
1:A:1063:MET:CE	1:A:1436:ILE:HG13	2.12	0.79
6:H:111:LEU:O	6:H:112:ILE:HD13	1.83	0.79
12:N:3:DG:H1'	12:N:4:DC:H5'	1.62	0.79
1:A:316:GLN:CG	1:A:319:GLY:HA2	2.13	0.79
1:A:839:ARG:HG2	1:A:839:ARG:HH11	1.45	0.79
1:A:804:TYR:HE2	2:B:1021:MET:HE3	1.47	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:169:ARG:H	2:B:454:THR:HG23	1.48	0.78
12:N:3:DG:H1'	12:N:4:DC:C5'	2.13	0.78
1:A:316:GLN:HE21	1:A:319:GLY:HA2	1.47	0.78
2:B:436:VAL:O	2:B:437:GLU:HG3	1.82	0.78
1:A:147:VAL:HG12	1:A:170:THR:HA	1.65	0.78
1:A:666:ILE:HD11	2:B:1030:LEU:HD13	1.64	0.78
11:T:7:DA:P	11:T:7:DA:H8	2.06	0.78
1:A:444:PHE:HE2	1:A:470:LEU:HD23	1.47	0.78
1:A:885:THR:HG23	1:A:943:LEU:HD12	1.65	0.78
1:A:43:GLU:HB2	1:A:50:ILE:HD12	0.80	0.78
1:A:304:MET:O	1:A:324:SER:HB2	1.83	0.78
7:I:78:CYS:SG	7:I:80:SER:HB3	2.24	0.78
10:L:38:LEU:HD12	10:L:40:LEU:CD1	2.13	0.78
2:B:642:ASP:HB3	2:B:649:LYS:HG3	1.64	0.77
3:C:56:THR:HG23	3:C:58:LEU:H	1.48	0.77
1:A:1063:MET:HE2	1:A:1436:ILE:HG13	1.64	0.77
2:B:195:CYS:HB2	2:B:784:ASN:OD1	1.85	0.77
6:H:136:LYS:O	6:H:137:GLN:HG2	1.85	0.77
2:B:1173:ALA:HA	2:B:1180:PHE:HD1	1.49	0.76
13:R:1:A:H2'	13:R:2:U:C5'	2.15	0.76
11:T:15:DA:C8	11:T:16:DC:C5	2.74	0.76
1:A:316:GLN:HB2	1:A:318:SER:HA	1.68	0.76
1:A:1176:LEU:H	1:A:1176:LEU:HD12	1.48	0.76
2:B:254:LEU:HD23	2:B:381:MET:HE1	1.68	0.76
12:N:2:DT:C2	12:N:3:DG:O6	2.39	0.76
1:A:849:MET:HB3	1:A:1063:MET:CE	2.16	0.76
1:A:399:HIS:CE1	1:A:462:VAL:HG21	2.20	0.76
2:B:519:TRP:CZ2	2:B:705:MET:HE1	2.22	0.75
10:L:29:TYR:HE1	10:L:58:LYS:HD2	1.52	0.75
2:B:1072:MET:HG3	2:B:1085:ILE:HB	1.67	0.75
10:L:38:LEU:HD11	10:L:49:LYS:HD3	1.66	0.75
1:A:1435:PRO:O	1:A:1436:ILE:HD12	1.86	0.75
2:B:711:GLU:C	2:B:713:ALA:HA	2.12	0.75
11:T:2:DT:O4	12:N:13:DA:N6	2.20	0.75
2:B:864:LYS:HD2	2:B:866:TYR:H	1.52	0.75
1:A:68:GLN:HE22	1:A:80:HIS:CD2	2.05	0.75
2:B:955:THR:HG23	2:B:956:THR:O	1.86	0.75
1:A:249:SER:HB2	1:A:250:ILE:CB	2.15	0.74
1:A:871:ASP:HB3	4:E:204:THR:HG23	1.68	0.74
2:B:257:LYS:NZ	2:B:279:ASP:OD2	2.20	0.74
2:B:1077:THR:HG23	2:B:1079:LYS:H	1.51	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:38:LEU:HD11	10:L:40:LEU:HD21	1.67	0.74
10:L:38:LEU:HD11	10:L:49:LYS:HD2	1.69	0.74
1:A:346:ASP:HB3	2:B:1107:ALA:O	1.87	0.74
3:C:41:ILE:HG13	3:C:172:PRO:CG	2.13	0.74
10:L:31:CYS:HB3	10:L:34:CYS:O	1.86	0.74
11:T:10:DA:H1'	11:T:11:DG:C8	2.22	0.74
2:B:640:VAL:HG22	2:B:651:LEU:HD23	1.68	0.74
2:B:1187:ASN:ND2	2:B:1190:ASP:HB2	2.03	0.74
1:A:310:GLY:C	1:A:312:PRO:HD3	2.11	0.74
1:A:821:ARG:O	1:A:825:ILE:HG12	1.87	0.74
2:B:702:LEU:HD23	2:B:737:THR:O	1.87	0.74
10:L:46:VAL:HB	10:L:47:ARG:CA	2.16	0.74
1:A:1035:TYR:O	1:A:1036:ARG:HB2	1.87	0.74
12:N:11:DG:H2''	12:N:12:DT:H72	1.67	0.74
11:T:5:DC:C2'	11:T:6:DG:C5'	2.51	0.74
1:A:570:PRO:HB2	1:A:572:TRP:HZ3	1.53	0.73
2:B:883:LEU:O	2:B:884:ARG:HB2	1.86	0.73
6:H:80:ARG:HG2	9:K:57:LEU:HD22	1.69	0.73
8:J:8:PHE:CD1	8:J:49:MET:SD	2.82	0.73
11:T:6:DG:H1'	11:T:7:DA:C5	2.24	0.73
2:B:25:ILE:HG23	2:B:29:ASP:HB2	1.70	0.73
2:B:789:MET:HE2	2:B:965:LYS:HB3	1.71	0.73
1:A:567:LYS:HB2	6:H:96:VAL:HB	1.69	0.73
1:A:1162:VAL:HG11	7:I:41:PRO:HG3	1.71	0.73
1:A:254:GLU:OE2	2:B:918:ILE:HD12	1.89	0.73
1:A:1420:ASP:HB3	1:A:1422:ARG:HG2	1.71	0.73
12:N:6:DT:C2'	12:N:7:DA:OP2	2.31	0.73
2:B:470:LYS:HB3	2:B:471:LYS:HA	1.71	0.72
1:A:1063:MET:SD	1:A:1436:ILE:HG13	2.28	0.72
2:B:714:GLU:CG	2:B:715:ALA:HB3	2.19	0.72
1:A:399:HIS:CD2	1:A:400:PRO:HB3	2.24	0.72
1:A:901:LEU:HD22	1:A:919:ILE:HG23	1.68	0.72
1:A:164:ARG:HG2	1:A:165:GLY:H	1.54	0.72
2:B:801:LYS:O	8:J:52:THR:HG23	1.89	0.72
1:A:963:ILE:HD12	1:A:1049:ILE:HG13	1.71	0.72
1:A:469:ARG:NH2	2:B:991:GLY:O	2.23	0.72
11:T:5:DC:H1'	11:T:6:DG:C5'	2.20	0.72
1:A:403:LYS:CB	1:A:404:TYR:HD1	2.01	0.71
2:B:213:ILE:O	2:B:215:GLN:NE2	2.23	0.71
2:B:244:LEU:H	2:B:244:LEU:HD12	1.55	0.71
4:E:169:ARG:HG2	4:E:169:ARG:HH11	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:606:LEU:HD23	1:A:614:PHE:CE2	2.25	0.71
8:J:48:ARG:HD2	8:J:48:ARG:C	2.15	0.71
1:A:330:LYS:O	1:A:334:GLY:HA3	1.90	0.71
1:A:853:ASP:OD1	1:A:855:THR:HB	1.90	0.71
4:E:169:ARG:HG2	4:E:169:ARG:NH1	2.04	0.71
2:B:460:ALA:HB1	2:B:466:TRP:CE3	2.25	0.71
2:B:642:ASP:HA	2:B:649:LYS:HA	1.73	0.71
2:B:899:ILE:HG21	2:B:949:VAL:HG21	1.72	0.71
2:B:1117:GLN:NE2	2:B:1199:ALA:HB2	2.06	0.71
1:A:38:PRO:HG2	1:A:39:GLU:CD	2.15	0.71
2:B:487:THR:HG22	2:B:490:SER:H	1.55	0.71
6:H:38:LEU:HD12	6:H:125:LEU:HD21	1.72	0.71
10:L:47:ARG:HB3	10:L:54:ARG:CB	2.21	0.71
1:A:316:GLN:HE21	1:A:319:GLY:CA	2.03	0.70
1:A:317:LYS:CA	1:A:318:SER:CB	2.66	0.70
1:A:152:VAL:CG1	1:A:153:PRO:HD2	2.22	0.70
1:A:316:GLN:CB	1:A:317:LYS:CA	2.66	0.70
1:A:981:LEU:HD23	1:A:981:LEU:H	1.55	0.70
11:T:5:DC:C5	11:T:6:DG:C5	2.80	0.70
1:A:57:ARG:CG	1:A:68:GLN:HB3	2.21	0.70
2:B:778:MET:HE1	2:B:1094:ARG:HD2	1.74	0.70
2:B:980:PHE:CE2	2:B:1094:ARG:HG3	2.26	0.70
3:C:45:ALA:HB3	3:C:170:TRP:NE1	2.07	0.70
1:A:84:ILE:CD1	1:A:270:LEU:HG	2.21	0.70
4:E:79:TRP:HB2	4:E:105:PHE:HD2	1.54	0.70
1:A:114:LEU:HD13	1:A:145:LYS:CB	2.22	0.69
1:A:1329:THR:HB	1:A:1331:SER:H	1.56	0.69
11:T:3:DA:N6	12:N:11:DG:C6	2.60	0.69
2:B:269:ILE:HD11	2:B:386:LEU:HD21	1.74	0.69
6:H:5:LEU:HB2	6:H:59:ILE:O	1.92	0.69
1:A:57:ARG:HG2	1:A:68:GLN:HB3	1.72	0.69
3:C:45:ALA:HB3	3:C:170:TRP:CD1	2.26	0.69
11:T:15:DA:C5	11:T:16:DC:C4	2.81	0.69
1:A:50:ILE:HG23	1:A:51:GLY:N	2.07	0.69
1:A:249:SER:HA	1:A:250:ILE:HB	1.72	0.69
1:A:875:ALA:HB2	1:A:1366:ARG:HD2	1.74	0.69
1:A:885:THR:CG2	1:A:943:LEU:CD1	2.68	0.69
11:T:10:DA:C2	11:T:11:DG:C2	2.81	0.69
1:A:1356:ILE:HG22	1:A:1361:SER:HB2	1.74	0.69
1:A:67:CYS:SG	1:A:68:GLN:CD	2.76	0.69
1:A:668:ASP:HB3	1:A:743:VAL:HG23	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1111:MET:HG3	1:A:1114:PRO:HG3	1.74	0.69
2:B:378:LEU:O	2:B:382:ILE:HG12	1.92	0.69
11:T:2:DT:H2''	11:T:3:DA:OP2	1.92	0.69
11:T:17:DG:H2''	11:T:18:DA:O5'	1.93	0.69
12:N:7:DA:H2''	12:N:8:DT:H71	1.72	0.69
1:A:30:ILE:HG12	2:B:1170:THR:HG21	1.75	0.69
1:A:1277:GLU:O	1:A:1278:ASN:HB2	1.93	0.69
8:J:8:PHE:CE1	8:J:49:MET:SD	2.86	0.69
11:T:10:DA:H2''	11:T:11:DG:C8	2.28	0.69
11:T:10:DA:H1'	11:T:11:DG:N9	2.08	0.69
2:B:287:ARG:NH1	2:B:324:ILE:O	2.26	0.68
7:I:111:THR:HG22	7:I:113:ASP:H	1.56	0.68
1:A:919:ILE:CG2	1:A:920:LEU:N	2.56	0.68
11:T:5:DC:H1'	11:T:6:DG:H5'	1.75	0.68
8:J:3:VAL:HG21	8:J:18:TRP:HB2	1.75	0.68
1:A:57:ARG:CA	1:A:68:GLN:HG2	2.23	0.68
1:A:112:LYS:HG2	1:A:113:LEU:N	2.06	0.68
1:A:399:HIS:CD2	1:A:400:PRO:CB	2.77	0.68
1:A:779:PHE:CE2	1:A:785:PRO:HD3	2.29	0.68
1:A:343:LYS:HD2	2:B:1151:LEU:HA	1.76	0.68
1:A:901:LEU:HB2	1:A:926:GLN:HG2	1.75	0.68
2:B:824:ILE:HG12	8:J:48:ARG:HH22	1.59	0.68
11:T:6:DG:H2''	11:T:7:DA:N7	2.08	0.68
1:A:1345:ARG:HD2	1:A:1373:ASP:OD1	1.93	0.68
2:B:855:PHE:CZ	2:B:857:ARG:NH1	2.60	0.68
10:L:31:CYS:CB	10:L:34:CYS:SG	2.81	0.68
2:B:784:ASN:HD21	2:B:788:ARG:HD2	1.57	0.68
9:K:41:THR:HG22	9:K:42:LEU:N	2.07	0.68
1:A:780:VAL:HG23	1:A:789:LYS:HE2	1.76	0.68
2:B:710:LEU:O	2:B:711:GLU:CB	2.41	0.68
12:N:2:DT:C2	12:N:3:DG:C6	2.81	0.68
2:B:1084:GLN:HE22	3:C:191:TYR:HA	1.58	0.67
2:B:1031:LEU:HD13	2:B:1055:ILE:HD13	1.76	0.67
3:C:69:LEU:HB2	8:J:5:VAL:HG11	1.76	0.67
11:T:10:DA:C2	11:T:11:DG:N3	2.62	0.67
1:A:849:MET:HB3	1:A:1063:MET:HE3	1.76	0.67
1:A:129:LYS:HA	1:A:134:ARG:HH21	1.59	0.67
2:B:33:VAL:HG21	2:B:638:PHE:CZ	2.30	0.67
2:B:428:ILE:HD11	2:B:448:ILE:HA	1.76	0.67
2:B:710:LEU:C	2:B:711:GLU:HG2	2.18	0.67
3:C:66:ARG:NH2	8:J:3:VAL:O	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:550:LEU:HG	1:A:556:TRP:CE2	2.30	0.67
2:B:955:THR:OG1	10:L:55:ILE:HA	1.93	0.67
2:B:475:SER:O	2:B:476:ARG:HB2	1.94	0.67
6:H:38:LEU:C	6:H:38:LEU:HD23	2.19	0.67
11:T:3:DA:C2	12:N:13:DA:N1	2.63	0.67
1:A:1134:ILE:O	1:A:1138:ILE:HG12	1.95	0.67
3:C:34:ARG:HA	3:C:37:MET:HE3	1.76	0.67
3:C:38:ILE:HG13	3:C:176:ILE:HD12	1.76	0.67
11:T:16:DC:C2'	11:T:17:DG:H5''	2.21	0.67
1:A:38:PRO:HD3	1:A:270:LEU:HD22	1.77	0.67
3:C:11:ARG:HH21	3:C:229:TYR:HD2	1.43	0.67
6:H:93:TYR:CG	6:H:145:ARG:HD3	2.30	0.67
1:A:351:THR:HG21	1:A:466:SER:O	1.95	0.67
1:A:744:LYS:HE2	1:A:748:MET:HE3	1.76	0.67
2:B:356:LEU:HA	2:B:360:PHE:HB3	1.76	0.66
1:A:264:PHE:CE2	1:A:317:LYS:HD3	2.30	0.66
1:A:899:VAL:CB	1:A:929:LEU:HD13	2.25	0.66
2:B:648:HIS:CD2	2:B:711:GLU:CG	2.78	0.66
4:E:135:PHE:HD2	4:E:140:LEU:HD21	1.60	0.66
6:H:116:TYR:HB2	6:H:123:MET:HB3	1.77	0.66
11:T:6:DG:C1'	11:T:7:DA:N7	2.57	0.66
1:A:693:VAL:HG21	1:A:721:PHE:HE2	1.61	0.66
1:A:981:LEU:HD12	1:A:986:ILE:CD1	2.23	0.66
2:B:1181:GLU:HG2	2:B:1188:LYS:HG3	1.78	0.66
3:C:142:VAL:H	8:J:16:ASP:HB3	1.60	0.66
10:L:47:ARG:H	10:L:47:ARG:CD	2.07	0.66
6:H:136:LYS:O	6:H:137:GLN:CG	2.44	0.66
1:A:343:LYS:O	1:A:345:VAL:HG13	1.96	0.65
1:A:67:CYS:O	1:A:70:CYS:SG	2.54	0.65
1:A:215:SER:HB3	1:A:218:ASP:HB2	1.78	0.65
1:A:71:GLN:O	1:A:72:GLU:HB2	1.95	0.65
2:B:784:ASN:ND2	2:B:788:ARG:CD	2.60	0.65
7:I:78:CYS:O	7:I:79:HIS:HB2	1.97	0.65
2:B:1084:GLN:HE22	3:C:192:TRP:H	1.41	0.65
3:C:57:VAL:HG12	3:C:58:LEU:HD23	1.79	0.65
1:A:353:ILE:HD13	1:A:487:MET:HE3	1.79	0.65
1:A:378:GLU:OE1	1:A:434:ARG:HD3	1.96	0.65
1:A:147:VAL:O	1:A:148:CYS:C	2.39	0.65
1:A:392:VAL:CG1	1:A:415:LEU:HD11	2.25	0.65
2:B:465:ASN:HD22	2:B:465:ASN:N	1.94	0.65
2:B:976:ILE:O	2:B:1099:VAL:HG21	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1174:PHE:O	1:A:1176:LEU:HB2	1.96	0.65
2:B:806:THR:HG22	2:B:808:ALA:H	1.61	0.65
1:A:563:PRO:CB	1:A:572:TRP:CZ2	2.79	0.64
11:T:15:DA:H2''	11:T:16:DC:H5'	1.79	0.64
2:B:460:ALA:HB1	2:B:466:TRP:CZ3	2.32	0.64
1:A:114:LEU:HD13	1:A:145:LYS:HB3	1.80	0.64
4:E:117:THR:O	4:E:120:ALA:N	2.31	0.64
7:I:34:TYR:HE1	7:I:36:GLU:HB3	1.63	0.64
8:J:6:ARG:HG2	8:J:11:GLY:O	1.96	0.64
12:N:9:DC:C2	12:N:10:DG:C6	2.85	0.64
12:N:13:DA:H2''	12:N:14:DG:C8	2.32	0.64
1:A:572:TRP:HH2	6:H:79:TRP:CZ3	2.15	0.64
2:B:711:GLU:CB	2:B:713:ALA:CA	2.68	0.64
2:B:969:ARG:NH1	3:C:61:GLU:OE1	2.31	0.64
6:H:93:TYR:CD2	6:H:145:ARG:HD3	2.33	0.64
8:J:42:LYS:HG3	8:J:43:ARG:H	1.63	0.64
1:A:145:LYS:HG3	1:A:146:MET:H	1.63	0.64
1:A:888:GLY:O	1:A:940:ARG:NH2	2.31	0.64
2:B:797:TYR:HB3	2:B:798:TYR:CD1	2.32	0.64
2:B:857:ARG:HD3	2:B:859:TYR:CZ	2.32	0.64
1:A:783:THR:HG21	1:A:796:SER:O	1.97	0.64
2:B:711:GLU:HB3	2:B:713:ALA:CB	2.28	0.64
11:T:6:DG:C1'	11:T:7:DA:C8	2.80	0.64
2:B:955:THR:HG23	2:B:956:THR:N	2.13	0.64
1:A:44:THR:O	1:A:45:GLN:HG3	1.98	0.64
2:B:977:GLY:C	2:B:1099:VAL:HG23	2.23	0.64
6:H:91:ASP:O	6:H:93:TYR:CD1	2.51	0.64
10:L:38:LEU:HD21	10:L:49:LYS:HD2	1.80	0.64
11:T:12:DC:H3'	11:T:12:DC:OP2	1.97	0.64
5:F:110:ASP:O	5:F:111:LEU:HB2	1.97	0.63
1:A:761:MET:HG3	2:B:1021:MET:HG2	1.80	0.63
2:B:62:ILE:HG23	2:B:418:LYS:HG2	1.80	0.63
2:B:784:ASN:HD21	2:B:788:ARG:CD	2.11	0.63
7:I:74:GLU:HB3	7:I:81:ARG:NE	2.13	0.63
11:T:6:DG:O3'	11:T:7:DA:C8	2.51	0.63
2:B:301:ILE:HG21	2:B:314:LEU:HD11	1.81	0.63
8:J:8:PHE:HE1	8:J:49:MET:HE1	1.63	0.63
1:A:134:ARG:NH1	1:A:220:THR:O	2.31	0.63
1:A:316:GLN:NE2	1:A:319:GLY:HA2	2.14	0.63
2:B:884:ARG:HB2	2:B:936:ASP:H	1.62	0.63
10:L:47:ARG:H	10:L:47:ARG:HD2	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:T:3:DA:H2''	11:T:4:DC:H5'	1.80	0.63
11:T:7:DA:C2'	11:T:8:DT:C6	2.80	0.63
1:A:41:MET:O	1:A:42:ASP:HB3	1.99	0.63
1:A:629:LEU:HD13	1:A:645:LEU:HD21	1.78	0.63
1:A:977:LYS:HG3	1:A:978:PRO:HD2	1.81	0.63
2:B:33:VAL:HG21	2:B:638:PHE:HZ	1.64	0.63
4:E:79:TRP:HB2	4:E:105:PHE:CD2	2.32	0.63
6:H:137:GLN:CG	6:H:138:GLU:HA	2.29	0.63
1:A:420:ARG:O	1:A:424:ILE:HG13	1.99	0.63
2:B:708:GLU:O	2:B:712:PRO:CB	2.45	0.63
2:B:1051:THR:HG22	2:B:1053:GLU:H	1.62	0.63
8:J:3:VAL:HG21	8:J:18:TRP:CB	2.28	0.63
10:L:27:LEU:O	10:L:39:SER:HA	1.98	0.63
7:I:109:ILE:HG21	7:I:120:GLN:HG3	1.79	0.63
10:L:40:LEU:HD11	10:L:49:LYS:HE3	1.81	0.63
1:A:1176:LEU:HD12	1:A:1176:LEU:N	2.13	0.63
11:T:1:DC:H2'	11:T:2:DT:C6	2.34	0.63
11:T:9:DA:H61	12:N:6:DT:H3	0.79	0.63
1:A:269:ILE:HD11	1:A:300:VAL:HA	1.80	0.63
2:B:1032:SER:HB3	2:B:1089:PRO:HB2	1.81	0.63
11:T:7:DA:C2'	11:T:8:DT:H5'	2.28	0.63
1:A:42:ASP:HA	1:A:50:ILE:HB	1.81	0.62
1:A:563:PRO:CB	1:A:572:TRP:CE2	2.81	0.62
1:A:600:PRO:HA	6:H:25:ARG:NH1	2.13	0.62
1:A:316:GLN:HB3	1:A:319:GLY:C	2.24	0.62
1:A:79:GLY:O	1:A:243:PRO:HG3	1.99	0.62
1:A:472:LEU:O	1:A:475:THR:HB	1.99	0.62
2:B:416:LEU:HD12	2:B:466:TRP:CE2	2.33	0.62
1:A:42:ASP:OD1	1:A:43:GLU:N	2.31	0.62
1:A:705:LYS:HD2	1:A:708:MET:HE1	1.81	0.62
1:A:44:THR:O	1:A:45:GLN:C	2.42	0.62
1:A:870:GLU:HB2	4:E:204:THR:HG21	1.81	0.62
2:B:714:GLU:HA	2:B:715:ALA:HB2	0.65	0.62
4:E:20:LYS:NZ	4:E:34:GLU:O	2.32	0.62
6:H:91:ASP:O	6:H:93:TYR:HD1	1.83	0.62
10:L:29:TYR:HD1	10:L:58:LYS:HA	1.65	0.62
3:C:167:HIS:HD2	3:C:169:LYS:H	1.46	0.62
6:H:47:PHE:HB3	6:H:95:TYR:CD2	2.35	0.62
1:A:354:SER:HA	1:A:482:PHE:CD1	2.35	0.62
1:A:981:LEU:HD22	1:A:1038:THR:C	2.25	0.62
2:B:977:GLY:HA3	2:B:1099:VAL:CG2	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:987:LYS:NZ	13:R:9:G:OP1	2.27	0.62
1:A:57:ARG:CB	1:A:68:GLN:CG	2.55	0.61
1:A:1400:CYS:O	1:A:1405:THR:HG22	2.00	0.61
8:J:28:ASP:OD1	8:J:28:ASP:N	2.32	0.61
11:T:6:DG:N3	11:T:7:DA:C6	2.68	0.61
1:A:283:GLY:O	1:A:285:PRO:HD3	2.00	0.61
1:A:316:GLN:CB	1:A:318:SER:CA	2.65	0.61
11:T:6:DG:O3'	11:T:7:DA:H8	1.83	0.61
2:B:1048:THR:OG1	2:B:1050:ILE:HD12	1.99	0.61
5:F:97:ARG:NH1	5:F:100:GLN:OE1	2.33	0.61
1:A:317:LYS:HA	1:A:318:SER:CB	2.31	0.61
1:A:650:GLN:O	1:A:654:ASN:HB2	2.00	0.61
1:A:244:PRO:O	1:A:247:ARG:N	2.29	0.61
3:C:114:TYR:CG	3:C:140:ASN:HB2	2.35	0.61
5:F:85:MET:HE1	5:F:148:VAL:HG13	1.81	0.61
1:A:981:LEU:CD1	1:A:986:ILE:HD11	2.28	0.61
2:B:1163:CYS:HA	2:B:1191:ILE:HD12	1.82	0.61
1:A:70:CYS:HA	2:B:1174:LYS:HD3	1.83	0.61
4:E:169:ARG:HH11	4:E:169:ARG:CG	2.14	0.61
10:L:55:ILE:HG23	10:L:55:ILE:O	2.01	0.61
11:T:6:DG:C2'	11:T:7:DA:C8	2.84	0.61
1:A:381:THR:HG23	1:A:383:TYR:H	1.66	0.61
1:A:466:SER:HB2	2:B:1099:VAL:HG11	1.82	0.61
1:A:705:LYS:HB2	1:A:708:MET:HE2	1.82	0.61
1:A:981:LEU:HD12	1:A:986:ILE:CG1	2.30	0.61
2:B:114:PRO:HG2	2:B:181:LEU:HD11	1.81	0.60
1:A:479:ASN:ND2	16:T:101:G2P:O3'	2.34	0.60
1:A:563:PRO:HB3	1:A:572:TRP:CH2	2.36	0.60
2:B:435:THR:O	2:B:435:THR:HG22	2.00	0.60
1:A:114:LEU:HD12	1:A:142:CYS:SG	2.41	0.60
5:F:119:ARG:HH11	5:F:119:ARG:HG3	1.67	0.60
7:I:34:TYR:CE1	7:I:36:GLU:HB3	2.36	0.60
10:L:28:LYS:HA	10:L:39:SER:HA	1.82	0.60
2:B:724:ASP:HB3	2:B:727:LYS:HG3	1.84	0.60
1:A:38:PRO:CG	1:A:39:GLU:OE1	2.44	0.60
1:A:912:LEU:HD22	1:A:1036:ARG:HH21	1.61	0.60
1:A:901:LEU:HD22	1:A:919:ILE:CG2	2.32	0.60
2:B:470:LYS:CB	2:B:471:LYS:HA	2.29	0.60
11:T:6:DG:N2	11:T:7:DA:C2	2.70	0.60
6:H:47:PHE:HZ	6:H:146:ARG:HG3	1.65	0.60
1:A:869:GLY:O	4:E:204:THR:HG21	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:980:ASP:H	1:A:981:LEU:HD23	1.65	0.60
10:L:47:ARG:HB2	10:L:54:ARG:HA	1.83	0.60
11:T:18:DA:C2'	11:T:19:1CC:OP2	2.37	0.60
1:A:768:GLN:HG2	1:A:816:HIS:HA	1.82	0.60
1:A:963:ILE:HD13	1:A:1048:ASN:HB3	1.83	0.60
2:B:470:LYS:HB3	2:B:471:LYS:CA	2.32	0.60
2:B:884:ARG:O	2:B:936:ASP:HB3	2.02	0.60
6:H:91:ASP:OD1	6:H:92:ASP:N	2.35	0.60
11:T:6:DG:H2''	11:T:7:DA:C8	2.37	0.60
2:B:244:LEU:HD12	2:B:244:LEU:N	2.17	0.59
2:B:911:ILE:CD1	2:B:941:LEU:HD23	2.31	0.59
1:A:406:ILE:HD13	1:A:431:LYS:CB	2.32	0.59
2:B:65:GLU:HG3	2:B:246:LYS:NZ	2.17	0.59
2:B:284:ILE:HG21	2:B:333:PHE:HD2	1.66	0.59
2:B:487:THR:O	2:B:490:SER:HB3	2.02	0.59
5:F:97:ARG:HE	5:F:124:GLU:CD	2.10	0.59
9:K:41:THR:CG2	9:K:42:LEU:N	2.65	0.59
1:A:53:LEU:HD23	1:A:53:LEU:C	2.27	0.59
1:A:406:ILE:CD1	1:A:431:LYS:HB2	2.32	0.59
2:B:977:GLY:C	2:B:1099:VAL:CG2	2.76	0.59
2:B:1164:GLY:HA3	2:B:1190:ASP:HB3	1.83	0.59
1:A:265:LYS:CE	1:A:302:THR:HG23	2.23	0.59
1:A:355:GLY:CA	1:A:482:PHE:CZ	2.85	0.59
1:A:185:TRP:HZ3	1:A:200:ARG:HG2	1.68	0.59
6:H:130:ARG:HG2	6:H:130:ARG:NH1	2.15	0.59
11:T:10:DA:N3	11:T:11:DG:N3	2.51	0.59
1:A:920:LEU:HD23	1:A:921:GLY:H	1.66	0.59
1:A:977:LYS:HA	1:A:977:LYS:HE3	1.84	0.59
2:B:1220:ARG:O	2:B:1221:SER:HB2	2.01	0.59
5:F:119:ARG:HH11	5:F:119:ARG:CG	2.16	0.59
2:B:1162:ILE:HG22	2:B:1163:CYS:H	1.67	0.59
1:A:606:LEU:HG	1:A:613:ILE:HB	1.84	0.59
1:A:1155:ASP:O	1:A:1241:ARG:NH1	2.35	0.59
2:B:287:ARG:HG2	2:B:292:ILE:HA	1.84	0.59
2:B:977:GLY:HA3	2:B:1099:VAL:HG21	1.84	0.59
1:A:247:ARG:N	1:A:248:PRO:HD3	2.18	0.59
2:B:30:SER:OG	2:B:743:ILE:O	2.21	0.59
2:B:714:GLU:CA	2:B:715:ALA:HB3	2.25	0.59
12:N:11:DG:H2''	12:N:12:DT:C7	2.33	0.59
2:B:737:THR:O	2:B:737:THR:HG23	2.03	0.59
2:B:1084:GLN:NE2	3:C:191:TYR:HA	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:45:ALA:HA	3:C:72:LEU:HD12	1.84	0.59
1:A:565:ILE:O	1:A:570:PRO:HA	2.03	0.58
1:A:979:SER:HB2	1:A:981:LEU:CD2	2.30	0.58
2:B:696:GLU:O	2:B:699:GLU:HB2	2.03	0.58
7:I:4:PHE:CD2	7:I:13:MET:HE2	2.38	0.58
1:A:251:SER:CB	1:A:252:PHE:HB3	2.22	0.58
2:B:108:VAL:HG12	2:B:109:THR:N	2.16	0.58
12:N:11:DG:H2''	12:N:12:DT:C5	2.38	0.58
1:A:1011:GLN:NE2	1:A:1015:VAL:HG21	2.17	0.58
9:K:49:GLU:HG3	9:K:94:ILE:HG12	1.84	0.58
1:A:244:PRO:O	1:A:248:PRO:HD3	2.03	0.58
1:A:316:GLN:CG	1:A:319:GLY:O	2.51	0.58
2:B:570:VAL:HB	2:B:573:GLN:HG2	1.84	0.58
10:L:47:ARG:HG2	10:L:48:CYS:N	2.12	0.58
1:A:323:LYS:HE2	1:A:328:ARG:NE	2.12	0.58
10:L:32:ALA:HB2	10:L:55:ILE:HG23	1.85	0.58
1:A:259:GLU:HB3	1:A:264:PHE:CZ	2.38	0.58
1:A:401:GLY:C	1:A:435:HIS:CD2	2.82	0.58
6:H:4:THR:HG22	6:H:5:LEU:N	2.18	0.58
6:H:139:ASN:O	6:H:140:ALA:HB2	2.03	0.58
7:I:113:ASP:OD2	7:I:116:ASN:ND2	2.37	0.58
1:A:316:GLN:HG2	1:A:319:GLY:CA	2.34	0.58
1:A:920:LEU:HD23	1:A:921:GLY:N	2.18	0.58
3:C:183:TRP:CZ2	3:C:207:CYS:HB3	2.39	0.58
1:A:45:GLN:HG3	1:A:45:GLN:O	2.02	0.58
1:A:946:VAL:HG22	4:E:201:LYS:HD3	1.86	0.58
2:B:1095:LEU:C	2:B:1097:HIS:H	2.12	0.58
11:T:3:DA:N6	12:N:11:DG:C5	2.72	0.58
1:A:606:LEU:HD23	1:A:614:PHE:HE2	1.68	0.58
1:A:709:THR:HG23	1:A:712:GLU:CB	2.33	0.58
1:A:1444:MET:HB2	5:F:133:VAL:HG12	1.84	0.58
2:B:1187:ASN:ND2	2:B:1190:ASP:CB	2.61	0.58
1:A:164:ARG:CG	1:A:165:GLY:H	2.16	0.57
9:K:42:LEU:CD1	9:K:46:ILE:HG13	2.34	0.57
11:T:1:DC:H2''	11:T:2:DT:O4'	2.04	0.57
2:B:824:ILE:HG12	8:J:48:ARG:NH2	2.19	0.57
8:J:48:ARG:HE	8:J:49:MET:HG2	1.69	0.57
1:A:526:ASP:HB2	2:B:835:GLN:CD	2.30	0.57
1:A:588:LEU:HD23	1:A:632:VAL:HG21	1.86	0.57
2:B:106:ASP:OD1	2:B:107:GLY:N	2.36	0.57
3:C:66:ARG:HB3	8:J:5:VAL:CG2	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:30:ILE:HG22	10:L:36:SER:O	2.04	0.57
2:B:468:GLU:C	2:B:470:LYS:H	2.13	0.57
2:B:778:MET:HE1	2:B:1094:ARG:HH11	1.70	0.57
2:B:1051:THR:HG22	2:B:1053:GLU:N	2.19	0.57
3:C:162:GLY:HA3	3:C:170:TRP:CD2	2.39	0.57
12:N:3:DG:H1'	12:N:4:DC:H5''	1.86	0.57
2:B:857:ARG:HH11	2:B:857:ARG:HB2	1.69	0.57
2:B:864:LYS:HB3	2:B:872:GLU:H	1.69	0.57
4:E:9:ILE:HD11	4:E:53:PRO:HD3	1.87	0.57
8:J:2:ILE:O	8:J:3:VAL:O	2.23	0.57
1:A:316:GLN:CG	1:A:319:GLY:CA	2.82	0.57
2:B:58:THR:O	2:B:62:ILE:HG12	2.04	0.57
2:B:465:ASN:CG	2:B:477:ALA:HB2	2.29	0.57
2:B:475:SER:O	2:B:476:ARG:CB	2.52	0.57
3:C:77:ILE:HD12	3:C:161:LYS:HG3	1.86	0.57
1:A:251:SER:HB2	1:A:252:PHE:CA	2.35	0.57
2:B:280:ILE:HB	2:B:285:ILE:HD11	1.87	0.57
3:C:69:LEU:CB	8:J:5:VAL:HG11	2.35	0.57
1:A:152:VAL:HG12	1:A:153:PRO:HD2	1.86	0.57
1:A:173:THR:HB	1:A:184:SER:HB3	1.85	0.57
1:A:268:ASP:O	1:A:299:HIS:ND1	2.34	0.57
2:B:712:PRO:N	2:B:713:ALA:HA	2.16	0.57
3:C:148:ARG:HG2	3:C:149:LYS:H	1.70	0.57
6:H:130:ARG:HH11	6:H:130:ARG:CG	2.14	0.57
1:A:378:GLU:HG2	1:A:388:LEU:HD11	1.86	0.57
2:B:31:TRP:HA	2:B:34:ILE:HD12	1.87	0.56
2:B:799:PRO:HB2	2:B:818:PRO:HG2	1.87	0.56
11:T:5:DC:N4	12:N:10:DG:H1	2.03	0.56
11:T:6:DG:C2	11:T:7:DA:N1	2.74	0.56
1:A:840:ARG:HG2	1:A:1402:PHE:HZ	1.70	0.56
1:A:1038:THR:O	1:A:1042:PHE:HB3	2.05	0.56
1:A:1441:PHE:CZ	5:F:89:GLU:HA	2.40	0.56
2:B:102:VAL:HG22	2:B:112:LEU:HD22	1.87	0.56
2:B:710:LEU:C	2:B:711:GLU:CG	2.76	0.56
2:B:711:GLU:CA	2:B:713:ALA:HA	2.35	0.56
6:H:103:LYS:HB3	6:H:115:TYR:HD2	1.69	0.56
10:L:47:ARG:CB	10:L:54:ARG:HB3	2.26	0.56
11:T:10:DA:C4	11:T:11:DG:C4	2.93	0.56
2:B:205:ILE:HG13	2:B:461:LEU:HB3	1.87	0.56
2:B:258:LEU:HB2	2:B:385:LEU:HD21	1.86	0.56
4:E:157:SER:N	4:E:160:GLU:OE1	2.30	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:32:ALA:CB	10:L:55:ILE:HG23	2.35	0.56
11:T:3:DA:H2'	11:T:4:DC:O4'	2.05	0.56
1:A:152:VAL:HG13	1:A:153:PRO:HD2	1.87	0.56
1:A:1209:MET:SD	1:A:1236:LEU:HB3	2.45	0.56
1:A:316:GLN:HG2	1:A:319:GLY:C	2.30	0.56
11:T:8:DT:H3'	11:T:8:DT:OP2	2.05	0.56
1:A:32:VAL:HG21	1:A:57:ARG:O	2.06	0.56
1:A:980:ASP:N	1:A:981:LEU:HD23	2.21	0.56
2:B:370:PHE:HD2	2:B:373:ARG:HG3	1.71	0.56
2:B:373:ARG:HA	2:B:566:LEU:HD23	1.86	0.56
2:B:847:ASP:OD2	9:K:6:ARG:NH2	2.35	0.56
3:C:177:GLU:HB2	3:C:231:ASN:HB3	1.87	0.56
11:T:10:DA:C1'	11:T:11:DG:C8	2.87	0.56
1:A:563:PRO:HB3	1:A:572:TRP:CD2	2.38	0.56
2:B:246:LYS:HG3	2:B:246:LYS:O	2.05	0.56
2:B:762:ASN:ND2	2:B:1022:THR:HA	2.20	0.56
11:T:8:DT:C1'	11:T:9:DA:C8	2.80	0.56
1:A:302:THR:HA	1:A:305:ASP:O	2.06	0.56
1:A:1312:ASN:O	1:A:1316:VAL:HG23	2.06	0.56
2:B:104:GLU:CD	10:L:54:ARG:NH1	2.64	0.56
11:T:12:DC:C1'	11:T:13:DA:C1'	2.81	0.56
1:A:679:ILE:HG23	1:A:729:ALA:HB1	1.88	0.55
2:B:844:SER:HB2	2:B:996:ARG:H	1.69	0.55
2:B:979:LYS:HE3	2:B:987:LYS:HG3	1.86	0.55
1:A:546:VAL:HG13	1:A:577:ILE:HG21	1.87	0.55
1:A:885:THR:HG21	1:A:943:LEU:HD12	1.84	0.55
11:T:5:DC:H42	12:N:10:DG:H1	1.55	0.55
11:T:6:DG:C2'	11:T:7:DA:N7	2.68	0.55
2:B:95:ILE:HD12	2:B:130:VAL:HG22	1.87	0.55
3:C:66:ARG:CA	8:J:5:VAL:HG21	2.33	0.55
3:C:251:LEU:O	3:C:255:VAL:HG23	2.05	0.55
1:A:545:GLN:HG2	1:A:549:MET:HE3	1.88	0.55
1:A:795:GLU:HG2	1:A:796:SER:N	2.21	0.55
2:B:129:PHE:CE1	2:B:166:PHE:HB2	2.42	0.55
2:B:883:LEU:HD22	2:B:884:ARG:H	1.72	0.55
6:H:40:LEU:HD13	6:H:123:MET:HG3	1.89	0.55
7:I:47:GLU:HG2	7:I:50:THR:HG23	1.87	0.55
2:B:640:VAL:HG22	2:B:651:LEU:CD2	2.37	0.55
4:E:46:TYR:CD1	4:E:58:MET:HG3	2.42	0.55
1:A:406:ILE:CD1	1:A:431:LYS:CB	2.85	0.55
1:A:497:THR:HG21	2:B:1149:GLU:OE2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1118:VAL:HB	1:A:1306:LEU:HB2	1.87	0.55
2:B:469:GLN:HG3	2:B:469:GLN:O	2.05	0.55
2:B:1162:ILE:O	2:B:1191:ILE:HG13	2.06	0.55
6:H:38:LEU:CD1	6:H:125:LEU:HD21	2.37	0.55
11:T:13:DA:C5'	11:T:14:DG:OP2	2.48	0.55
1:A:447:GLN:NE2	11:T:21:DC:H4'	2.21	0.55
2:B:486:TYR:CZ	2:B:1096:ARG:HB3	2.42	0.55
2:B:756:ILE:HG12	2:B:770:GLN:HG2	1.89	0.55
3:C:44:LEU:HD12	3:C:160:LYS:C	2.32	0.55
1:A:1161:THR:HG22	1:A:1163:ILE:N	2.15	0.55
1:A:1323:ASP:OD1	1:A:1325:THR:HG22	2.07	0.55
2:B:62:ILE:HD12	2:B:418:LYS:HG3	1.89	0.55
2:B:1000:PRO:HB2	2:B:1072:MET:HE3	1.89	0.55
1:A:241:VAL:HG13	1:A:266:LEU:HD13	1.89	0.55
1:A:981:LEU:CD2	1:A:1038:THR:HA	2.37	0.55
5:F:123:LYS:NZ	5:F:127:GLU:OE2	2.39	0.55
1:A:949:ASP:OD1	1:A:949:ASP:N	2.40	0.55
3:C:7:GLN:HB2	3:C:23:SER:HB2	1.89	0.55
1:A:783:THR:HG22	1:A:787:PHE:CD2	2.43	0.54
9:K:45:LEU:HG	9:K:94:ILE:HD13	1.88	0.54
10:L:48:CYS:SG	10:L:49:LYS:N	2.80	0.54
2:B:429:PHE:HA	2:B:432:MET:HE2	1.89	0.54
11:T:3:DA:C2'	11:T:4:DC:O4'	2.56	0.54
1:A:899:VAL:CG1	1:A:929:LEU:HD13	2.37	0.54
1:A:1116:LEU:HD22	1:A:1311:VAL:HG22	1.88	0.54
2:B:345:LYS:HG2	2:B:348:ARG:HH12	1.73	0.54
3:C:22:LEU:HD22	3:C:25:VAL:HG21	1.88	0.54
3:C:181:ASP:CG	3:C:186:LEU:HD13	2.32	0.54
1:A:436:ILE:HD11	1:A:491:VAL:HG11	1.88	0.54
2:B:363:HIS:O	2:B:364:ILE:HB	2.07	0.54
2:B:955:THR:CG2	2:B:956:THR:O	2.55	0.54
11:T:5:DC:N4	12:N:10:DG:N1	2.56	0.54
1:A:145:LYS:HG3	1:A:146:MET:N	2.22	0.54
2:B:839:MET:HE2	2:B:1010:LEU:HD11	1.90	0.54
2:B:1002:THR:HG22	2:B:1006:ILE:N	2.22	0.54
4:E:179:GLN:O	4:E:182:ASP:HB2	2.08	0.54
8:J:8:PHE:CE1	8:J:49:MET:HE1	2.43	0.54
2:B:714:GLU:CB	2:B:715:ALA:HB3	2.37	0.54
6:H:89:LEU:HD23	6:H:92:ASP:H	1.72	0.54
8:J:8:PHE:HD1	8:J:49:MET:SD	2.28	0.54
1:A:167:CYS:SG	1:A:169:ASN:OD1	2.66	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:590:HIS:HD2	2:B:596:LEU:HD22	1.72	0.54
2:B:1002:THR:HG23	2:B:1004:GLU:N	2.16	0.54
2:B:1084:GLN:NE2	3:C:192:TRP:H	2.04	0.54
8:J:49:MET:HA	8:J:49:MET:CE	2.33	0.54
1:A:1017:LEU:HB2	4:E:205:SER:C	2.33	0.54
1:A:1342:GLU:HG3	4:E:198:ILE:HD13	1.89	0.54
3:C:60:ASP:HB3	10:L:67:PHE:CE2	2.43	0.54
2:B:325:GLN:OE1	7:I:12:ASN:ND2	2.39	0.54
2:B:549:THR:HG21	2:B:610:ASN:HD22	1.73	0.54
3:C:120:ILE:HG21	3:C:124:LEU:HD21	1.90	0.54
6:H:44:VAL:HG13	6:H:48:PRO:HA	1.90	0.54
2:B:792:MET:HE1	11:T:25:DC:P	2.48	0.53
6:H:36:CYS:SG	6:H:130:ARG:NH2	2.82	0.53
11:T:9:DA:H2'	11:T:10:DA:C8	2.43	0.53
11:T:12:DC:N4	12:N:3:DG:O6	2.41	0.53
1:A:765:VAL:HG22	1:A:800:VAL:HB	1.88	0.53
1:A:981:LEU:N	1:A:981:LEU:CD2	2.64	0.53
4:E:16:PHE:CD1	4:E:58:MET:HE3	2.44	0.53
5:F:111:LEU:O	5:F:112:GLU:CG	2.51	0.53
1:A:90:VAL:HB	1:A:297:GLN:NE2	2.24	0.53
1:A:492:PRO:HB2	1:A:497:THR:HG23	1.89	0.53
10:L:47:ARG:HD2	10:L:47:ARG:N	2.24	0.53
1:A:1376:THR:HG23	4:E:212:ARG:HH22	1.71	0.53
4:E:15:ALA:O	4:E:19:VAL:HG23	2.08	0.53
8:J:1:MET:H1	8:J:56:LEU:HD12	1.73	0.53
10:L:38:LEU:CD1	10:L:40:LEU:CD1	2.85	0.53
1:A:404:TYR:CD1	1:A:404:TYR:N	2.76	0.53
1:A:839:ARG:HH11	1:A:839:ARG:CG	2.14	0.53
2:B:247:GLY:HA3	2:B:418:LYS:HE3	1.90	0.53
2:B:849:GLY:C	8:J:8:PHE:HE2	2.16	0.53
6:H:58:THR:HG21	6:H:93:TYR:CZ	2.44	0.53
6:H:81:PRO:HB2	6:H:82:PRO:HD2	1.90	0.53
1:A:45:GLN:O	1:A:45:GLN:CG	2.52	0.53
7:I:5:ARG:HH21	7:I:36:GLU:CD	2.16	0.53
10:L:38:LEU:CD1	10:L:40:LEU:HD11	2.38	0.53
11:T:11:DG:OP2	11:T:11:DG:H8	1.90	0.53
1:A:599:SER:O	1:A:601:LYS:N	2.41	0.53
1:A:1349:TYR:HB2	1:A:1372:VAL:HG21	1.91	0.53
2:B:714:GLU:HG3	2:B:715:ALA:HB3	1.91	0.53
11:T:15:DA:N7	11:T:16:DC:C5	2.77	0.53
1:A:114:LEU:HB3	1:A:145:LYS:HG2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:ARG:NH1	2:B:1206:GLU:OE1	2.41	0.53
1:A:463:ILE:HB	1:A:464:PRO:HD2	1.91	0.53
1:A:1142:THR:O	1:A:1145:SER:OG	2.26	0.53
2:B:778:MET:CE	2:B:1094:ARG:HD2	2.38	0.53
2:B:983:ARG:NH1	2:B:1091:TYR:HB3	2.24	0.53
3:C:75:MET:O	3:C:246:ARG:NH2	2.42	0.53
7:I:117:LYS:HE2	7:I:117:LYS:O	2.08	0.53
8:J:30:LEU:HD22	8:J:34:THR:HG21	1.91	0.53
11:T:11:DG:C2	11:T:12:DC:N4	2.77	0.53
2:B:998:ASP:OD1	3:C:35:ARG:NH2	2.41	0.53
2:B:1095:LEU:O	2:B:1097:HIS:N	2.41	0.53
1:A:252:PHE:N	1:A:252:PHE:CD1	2.76	0.53
1:A:1038:THR:O	1:A:1042:PHE:CB	2.57	0.53
3:C:164:ALA:HB2	3:C:171:GLY:HA2	1.90	0.53
1:A:903:ASN:HD22	1:A:904:THR:H	1.57	0.52
2:B:842:ASN:ND2	2:B:845:SER:OG	2.42	0.52
7:I:103:CYS:HB3	7:I:108:HIS:H	1.73	0.52
1:A:39:GLU:HA	1:A:40:THR:CB	2.14	0.52
1:A:311:GLN:N	1:A:312:PRO:HD3	2.23	0.52
1:A:317:LYS:CB	1:A:318:SER:CB	2.58	0.52
1:A:1015:VAL:HG12	1:A:1019:CYS:SG	2.49	0.52
1:A:1324:PRO:HB2	4:E:142:VAL:HG11	1.90	0.52
6:H:58:THR:CG2	6:H:93:TYR:CE2	2.92	0.52
1:A:351:THR:HG23	2:B:1103:ILE:HG12	1.90	0.52
1:A:353:ILE:HG22	1:A:468:PHE:HB2	1.90	0.52
1:A:503:GLN:OE1	5:F:90:ARG:NH2	2.42	0.52
2:B:1179:GLN:O	2:B:1180:PHE:CD1	2.62	0.52
3:C:76:ASP:OD2	3:C:128:ASN:N	2.35	0.52
4:E:55:ARG:HD2	4:E:83:CYS:O	2.10	0.52
4:E:100:ILE:HG23	4:E:105:PHE:HB2	1.90	0.52
7:I:116:ASN:OD1	7:I:116:ASN:N	2.41	0.52
1:A:594:GLY:O	1:A:596:THR:CG2	2.58	0.52
2:B:1081:LEU:O	3:C:189:THR:HG23	2.09	0.52
1:A:569:LYS:HG2	1:A:570:PRO:HD2	1.92	0.52
1:A:24:PRO:HD2	1:A:233:TRP:CD1	2.45	0.52
2:B:476:ARG:O	2:B:477:ALA:C	2.51	0.52
2:B:714:GLU:CB	2:B:715:ALA:CB	2.87	0.52
4:E:54:GLN:HG2	4:E:57:MET:HE3	1.90	0.52
6:H:115:TYR:CE1	6:H:124:ARG:HG3	2.45	0.52
11:T:5:DC:H1'	11:T:6:DG:H5''	1.89	0.52
1:A:466:SER:HB2	2:B:1099:VAL:CG1	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:540:PHE:HB3	1:A:571:LEU:HB3	1.92	0.52
2:B:1002:THR:HG22	2:B:1006:ILE:H	1.74	0.52
4:E:156:LEU:HD11	4:E:195:VAL:HB	1.91	0.52
1:A:351:THR:HG22	1:A:352:VAL:N	2.25	0.52
1:A:1130:GLN:O	1:A:1134:ILE:HD12	2.10	0.52
3:C:114:TYR:CD2	3:C:140:ASN:HB2	2.45	0.52
10:L:54:ARG:O	10:L:55:ILE:HB	2.10	0.52
1:A:114:LEU:HD11	1:A:171:GLN:OE1	2.10	0.52
1:A:470:LEU:HD21	1:A:487:MET:HE3	1.91	0.52
1:A:1206:ASP:O	1:A:1274:ARG:NH1	2.43	0.52
1:A:1224:LEU:CD2	1:A:1240:CYS:HB3	2.37	0.52
2:B:293:PRO:HG2	2:B:296:GLU:HB3	1.92	0.52
2:B:1165:ILE:HB	2:B:1185:CYS:SG	2.50	0.52
12:N:3:DG:H2''	12:N:4:DC:C5'	2.24	0.52
12:N:9:DC:C2	12:N:10:DG:O6	2.63	0.52
2:B:661:LEU:HD11	2:B:684:LEU:HD11	1.91	0.52
1:A:534:LEU:O	1:A:574:GLY:HA3	2.10	0.51
1:A:919:ILE:HG22	1:A:920:LEU:N	2.26	0.51
1:A:1132:LYS:HG3	1:A:1135:ARG:NH1	2.21	0.51
1:A:1176:LEU:N	1:A:1176:LEU:CD1	2.73	0.51
2:B:345:LYS:HG2	2:B:348:ARG:NH1	2.24	0.51
2:B:712:PRO:N	2:B:713:ALA:CA	2.73	0.51
6:H:47:PHE:HB3	6:H:95:TYR:HD2	1.75	0.51
6:H:129:TYR:CE1	6:H:130:ARG:NH1	2.77	0.51
1:A:50:ILE:HG23	1:A:52:GLY:H	1.74	0.51
1:A:399:HIS:HD2	1:A:400:PRO:CA	2.07	0.51
2:B:487:THR:HG22	2:B:490:SER:N	2.22	0.51
2:B:487:THR:H	2:B:490:SER:HB3	1.75	0.51
5:F:77:ASP:OD1	5:F:77:ASP:N	2.43	0.51
6:H:93:TYR:HA	6:H:145:ARG:HG3	1.91	0.51
11:T:3:DA:H2''	11:T:4:DC:C5'	2.39	0.51
1:A:65:LEU:HA	1:A:73:GLY:HA2	1.93	0.51
1:A:1004:ASN:ND2	4:E:167:ARG:HD2	2.26	0.51
1:A:50:ILE:CG2	1:A:51:GLY:H	2.18	0.51
1:A:185:TRP:HE3	1:A:199:LEU:HB2	1.74	0.51
1:A:219:PHE:HB3	1:A:224:PHE:HB2	1.93	0.51
1:A:500:GLU:O	1:A:504:LEU:HB2	2.11	0.51
1:A:828:ALA:O	1:A:831:THR:CG2	2.51	0.51
2:B:1002:THR:CG2	2:B:1006:ILE:HB	2.41	0.51
2:B:1162:ILE:HG22	2:B:1163:CYS:N	2.24	0.51
1:A:35:ILE:CG2	1:A:52:GLY:O	2.52	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:97:MET:HB2	6:H:118:PHE:CD2	2.46	0.51
1:A:482:PHE:HB2	2:B:838:SER:HB3	1.91	0.51
1:A:599:SER:C	1:A:601:LYS:N	2.66	0.51
1:A:966:ASN:O	1:A:970:THR:HG22	2.10	0.51
3:C:17:ASN:HD22	3:C:231:ASN:HD21	1.58	0.51
11:T:10:DA:N3	11:T:11:DG:C4	2.79	0.51
1:A:785:PRO:HB2	2:B:703:ILE:HD12	1.93	0.51
1:A:1383:SER:O	1:A:1388:GLY:HA3	2.10	0.51
2:B:48:LEU:HD23	2:B:173:MET:SD	2.50	0.51
2:B:840:ILE:HG12	2:B:992:ILE:HG22	1.93	0.51
2:B:1159:ARG:HE	2:B:1193:GLN:NE2	2.08	0.51
11:T:7:DA:H8	11:T:7:DA:OP2	1.93	0.51
1:A:51:GLY:HA2	1:A:55:ASP:HB2	1.93	0.51
1:A:871:ASP:OD1	1:A:1366:ARG:NH2	2.43	0.51
2:B:637:LEU:HD12	2:B:693:ILE:HG13	1.93	0.51
2:B:955:THR:HG22	2:B:963:PHE:HE1	1.75	0.51
3:C:3:GLU:HB3	9:K:104:ASN:OD1	2.11	0.51
11:T:7:DA:OP2	11:T:8:DT:H73	2.09	0.51
1:A:250:ILE:CG1	1:A:251:SER:N	2.73	0.51
1:A:1345:ARG:HG2	1:A:1372:VAL:CG1	2.40	0.51
2:B:247:GLY:CA	2:B:418:LYS:HE3	2.39	0.51
2:B:651:LEU:HG	2:B:710:LEU:HD12	1.93	0.51
2:B:1135:ARG:NH2	2:B:1136:ASP:OD1	2.44	0.51
3:C:29:MET:HE2	9:K:94:ILE:HG23	1.93	0.51
8:J:64:ASN:N	8:J:65:PRO:HD2	2.26	0.51
1:A:567:LYS:CB	6:H:96:VAL:HB	2.39	0.51
1:A:697:ALA:HA	1:A:702:LEU:HB2	1.93	0.51
1:A:818:MET:HE3	2:B:514:LEU:O	2.11	0.51
1:A:1409:LEU:HD13	2:B:1207:LEU:HD21	1.92	0.51
6:H:103:LYS:HB3	6:H:115:TYR:CD2	2.46	0.51
1:A:746:MET:SD	2:B:1015:HIS:HD2	2.33	0.50
1:A:1072:ILE:HD11	1:A:1368:MET:HA	1.92	0.50
2:B:117:ALA:HA	2:B:122:LEU:HB2	1.93	0.50
2:B:784:ASN:ND2	2:B:784:ASN:O	2.44	0.50
6:H:36:CYS:HB2	6:H:130:ARG:NH2	2.25	0.50
6:H:127:GLY:HA3	6:H:130:ARG:CZ	2.41	0.50
9:K:91:CYS:O	9:K:95:ILE:HG13	2.11	0.50
12:N:4:DC:H2"	12:N:5:DT:H72	1.93	0.50
1:A:78:PRO:O	2:B:1205:GLN:NE2	2.43	0.50
1:A:117:GLU:H	1:A:117:GLU:CD	2.19	0.50
1:A:145:LYS:CG	1:A:146:MET:H	2.24	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:100:PRO:HD2	2:B:180:TYR:CE2	2.46	0.50
2:B:912:ILE:HD11	2:B:966:VAL:HG23	1.93	0.50
6:H:128:ASN:OD1	6:H:129:TYR:N	2.44	0.50
1:A:67:CYS:CB	1:A:70:CYS:SG	2.92	0.50
1:A:407:ARG:HG2	1:A:430:TRP:CZ2	2.47	0.50
1:A:114:LEU:HB2	1:A:142:CYS:SG	2.52	0.50
1:A:494:SER:H	1:A:497:THR:CG2	2.24	0.50
1:A:1223:ASP:O	1:A:1224:LEU:HB2	2.12	0.50
2:B:550:ASP:OD1	2:B:551:PRO:HD2	2.12	0.50
6:H:130:ARG:NH1	6:H:130:ARG:CG	2.73	0.50
1:A:896:ARG:HD2	1:A:897:TYR:CE2	2.46	0.50
2:B:711:GLU:C	2:B:714:GLU:H	2.19	0.50
2:B:859:TYR:OH	2:B:941:LEU:HD22	2.11	0.50
2:B:977:GLY:CA	2:B:1099:VAL:CG2	2.90	0.50
10:L:47:ARG:NH1	10:L:54:ARG:HE	2.10	0.50
1:A:251:SER:CB	1:A:252:PHE:CA	2.89	0.50
1:A:778:GLY:HA3	2:B:516:ASN:HB2	1.92	0.50
2:B:361:LEU:HD21	2:B:377:PHE:CD2	2.47	0.50
3:C:69:LEU:CB	8:J:5:VAL:CG1	2.89	0.50
6:H:58:THR:HG23	6:H:143:LEU:HB2	1.92	0.50
2:B:519:TRP:HZ2	2:B:705:MET:HE1	1.73	0.50
3:C:145:CYS:SG	3:C:146:LYS:N	2.85	0.50
4:E:55:ARG:C	4:E:57:MET:H	2.18	0.50
6:H:84:ALA:HA	6:H:87:ARG:HB2	1.92	0.50
8:J:2:ILE:O	8:J:3:VAL:C	2.55	0.50
11:T:18:DA:H2"	11:T:19:1CC:H2	1.70	0.50
2:B:637:LEU:HA	2:B:743:ILE:HG12	1.93	0.50
3:C:235:VAL:HG21	8:J:6:ARG:HH21	1.77	0.50
6:H:104:PHE:CE2	6:H:114:VAL:HG23	2.47	0.50
1:A:49:LYS:HD2	1:A:49:LYS:N	2.27	0.50
1:A:57:ARG:C	1:A:68:GLN:HG2	2.37	0.50
1:A:839:ARG:CG	1:A:839:ARG:NH1	2.73	0.50
2:B:899:ILE:HG13	2:B:911:ILE:HG23	1.94	0.50
3:C:185:LYS:HG2	3:C:213:PRO:HG3	1.94	0.50
7:I:73:ARG:O	7:I:83:ASN:ND2	2.44	0.50
8:J:13:VAL:HG13	8:J:13:VAL:O	2.12	0.50
10:L:29:TYR:CD1	10:L:58:LYS:HA	2.46	0.50
1:A:185:TRP:HB2	1:A:199:LEU:HD13	1.93	0.49
1:A:249:SER:HA	1:A:250:ILE:CB	2.36	0.49
1:A:746:MET:SD	2:B:1015:HIS:CD2	3.05	0.49
1:A:899:VAL:CG1	1:A:929:LEU:CD1	2.90	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:532:ALA:HB1	2:B:536:VAL:HG23	1.93	0.49
2:B:796:LEU:O	2:B:799:PRO:HD3	2.12	0.49
3:C:46:ILE:HA	3:C:159:ALA:HA	1.94	0.49
4:E:48:ASP:O	4:E:49:SER:C	2.55	0.49
1:A:38:PRO:HA	1:A:270:LEU:HD13	1.94	0.49
1:A:645:LEU:HD11	1:A:649:ILE:HD11	1.94	0.49
2:B:834:ASN:HB3	2:B:840:ILE:HG13	1.94	0.49
4:E:55:ARG:HG3	4:E:55:ARG:HH11	1.77	0.49
1:A:40:THR:HG23	1:A:41:MET:N	2.27	0.49
1:A:594:GLY:O	1:A:596:THR:HG23	2.12	0.49
1:A:605:MET:HG3	1:A:606:LEU:N	2.26	0.49
1:A:804:TYR:CE2	2:B:1021:MET:HE3	2.38	0.49
1:A:1169:ILE:H	1:A:1169:ILE:HD12	1.76	0.49
1:A:508:PRO:O	1:A:511:ILE:HG13	2.13	0.49
1:A:855:THR:CG2	1:A:857:ARG:HE	2.26	0.49
2:B:710:LEU:O	2:B:711:GLU:HB2	2.13	0.49
2:B:714:GLU:CD	2:B:715:ALA:HB3	2.38	0.49
3:C:15:LYS:O	3:C:240:VAL:HG22	2.12	0.49
7:I:74:GLU:O	7:I:74:GLU:HG3	2.12	0.49
11:T:10:DA:H1'	11:T:11:DG:C1'	2.43	0.49
12:N:12:DT:H2''	12:N:13:DA:OP2	2.12	0.49
2:B:251:ILE:HG23	2:B:251:ILE:O	2.12	0.49
2:B:651:LEU:HG	2:B:710:LEU:CD1	2.43	0.49
6:H:58:THR:HG21	6:H:93:TYR:CE2	2.47	0.49
1:A:64:ASN:O	1:A:66:LYS:N	2.38	0.49
1:A:339:ASN:HB3	2:B:1117:GLN:HE22	1.77	0.49
1:A:606:LEU:HD11	1:A:608:ILE:HG12	1.95	0.49
1:A:842:VAL:HG11	2:B:1136:ASP:OD2	2.12	0.49
2:B:732:SER:HB2	2:B:734:HIS:CE1	2.47	0.49
6:H:80:ARG:HG2	9:K:57:LEU:CD2	2.40	0.49
1:A:32:VAL:CG2	1:A:57:ARG:O	2.60	0.49
2:B:416:LEU:HD11	2:B:460:ALA:CB	2.42	0.49
2:B:899:ILE:HG22	2:B:900:ALA:N	2.28	0.49
4:E:161:LYS:HD2	4:E:195:VAL:HG23	1.95	0.49
11:T:5:DC:C5	11:T:6:DG:C6	3.00	0.49
1:A:357:PRO:HD2	2:B:833:TYR:CZ	2.47	0.49
1:A:599:SER:C	1:A:601:LYS:H	2.21	0.49
2:B:65:GLU:HG3	2:B:246:LYS:CE	2.43	0.49
2:B:169:ARG:N	2:B:454:THR:HG23	2.24	0.49
2:B:710:LEU:C	2:B:712:PRO:HA	2.37	0.49
2:B:776:GLN:HG2	2:B:1096:ARG:HD3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:I:34:TYR:C	7:I:34:TYR:CD1	2.90	0.49
1:A:372:LYS:HA	1:A:435:HIS:CE1	2.47	0.49
1:A:912:LEU:HD11	1:A:1033:GLN:HG3	1.95	0.49
1:A:1325:THR:OG1	4:E:146:HIS:O	2.31	0.49
1:A:1438:THR:HG23	2:B:1142:GLY:O	2.13	0.49
2:B:275:TYR:HE1	2:B:355:ILE:HG12	1.78	0.49
2:B:287:ARG:NH1	2:B:321:GLY:O	2.46	0.49
3:C:167:HIS:HD2	3:C:169:LYS:N	2.10	0.49
6:H:26:ILE:HG22	6:H:40:LEU:HB3	1.93	0.49
7:I:109:ILE:HG22	7:I:120:GLN:HG3	1.92	0.49
11:T:5:DC:N4	12:N:10:DG:C6	2.81	0.49
12:N:12:DT:HI1'	12:N:13:DA:C8	2.48	0.49
1:A:57:ARG:CB	1:A:68:GLN:CB	2.67	0.49
1:A:770:VAL:HA	1:A:822:GLU:OE2	2.13	0.49
1:A:1116:LEU:HD13	1:A:1329:THR:HG23	1.95	0.49
2:B:247:GLY:HA3	2:B:418:LYS:CE	2.42	0.49
2:B:358:LYS:HA	2:B:366:GLN:HG2	1.94	0.49
2:B:859:TYR:N	2:B:966:VAL:O	2.39	0.49
2:B:882:THR:O	2:B:882:THR:HG22	2.13	0.49
2:B:884:ARG:HG3	2:B:935:ARG:CG	2.32	0.49
2:B:896:ASP:OD2	10:L:29:TYR:OH	2.29	0.49
3:C:46:ILE:HG23	3:C:157:CYS:HB3	1.95	0.49
8:J:48:ARG:O	8:J:52:THR:HB	2.12	0.49
4:E:46:TYR:CE1	4:E:58:MET:HG2	2.47	0.48
5:F:83:PRO:HA	5:F:146:TRP:CZ3	2.47	0.48
1:A:261:ASP:HB2	1:A:323:LYS:NZ	2.28	0.48
2:B:955:THR:HG22	2:B:963:PHE:CE1	2.48	0.48
3:C:69:LEU:HB2	8:J:5:VAL:CG1	2.43	0.48
4:E:198:ILE:HD11	4:E:212:ARG:HG3	1.95	0.48
7:I:32:CYS:SG	7:I:33:SER:N	2.78	0.48
9:K:7:PHE:HB2	9:K:11:LEU:HD22	1.95	0.48
9:K:42:LEU:HD13	9:K:46:ILE:HG13	1.95	0.48
1:A:46:THR:CG2	1:A:47:ARG:H	2.00	0.48
1:A:86:LEU:HD13	1:A:90:VAL:HG22	1.94	0.48
1:A:169:ASN:O	1:A:169:ASN:ND2	2.46	0.48
1:A:552:TRP:NE1	1:A:655:PHE:CD2	2.81	0.48
1:A:1155:ASP:OD1	1:A:1162:VAL:HG23	2.13	0.48
1:A:1215:ARG:HG2	1:A:1273:LEU:HA	1.95	0.48
2:B:708:GLU:O	2:B:712:PRO:HG3	2.13	0.48
3:C:52:GLU:HA	10:L:64:LEU:HD11	1.95	0.48
3:C:133:ILE:HD11	3:C:237:SER:HA	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:136:ASN:OD1	4:E:137:GLU:N	2.46	0.48
11:T:10:DA:C2'	11:T:11:DG:C8	2.94	0.48
1:A:53:LEU:CD2	1:A:54:ASN:HB2	2.41	0.48
1:A:268:ASP:HB3	1:A:299:HIS:CE1	2.49	0.48
1:A:962:ARG:O	1:A:966:ASN:HB2	2.13	0.48
2:B:582:VAL:HG22	2:B:626:ILE:HB	1.94	0.48
2:B:778:MET:HE1	2:B:1094:ARG:CD	2.41	0.48
2:B:995:ARG:NH1	2:B:997:GLU:OE2	2.46	0.48
1:A:115:LEU:HD22	1:A:119:ASN:HB2	1.94	0.48
1:A:260:ASP:OD1	1:A:261:ASP:N	2.47	0.48
1:A:310:GLY:CA	1:A:312:PRO:HD3	2.43	0.48
1:A:315:LEU:HA	1:A:320:ARG:HG2	1.95	0.48
1:A:1402:PHE:CG	1:A:1403:GLU:HG2	2.47	0.48
11:T:6:DG:N2	12:N:10:DG:H1	2.11	0.48
1:A:406:ILE:CB	1:A:431:LYS:HB2	2.33	0.48
1:A:472:LEU:HD21	2:B:835:GLN:HB2	1.95	0.48
1:A:542:GLU:O	1:A:546:VAL:HG23	2.13	0.48
1:A:715:GLU:OE2	1:A:774:ARG:NH1	2.47	0.48
2:B:248:SER:C	2:B:250:PHE:H	2.22	0.48
2:B:376:PHE:CE1	2:B:569:TYR:HD2	2.32	0.48
2:B:792:MET:HG3	2:B:855:PHE:HE1	1.79	0.48
2:B:1174:LYS:HB3	2:B:1179:GLN:HB2	1.95	0.48
11:T:7:DA:H2'	11:T:8:DT:C5	2.45	0.48
2:B:487:THR:O	2:B:488:TYR:C	2.55	0.48
2:B:711:GLU:HB3	2:B:713:ALA:HB2	1.96	0.48
4:E:28:TYR:CE2	4:E:78:LEU:HD13	2.49	0.48
4:E:147:HIS:HB3	4:E:150:VAL:HG23	1.95	0.48
5:F:83:PRO:HG2	5:F:84:TYR:HD1	1.78	0.48
10:L:29:TYR:HE1	10:L:58:LYS:CD	2.22	0.48
1:A:24:PRO:HB3	1:A:237:THR:HB	1.96	0.48
1:A:1364:ASN:OD1	1:A:1366:ARG:HG2	2.14	0.48
2:B:707:PRO:C	2:B:709:ASP:N	2.71	0.48
8:J:8:PHE:HE1	8:J:49:MET:CE	2.27	0.48
9:K:39:ASP:OD1	9:K:39:ASP:N	2.45	0.48
11:T:3:DA:C2	12:N:13:DA:C2	3.01	0.48
1:A:109:HIS:HB3	1:A:167:CYS:SG	2.53	0.48
1:A:161:LEU:N	1:A:161:LEU:CD2	2.77	0.48
2:B:226:PHE:HA	2:B:395:GLN:HG3	1.95	0.48
2:B:1065:GLN:HE21	2:B:1069:PHE:HD2	1.62	0.48
6:H:131:ASN:OD1	6:H:132:LEU:HG	2.14	0.48
9:K:33:ILE:HD13	9:K:87:LEU:HD22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:908:LEU:CD1	1:A:983:ILE:HD11	2.44	0.47
1:A:1392:SER:O	1:A:1394:THR:N	2.47	0.47
2:B:1173:ALA:HA	2:B:1180:PHE:CD1	2.40	0.47
3:C:136:ASP:OD1	3:C:139:GLY:N	2.47	0.47
1:A:672:ASP:HB3	1:A:675:THR:H	1.79	0.47
2:B:65:GLU:OE2	2:B:246:LYS:HE3	2.14	0.47
2:B:203:PHE:HE2	2:B:212:LEU:HD12	1.79	0.47
2:B:332:ASP:C	2:B:334:ILE:H	2.22	0.47
2:B:364:ILE:HD13	2:B:585:VAL:HG13	1.95	0.47
2:B:1117:GLN:HE21	2:B:1199:ALA:HB2	1.77	0.47
1:A:565:ILE:HG22	1:A:569:LYS:O	2.14	0.47
1:A:628:GLY:O	1:A:632:VAL:HG23	2.13	0.47
1:A:1095:THR:HG21	1:A:1112:LYS:HE2	1.96	0.47
1:A:1189:SER:OG	1:A:1190:PRO:HD2	2.14	0.47
2:B:64:CYS:O	2:B:65:GLU:HB3	2.13	0.47
3:C:214:ASN:HB2	3:C:217:ASP:OD2	2.14	0.47
11:T:15:DA:C8	11:T:16:DC:H5	2.31	0.47
11:T:15:DA:C5	11:T:16:DC:N4	2.83	0.47
1:A:37:PHE:HB2	1:A:52:GLY:HA3	1.96	0.47
1:A:310:GLY:C	1:A:312:PRO:CD	2.86	0.47
2:B:394:ASP:OD1	2:B:394:ASP:N	2.35	0.47
2:B:492:LEU:HD23	2:B:492:LEU:HA	1.74	0.47
1:A:845:LEU:CD2	1:A:1374:VAL:HG11	2.45	0.47
2:B:209:GLU:OE1	2:B:788:ARG:NH2	2.47	0.47
11:T:16:DC:H1'	11:T:17:DG:O4'	2.15	0.47
1:A:1011:GLN:HE22	1:A:1015:VAL:HG21	1.78	0.47
2:B:314:LEU:O	2:B:317:CYS:HB2	2.13	0.47
2:B:620:ARG:NH1	7:I:68:LEU:HD21	2.29	0.47
2:B:1187:ASN:OD1	2:B:1188:LYS:N	2.47	0.47
4:E:23:VAL:HG12	4:E:28:TYR:HB2	1.97	0.47
9:K:44:ASN:HA	9:K:47:ARG:HG2	1.97	0.47
1:A:39:GLU:CA	1:A:40:THR:HB	2.27	0.47
1:A:152:VAL:HG12	1:A:153:PRO:CD	2.44	0.47
1:A:415:LEU:CD2	1:A:415:LEU:N	2.77	0.47
1:A:495:GLU:O	1:A:498:ARG:HG3	2.14	0.47
2:B:43:LEU:HD11	2:B:811:TYR:O	2.14	0.47
2:B:195:CYS:HB3	2:B:782:LEU:HD22	1.96	0.47
2:B:408:LEU:HB3	2:B:409:ALA:H	1.58	0.47
2:B:727:LYS:HD3	2:B:1049:ASP:CG	2.40	0.47
2:B:830:TYR:CE2	2:B:1000:PRO:HD3	2.50	0.47
7:I:32:CYS:O	7:I:33:SER:OG	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:8:PHE:HE1	8:J:49:MET:SD	2.38	0.47
9:K:12:LEU:H	9:K:12:LEU:HD12	1.79	0.47
11:T:10:DA:H1'	11:T:11:DG:O4'	2.15	0.47
13:R:1:A:C2'	13:R:2:U:C5'	2.91	0.47
1:A:605:MET:SD	1:A:621:THR:HG21	2.55	0.47
2:B:783:THR:HG23	8:J:60:PHE:CD1	2.50	0.47
3:C:99:LEU:N	3:C:99:LEU:HD23	2.30	0.47
7:I:10:CYS:SG	7:I:32:CYS:HB3	2.55	0.47
1:A:598:LEU:O	1:A:599:SER:C	2.58	0.47
1:A:606:LEU:C	1:A:606:LEU:HD12	2.40	0.47
1:A:1138:ILE:HG22	1:A:1279:ILE:HG21	1.97	0.47
1:A:1397:LEU:HB2	1:A:1426:GLU:OE2	2.15	0.47
2:B:702:LEU:HD21	2:B:735:ALA:HB1	1.97	0.47
5:F:107:VAL:HG11	5:F:111:LEU:HD11	1.96	0.47
1:A:399:HIS:NE2	1:A:400:PRO:HB3	2.29	0.47
1:A:492:PRO:CB	1:A:497:THR:HG23	2.44	0.47
1:A:1037:LEU:HD21	1:A:1045:VAL:HG21	1.96	0.47
2:B:468:GLU:CG	2:B:469:GLN:H	2.28	0.47
2:B:563:MET:HE1	2:B:580:VAL:HB	1.97	0.47
4:E:35:VAL:C	4:E:37:LEU:H	2.23	0.47
4:E:153:HIS:O	4:E:154:ILE:HD13	2.15	0.47
1:A:169:ASN:ND2	1:A:169:ASN:C	2.73	0.46
1:A:351:THR:CG2	2:B:1103:ILE:HG12	2.45	0.46
1:A:356:ASP:C	1:A:358:ASN:H	2.23	0.46
1:A:378:GLU:OE2	1:A:387:ARG:NH2	2.44	0.46
1:A:494:SER:O	1:A:497:THR:HG22	2.15	0.46
1:A:569:LYS:HZ1	3:C:221:TYR:HB2	1.80	0.46
1:A:569:LYS:NZ	3:C:221:TYR:HB2	2.30	0.46
2:B:211:VAL:O	2:B:480:SER:HA	2.14	0.46
10:L:31:CYS:SG	10:L:32:ALA:N	2.88	0.46
10:L:37:LYS:O	10:L:39:SER:N	2.47	0.46
11:T:12:DC:O2	11:T:13:DA:H1'	2.15	0.46
1:A:575:LYS:O	1:A:579:SER:OG	2.34	0.46
1:A:596:THR:O	1:A:596:THR:OG1	2.34	0.46
1:A:1402:PHE:CD1	1:A:1403:GLU:HG2	2.51	0.46
1:A:1431:GLY:HA3	2:B:1197:PRO:HD3	1.98	0.46
2:B:176:SER:O	2:B:182:SER:HB3	2.15	0.46
2:B:707:PRO:C	2:B:709:ASP:H	2.23	0.46
2:B:778:MET:CE	2:B:1094:ARG:CD	2.94	0.46
2:B:808:ALA:O	2:B:812:LEU:HG	2.16	0.46
4:E:19:VAL:O	4:E:23:VAL:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:SER:HB3	2:B:1193:GLN:OE1	2.16	0.46
1:A:68:GLN:O	1:A:69:THR:HB	2.16	0.46
1:A:1224:LEU:HD21	1:A:1240:CYS:CB	2.40	0.46
3:C:41:ILE:HD11	3:C:243:VAL:HG13	1.97	0.46
3:C:54:ASN:OD1	3:C:56:THR:HG22	2.15	0.46
7:I:50:THR:HG22	7:I:52:ILE:HG22	1.97	0.46
1:A:250:ILE:CG1	1:A:251:SER:H	2.29	0.46
1:A:285:PRO:HB2	1:A:288:ALA:HB3	1.97	0.46
1:A:938:LYS:HB2	1:A:938:LYS:HE3	1.78	0.46
1:A:1336:MET:HE2	1:A:1381:LEU:HG	1.97	0.46
2:B:797:TYR:HB3	2:B:798:TYR:HD1	1.80	0.46
2:B:834:ASN:O	2:B:1013:ASN:HB2	2.15	0.46
6:H:109:LYS:HA	6:H:109:LYS:HE3	1.98	0.46
11:T:8:DT:O2	11:T:9:DA:C5	2.69	0.46
1:A:35:ILE:HG23	1:A:53:LEU:HA	1.96	0.46
1:A:369:SER:HB3	9:K:2:ASN:OD1	2.15	0.46
1:A:402:ALA:CB	1:A:434:ARG:HA	2.46	0.46
1:A:845:LEU:HD21	1:A:1374:VAL:HG11	1.97	0.46
2:B:315:LYS:N	2:B:316:PRO:HD2	2.31	0.46
11:T:12:DC:HI'	11:T:13:DA:C4	2.44	0.46
1:A:577:ILE:HD12	1:A:578:LEU:N	2.29	0.46
2:B:487:THR:O	2:B:490:SER:N	2.47	0.46
2:B:848:ARG:HD2	8:J:7:CYS:O	2.16	0.46
3:C:167:HIS:CD2	3:C:169:LYS:H	2.31	0.46
8:J:36:LEU:HD11	8:J:51:LEU:HB2	1.98	0.46
10:L:33:GLU:OE2	10:L:53:HIS:CG	2.69	0.46
1:A:4:GLN:HB3	1:A:76:GLU:OE1	2.16	0.46
1:A:53:LEU:C	1:A:55:ASP:H	2.23	0.46
1:A:311:GLN:N	1:A:312:PRO:CD	2.79	0.46
1:A:642:CYS:O	1:A:645:LEU:HB3	2.15	0.46
1:A:761:MET:HG3	2:B:1021:MET:CG	2.46	0.46
1:A:848:ILE:HD11	1:A:1374:VAL:HG21	1.97	0.46
1:A:882:SER:HA	1:A:953:ASN:HA	1.97	0.46
1:A:1022:LEU:HD11	1:A:1026:LEU:HD12	1.97	0.46
1:A:1035:TYR:HB3	1:A:1037:LEU:HD12	1.97	0.46
2:B:28:GLU:C	2:B:30:SER:H	2.23	0.46
3:C:74:SER:O	3:C:77:ILE:HB	2.16	0.46
5:F:76:LYS:O	5:F:79:ARG:HD3	2.15	0.46
1:A:35:ILE:HA	1:A:52:GLY:O	2.15	0.46
1:A:224:PHE:CZ	1:A:231:PRO:HG3	2.51	0.46
1:A:316:GLN:NE2	1:A:318:SER:OG	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:396:PRO:HD3	1:A:415:LEU:HB3	1.97	0.46
1:A:399:HIS:NE2	1:A:437:MET:HG2	2.31	0.46
1:A:537:ARG:HD3	6:H:120:GLY:O	2.15	0.46
2:B:1110:PRO:HB2	2:B:1119:VAL:HG13	1.98	0.46
5:F:132:LEU:O	5:F:148:VAL:HG23	2.16	0.46
6:H:108:SER:C	6:H:110:ASP:N	2.74	0.46
7:I:78:CYS:O	7:I:79:HIS:CB	2.64	0.46
1:A:337:ARG:HB3	1:A:337:ARG:HH11	1.81	0.46
1:A:375:THR:HG21	1:A:433:GLU:OE1	2.15	0.46
1:A:416:ARG:C	1:A:417:TYR:CD1	2.94	0.46
1:A:768:GLN:CG	1:A:816:HIS:HA	2.45	0.46
1:A:908:LEU:HD11	1:A:983:ILE:HD11	1.96	0.46
2:B:261:ARG:HD3	2:B:261:ARG:HA	1.82	0.46
2:B:1077:THR:CG2	2:B:1079:LYS:H	2.26	0.46
8:J:1:MET:N	8:J:56:LEU:HD12	2.30	0.46
1:A:164:ARG:CG	1:A:165:GLY:N	2.79	0.46
1:A:387:ARG:HH11	1:A:437:MET:HE1	1.81	0.46
1:A:399:HIS:HE1	1:A:462:VAL:HG21	1.78	0.46
1:A:406:ILE:HD13	1:A:431:LYS:HB2	1.93	0.46
1:A:494:SER:O	1:A:498:ARG:HG2	2.15	0.46
1:A:592:ASP:O	1:A:593:GLU:CB	2.49	0.46
1:A:839:ARG:HG2	1:A:839:ARG:NH1	2.21	0.46
2:B:1034:VAL:HG22	2:B:1059:LEU:HB2	1.98	0.46
2:B:1110:PRO:C	2:B:1111:MET:HG2	2.40	0.46
4:E:79:TRP:HE1	4:E:81:GLU:HG3	1.81	0.46
5:F:119:ARG:CG	5:F:119:ARG:NH1	2.75	0.46
6:H:128:ASN:O	6:H:131:ASN:ND2	2.48	0.46
7:I:55:THR:HG21	7:I:120:GLN:HB3	1.98	0.46
10:L:42:ARG:H	10:L:42:ARG:HG3	1.43	0.46
10:L:47:ARG:CB	10:L:54:ARG:HA	2.44	0.46
11:T:24:DT:H2'	11:T:25:DC:O4'	2.16	0.46
1:A:363:GLN:O	1:A:458:HIS:ND1	2.48	0.45
1:A:550:LEU:HD21	1:A:561:PRO:HD2	1.98	0.45
2:B:434:ARG:HG2	2:B:434:ARG:O	2.16	0.45
2:B:789:MET:CE	2:B:965:LYS:HB3	2.44	0.45
2:B:864:LYS:HD2	2:B:866:TYR:N	2.24	0.45
4:E:116:ILE:CG2	4:E:121:MET:HG3	2.46	0.45
1:A:38:PRO:CA	1:A:270:LEU:HD13	2.47	0.45
1:A:406:ILE:HD13	1:A:431:LYS:HB3	1.96	0.45
1:A:868:TYR:CZ	1:A:1064:VAL:HG21	2.51	0.45
1:A:1410:PHE:HD1	2:B:1212:ILE:HD11	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:900:ALA:O	2:B:902:GLY:N	2.47	0.45
2:B:1084:GLN:OE1	2:B:1084:GLN:N	2.49	0.45
3:C:56:THR:HG23	3:C:58:LEU:N	2.25	0.45
1:A:261:ASP:HB2	1:A:323:LYS:HZ3	1.80	0.45
1:A:738:LYS:HB3	6:H:19:ARG:HH22	1.81	0.45
1:A:810:PRO:HB2	2:B:705:MET:SD	2.55	0.45
1:A:868:TYR:CE1	1:A:1064:VAL:HG21	2.51	0.45
1:A:903:ASN:ND2	1:A:904:THR:H	2.14	0.45
2:B:256:VAL:HG11	2:B:382:ILE:HD13	1.98	0.45
2:B:636:PRO:C	2:B:637:LEU:HG	2.40	0.45
4:E:204:THR:HG22	4:E:205:SER:N	2.31	0.45
6:H:10:PHE:HB3	6:H:28:ALA:HB1	1.97	0.45
6:H:109:LYS:HA	6:H:109:LYS:CE	2.46	0.45
11:T:6:DG:C4	11:T:7:DA:C6	3.05	0.45
1:A:318:SER:HA	1:A:319:GLY:HA2	1.64	0.45
1:A:765:VAL:HG13	1:A:802:ASN:O	2.16	0.45
1:A:833:GLU:O	1:A:837:ILE:HG12	2.17	0.45
1:A:1349:TYR:CD1	1:A:1349:TYR:C	2.94	0.45
2:B:620:ARG:CZ	7:I:68:LEU:HD21	2.47	0.45
2:B:763:GLN:HG2	2:B:765:PRO:HD2	1.99	0.45
1:A:102:VAL:C	1:A:104:GLU:H	2.25	0.45
1:A:209:ASN:HA	1:A:212:LYS:HB2	1.99	0.45
1:A:550:LEU:HG	1:A:556:TRP:NE1	2.32	0.45
1:A:707:GLY:C	1:A:708:MET:HG3	2.41	0.45
2:B:31:TRP:CE3	2:B:34:ILE:HD13	2.52	0.45
3:C:38:ILE:HG13	3:C:176:ILE:CD1	2.45	0.45
8:J:6:ARG:CG	8:J:12:LYS:O	2.64	0.45
2:B:648:HIS:HB2	2:B:711:GLU:CD	2.42	0.45
4:E:164:LEU:HD13	4:E:211:TYR:CE2	2.51	0.45
6:H:98:TYR:C	6:H:98:TYR:CD1	2.94	0.45
8:J:25:LEU:HA	8:J:25:LEU:HD23	1.78	0.45
1:A:68:GLN:CD	1:A:80:HIS:CD2	2.94	0.45
1:A:91:PHE:HA	1:A:235:ILE:HG22	1.99	0.45
1:A:399:HIS:HA	1:A:400:PRO:HA	1.68	0.45
1:A:606:LEU:CD2	1:A:614:PHE:CE2	2.99	0.45
2:B:436:VAL:O	2:B:436:VAL:HG13	2.17	0.45
2:B:554:ILE:HD11	2:B:609:ILE:HG23	1.98	0.45
3:C:8:VAL:HG11	9:K:105:PHE:CD1	2.51	0.45
3:C:67:LEU:HD23	3:C:144:ILE:HD11	1.99	0.45
4:E:117:THR:O	4:E:119:SER:N	2.50	0.45
6:H:91:ASP:C	6:H:93:TYR:HD1	2.24	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:39:GLU:OE1	1:A:39:GLU:N	2.50	0.45
1:A:44:THR:O	1:A:46:THR:N	2.49	0.45
1:A:821:ARG:HG3	1:A:825:ILE:HD11	1.99	0.45
1:A:849:MET:SD	1:A:1061:GLY:HA2	2.56	0.45
1:A:981:LEU:HD22	1:A:1038:THR:HA	1.98	0.45
4:E:112:TYR:CD1	4:E:116:ILE:HD11	2.52	0.45
5:F:94:LEU:HD13	5:F:122:MET:HG2	1.98	0.45
9:K:41:THR:HG22	9:K:42:LEU:H	1.80	0.45
11:T:12:DC:N4	12:N:3:DG:C6	2.84	0.45
1:A:393:ARG:C	1:A:395:GLY:H	2.25	0.45
1:A:401:GLY:C	1:A:435:HIS:HD2	2.25	0.45
1:A:404:TYR:HD1	1:A:404:TYR:N	2.14	0.45
1:A:483:ASP:HA	2:B:988:GLY:HA2	1.98	0.45
1:A:567:LYS:HA	1:A:568:PRO:HA	1.59	0.45
1:A:743:VAL:O	1:A:747:VAL:HG23	2.17	0.45
2:B:824:ILE:HG22	2:B:1008:PRO:HA	1.98	0.45
3:C:99:LEU:HB3	3:C:120:ILE:HA	1.99	0.45
4:E:28:TYR:HE1	4:E:76:GLY:O	1.99	0.45
10:L:42:ARG:NH2	10:L:43:THR:OG1	2.50	0.45
11:T:1:DC:H6	11:T:1:DC:H3'	1.80	0.45
1:A:960:ILE:HG12	1:A:1049:ILE:HD11	1.99	0.45
1:A:1301:GLU:HA	1:A:1302:PRO:HD3	1.83	0.45
2:B:387:LEU:HD22	2:B:387:LEU:HA	1.85	0.45
2:B:576:ASP:OD1	2:B:576:ASP:N	2.48	0.45
2:B:1001:PHE:CZ	2:B:1073:TYR:HB2	2.52	0.45
2:B:1110:PRO:HB2	2:B:1119:VAL:CG1	2.46	0.45
2:B:1189:ILE:HD12	2:B:1190:ASP:H	1.81	0.45
5:F:130:ILE:HA	5:F:131:PRO:HD3	1.77	0.45
8:J:42:LYS:HG3	8:J:43:ARG:N	2.30	0.45
1:A:164:ARG:HG2	1:A:165:GLY:N	2.28	0.44
1:A:1138:ILE:HD11	1:A:1319:VAL:HG11	1.97	0.44
2:B:275:TYR:CE1	2:B:355:ILE:HG12	2.52	0.44
2:B:955:THR:CG2	2:B:956:THR:N	2.73	0.44
11:T:15:DA:C2'	11:T:16:DC:H5'	2.44	0.44
1:A:12:ARG:HD3	2:B:1192:TYR:CD1	2.52	0.44
1:A:72:GLU:CD	2:B:1175:LEU:HB2	2.42	0.44
1:A:698:GLN:HA	7:I:97:MET:O	2.18	0.44
2:B:1174:LYS:HE3	2:B:1174:LYS:HB2	1.73	0.44
3:C:146:LYS:HB2	8:J:57:ILE:HD13	2.00	0.44
1:A:38:PRO:HB3	1:A:270:LEU:CG	2.45	0.44
1:A:298:PHE:O	1:A:302:THR:HG22	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:329:LEU:HA	1:A:335:ARG:H	1.82	0.44
1:A:403:LYS:O	1:A:415:LEU:HD23	2.18	0.44
1:A:446:ARG:HB2	1:A:487:MET:SD	2.57	0.44
1:A:588:LEU:CD2	1:A:632:VAL:HG21	2.46	0.44
1:A:840:ARG:HG2	1:A:1402:PHE:CZ	2.51	0.44
1:A:898:ARG:O	1:A:1029:ARG:NH1	2.51	0.44
2:B:637:LEU:CD1	2:B:693:ILE:HG13	2.47	0.44
2:B:1006:ILE:CG2	2:B:1087:PHE:HE2	2.30	0.44
4:E:55:ARG:C	4:E:57:MET:N	2.75	0.44
6:H:4:THR:O	6:H:5:LEU:HD22	2.18	0.44
6:H:38:LEU:HD21	6:H:40:LEU:HB2	1.99	0.44
10:L:38:LEU:CD1	10:L:49:LYS:HD2	2.43	0.44
1:A:323:LYS:HE3	1:A:328:ARG:HE	1.80	0.44
1:A:1212:VAL:O	1:A:1216:ILE:HG13	2.18	0.44
2:B:522:VAL:HG11	2:B:537:LYS:HD2	1.98	0.44
2:B:1002:THR:HG21	2:B:1006:ILE:HB	1.98	0.44
2:B:1084:GLN:HE22	3:C:192:TRP:N	2.13	0.44
7:I:118:ARG:HH11	7:I:118:ARG:CG	2.31	0.44
12:N:4:DC:H2"	12:N:5:DT:OP2	2.18	0.44
1:A:793:SER:HB2	1:A:794:PRO:HD2	2.00	0.44
1:A:1042:PHE:CD1	1:A:1042:PHE:C	2.95	0.44
1:A:1345:ARG:HG2	1:A:1372:VAL:HG12	2.00	0.44
3:C:242:GLN:HB3	3:C:246:ARG:HD2	1.99	0.44
5:F:109:VAL:HG11	5:F:123:LYS:HG2	2.00	0.44
1:A:354:SER:C	1:A:482:PHE:CE1	2.95	0.44
1:A:388:LEU:HD23	1:A:391:LEU:HD12	1.99	0.44
1:A:402:ALA:HA	1:A:435:HIS:HD2	1.83	0.44
1:A:451:HIS:CD2	1:A:451:HIS:H	2.36	0.44
1:A:1345:ARG:HG3	1:A:1376:THR:HG21	1.98	0.44
1:A:1389:PHE:O	1:A:1392:SER:OG	2.34	0.44
1:A:1389:PHE:HZ	1:A:1402:PHE:CE2	2.36	0.44
2:B:1036:ALA:O	8:J:47:ARG:HD3	2.18	0.44
6:H:82:PRO:C	6:H:84:ALA:H	2.25	0.44
11:T:15:DA:C5	11:T:16:DC:C5	3.05	0.44
12:N:7:DA:OP2	12:N:7:DA:C8	2.70	0.44
1:A:98:LYS:O	1:A:102:VAL:HG23	2.18	0.44
1:A:145:LYS:CG	1:A:146:MET:N	2.81	0.44
1:A:563:PRO:HD3	1:A:572:TRP:CZ2	2.52	0.44
2:B:800:GLN:HB3	8:J:52:THR:HG22	1.99	0.44
6:H:89:LEU:HD23	6:H:91:ASP:CG	2.43	0.44
11:T:7:DA:C8	11:T:7:DA:OP2	2.71	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:R:1:A:C2'	13:R:2:U:H5''	2.33	0.44
1:A:54:ASN:OD1	1:A:247:ARG:NH1	2.49	0.44
1:A:79:GLY:C	1:A:243:PRO:HG3	2.43	0.44
1:A:810:PRO:HD3	2:B:1047:PHE:CD1	2.53	0.44
1:A:899:VAL:HG22	1:A:1029:ARG:HG2	2.00	0.44
1:A:1155:ASP:OD2	1:A:1161:THR:HG23	2.18	0.44
2:B:708:GLU:HG3	2:B:712:PRO:CG	2.48	0.44
2:B:973:ILE:HG22	2:B:974:PRO:HD2	2.00	0.44
2:B:1002:THR:HG23	2:B:1004:GLU:HG3	1.99	0.44
3:C:94:LYS:HE2	3:C:94:LYS:HB3	1.90	0.44
6:H:139:ASN:O	6:H:140:ALA:CB	2.66	0.44
11:T:12:DC:H4'	11:T:13:DA:OP1	2.17	0.44
1:A:485:ASP:OD1	1:A:485:ASP:N	2.49	0.44
2:B:600:LEU:HD22	2:B:615:MET:SD	2.58	0.44
2:B:953:LEU:HD11	10:L:55:ILE:HG13	2.00	0.44
2:B:1160:VAL:HG11	2:B:1169:MET:SD	2.57	0.44
3:C:66:ARG:HB3	8:J:5:VAL:HG22	2.00	0.44
1:A:247:ARG:N	1:A:248:PRO:CD	2.81	0.43
1:A:415:LEU:N	1:A:415:LEU:HD22	2.33	0.43
1:A:912:LEU:CD1	1:A:1033:GLN:HG3	2.48	0.43
1:A:919:ILE:HG23	1:A:920:LEU:N	2.26	0.43
1:A:925:LEU:O	1:A:928:LEU:N	2.50	0.43
1:A:1109:LYS:HB3	1:A:1109:LYS:HE3	1.76	0.43
5:F:72:LYS:HE2	5:F:73:ALA:HA	1.99	0.43
8:J:3:VAL:CG2	8:J:18:TRP:HB2	2.45	0.43
1:A:545:GLN:O	1:A:549:MET:HG3	2.17	0.43
1:A:568:PRO:HD3	6:H:94:ASP:O	2.19	0.43
1:A:582:ILE:HA	1:A:583:PRO:HD3	1.86	0.43
1:A:722:LEU:HD11	1:A:794:PRO:HB3	2.01	0.43
1:A:987:VAL:HG23	1:A:1028:THR:OG1	2.17	0.43
2:B:118:ARG:HA	2:B:207:GLY:HA2	2.01	0.43
10:L:28:LYS:O	10:L:29:TYR:CG	2.71	0.43
10:L:42:ARG:C	10:L:44:ASP:H	2.26	0.43
1:A:365:GLY:O	1:A:468:PHE:HA	2.19	0.43
1:A:847:ASP:OD2	1:A:858:ASN:HB2	2.17	0.43
2:B:365:THR:HG21	2:B:370:PHE:CD1	2.54	0.43
2:B:464:GLY:CA	2:B:480:SER:OG	2.61	0.43
2:B:563:MET:HA	2:B:589:VAL:O	2.18	0.43
2:B:884:ARG:CB	2:B:936:ASP:H	2.27	0.43
2:B:1060:ARG:HD2	2:B:1060:ARG:HA	1.72	0.43
2:B:1187:ASN:HD21	2:B:1190:ASP:CA	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:21:TYR:CZ	8:J:25:LEU:HD11	2.53	0.43
11:T:12:DC:H2''	11:T:13:DA:C8	2.54	0.43
1:A:298:PHE:CE1	1:A:312:PRO:O	2.71	0.43
1:A:317:LYS:HG2	1:A:318:SER:N	2.33	0.43
1:A:518:LYS:HB2	1:A:519:PRO:HD2	2.00	0.43
1:A:994:GLN:HG2	1:A:1019:CYS:SG	2.58	0.43
2:B:188:ASP:O	2:B:192:LEU:HD12	2.18	0.43
12:N:3:DG:H2''	12:N:4:DC:OP2	2.17	0.43
1:A:64:ASN:C	1:A:66:LYS:H	2.23	0.43
1:A:224:PHE:HB3	1:A:229:SER:O	2.18	0.43
1:A:289:ILE:O	1:A:293:GLU:HG3	2.18	0.43
2:B:848:ARG:NH1	8:J:8:PHE:O	2.50	0.43
2:B:1065:GLN:NE2	2:B:1069:PHE:HD2	2.15	0.43
6:H:141:TYR:N	6:H:141:TYR:CD1	2.86	0.43
11:T:12:DC:C1'	11:T:13:DA:C8	2.97	0.43
11:T:14:DG:H2''	11:T:15:DA:OP2	2.19	0.43
16:T:101:G2P:O4'	13:R:9:G:H2'	2.18	0.43
1:A:308:ILE:H	1:A:308:ILE:HD12	1.84	0.43
1:A:397:ASN:HA	1:A:398:GLU:HA	1.46	0.43
1:A:1021:LEU:HD11	1:A:1025:ARG:NH1	2.34	0.43
1:A:1389:PHE:CZ	1:A:1402:PHE:CE2	3.06	0.43
2:B:222:ILE:HD11	2:B:627:PHE:CE1	2.54	0.43
2:B:402:GLY:HA2	2:B:695:ALA:HB3	2.00	0.43
2:B:846:ILE:HA	2:B:850:LEU:HB3	2.01	0.43
2:B:880:THR:C	2:B:882:THR:H	2.26	0.43
2:B:1017:ILE:HA	2:B:1017:ILE:HD13	1.79	0.43
3:C:268:ASP:OD1	3:C:268:ASP:N	2.52	0.43
5:F:111:LEU:C	5:F:113:GLY:H	2.27	0.43
8:J:9:SER:OG	8:J:48:ARG:NH1	2.51	0.43
1:A:317:LYS:HG2	1:A:318:SER:HB3	1.83	0.43
1:A:331:GLY:HA2	1:A:337:ARG:HG3	2.01	0.43
1:A:346:ASP:H	2:B:1154:ALA:HB1	1.81	0.43
1:A:779:PHE:CE1	2:B:517:THR:HG22	2.53	0.43
2:B:851:PHE:O	2:B:974:PRO:HD3	2.18	0.43
3:C:46:ILE:CG2	3:C:157:CYS:HB3	2.49	0.43
3:C:116:LYS:HG3	3:C:117:ASP:N	2.33	0.43
4:E:169:ARG:NH1	5:F:140:ASP:OD2	2.52	0.43
6:H:46:LEU:HD23	6:H:46:LEU:HA	1.76	0.43
6:H:89:LEU:HD22	6:H:91:ASP:H	1.84	0.43
6:H:97:MET:HE3	6:H:118:PHE:CG	2.54	0.43
7:I:120:GLN:CD	7:I:120:GLN:N	2.76	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:37:SER:OG	8:J:47:ARG:NH2	2.48	0.43
12:N:2:DT:O2	12:N:3:DG:N1	2.51	0.43
1:A:452:LYS:C	1:A:454:SER:H	2.27	0.43
1:A:550:LEU:HD23	1:A:556:TRP:CZ2	2.53	0.43
1:A:896:ARG:HB3	1:A:897:TYR:CD2	2.53	0.43
5:F:83:PRO:HG2	5:F:84:TYR:CD1	2.53	0.43
8:J:6:ARG:HG3	8:J:12:LYS:O	2.19	0.43
1:A:272:ALA:O	1:A:296:LEU:HB2	2.19	0.43
1:A:590:ARG:HH22	1:A:592:ASP:HB2	1.83	0.43
1:A:810:PRO:CB	2:B:705:MET:SD	3.07	0.43
1:A:968:GLN:HB3	1:A:973:ILE:HD11	2.01	0.43
2:B:997:GLU:H	2:B:997:GLU:HG3	1.30	0.43
4:E:116:ILE:HG21	4:E:121:MET:HG3	2.00	0.43
8:J:8:PHE:CE1	8:J:49:MET:CE	3.02	0.43
8:J:23:ASN:O	8:J:27:GLU:HB3	2.18	0.43
11:T:11:DG:OP2	11:T:11:DG:C8	2.71	0.43
1:A:407:ARG:HG2	1:A:430:TRP:CH2	2.54	0.43
1:A:598:LEU:HG	6:H:25:ARG:NH1	2.34	0.43
1:A:786:HIS:CD2	2:B:705:MET:HE3	2.54	0.43
1:A:1094:VAL:HA	1:A:1113:THR:HG21	2.00	0.43
1:A:1402:PHE:CD2	1:A:1403:GLU:HG2	2.54	0.43
2:B:118:ARG:HH22	2:B:194:GLU:CD	2.27	0.43
2:B:120:ARG:HG2	2:B:955:THR:HG21	2.00	0.43
2:B:190:TYR:CZ	2:B:196:PRO:HG3	2.54	0.43
2:B:307:ASP:OD2	2:B:310:MET:HE2	2.19	0.43
2:B:512:ARG:NH2	2:B:531:GLN:O	2.49	0.43
4:E:57:MET:HE3	4:E:57:MET:HB2	1.67	0.43
8:J:36:LEU:HD13	8:J:47:ARG:CG	2.49	0.43
1:A:251:SER:CB	1:A:252:PHE:HA	2.48	0.42
1:A:780:VAL:HG22	2:B:699:GLU:OE2	2.18	0.42
1:A:963:ILE:HD12	1:A:1049:ILE:CG1	2.44	0.42
2:B:90:ILE:HA	2:B:133:LYS:O	2.18	0.42
2:B:711:GLU:C	2:B:714:GLU:N	2.77	0.42
2:B:722:ASP:OD1	2:B:722:ASP:N	2.52	0.42
4:E:177:ARG:HD3	4:E:215:MET:SD	2.59	0.42
11:T:15:DA:N7	11:T:16:DC:N4	2.67	0.42
13:R:4:G:H2'	13:R:5:A:C8	2.54	0.42
1:A:172:PRO:HB3	1:A:185:TRP:CE2	2.54	0.42
1:A:562:THR:HG23	1:A:563:PRO:HD2	2.00	0.42
1:A:995:GLU:OE2	1:A:995:GLU:HA	2.19	0.42
1:A:1115:SER:HB3	1:A:1330:ASN:ND2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:469:GLN:O	2:B:470:LYS:HG3	2.19	0.42
2:B:711:GLU:O	2:B:714:GLU:N	2.50	0.42
4:E:43:LYS:O	4:E:47:CYS:HB2	2.20	0.42
4:E:176:PRO:O	4:E:212:ARG:HA	2.20	0.42
8:J:16:ASP:OD1	8:J:17:LYS:HG2	2.20	0.42
10:L:31:CYS:HA	10:L:56:LEU:HD23	2.01	0.42
1:A:355:GLY:HA3	1:A:482:PHE:CE2	2.54	0.42
1:A:388:LEU:HD23	1:A:388:LEU:HA	1.78	0.42
1:A:455:MET:HE3	2:B:1134:GLU:HG3	2.01	0.42
2:B:62:ILE:HD12	2:B:418:LYS:CG	2.48	0.42
2:B:779:GLY:HA2	2:B:796:LEU:HB2	2.01	0.42
2:B:783:THR:HG21	8:J:59:LYS:HB3	2.01	0.42
3:C:9:LYS:HB2	3:C:9:LYS:HE2	1.79	0.42
3:C:66:ARG:HB3	8:J:5:VAL:HG21	2.01	0.42
3:C:249:ASP:O	3:C:253:LYS:HB2	2.20	0.42
9:K:20:LYS:O	9:K:33:ILE:HA	2.19	0.42
9:K:47:ARG:HG3	9:K:48:ALA:N	2.33	0.42
1:A:44:THR:C	1:A:46:THR:N	2.73	0.42
1:A:316:GLN:CB	1:A:319:GLY:CA	2.77	0.42
1:A:577:ILE:HD12	1:A:578:LEU:H	1.85	0.42
1:A:783:THR:O	2:B:516:ASN:ND2	2.43	0.42
1:A:901:LEU:HD21	1:A:919:ILE:HD13	2.00	0.42
2:B:789:MET:HE2	2:B:965:LYS:CB	2.47	0.42
2:B:826:ALA:HB2	2:B:1087:PHE:CD1	2.54	0.42
1:A:42:ASP:CG	1:A:44:THR:H	2.27	0.42
1:A:179:LEU:HD22	1:A:297:GLN:HG3	2.02	0.42
1:A:315:LEU:HB2	1:A:316:GLN:H	1.63	0.42
1:A:329:LEU:HD12	1:A:1406:VAL:HG23	2.00	0.42
1:A:1342:GLU:HG2	4:E:212:ARG:HH11	1.84	0.42
2:B:402:GLY:CA	2:B:695:ALA:HB3	2.50	0.42
2:B:424:LEU:HD11	2:B:448:ILE:HG23	2.02	0.42
2:B:708:GLU:C	2:B:710:LEU:H	2.27	0.42
2:B:1023:VAL:O	2:B:1027:ILE:HG13	2.19	0.42
3:C:5:GLY:O	3:C:7:GLN:HG2	2.20	0.42
8:J:36:LEU:HD13	8:J:47:ARG:HG2	2.01	0.42
11:T:5:DC:C1'	11:T:6:DG:C5'	2.78	0.42
12:N:12:DT:H2''	12:N:13:DA:H8	1.83	0.42
1:A:129:LYS:HA	1:A:134:ARG:NH2	2.31	0.42
1:A:590:ARG:HG2	1:A:590:ARG:HH21	1.82	0.42
1:A:1044:TRP:O	1:A:1047:SER:N	2.53	0.42
2:B:244:LEU:O	2:B:246:LYS:N	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:423:LYS:O	2:B:427:ASP:HB2	2.19	0.42
6:H:16:ASP:HA	6:H:17:PRO:HD2	1.95	0.42
8:J:32:GLU:CD	8:J:32:GLU:H	2.28	0.42
11:T:3:DA:O5'	11:T:3:DA:H8	2.03	0.42
12:N:12:DT:C2	12:N:13:DA:C5	3.08	0.42
1:A:42:ASP:HA	1:A:50:ILE:CB	2.48	0.42
1:A:403:LYS:C	1:A:404:TYR:CD1	2.98	0.42
1:A:494:SER:H	1:A:497:THR:HG22	1.85	0.42
1:A:549:MET:HE1	1:A:656:TRP:HD1	1.83	0.42
1:A:1424:VAL:HG11	2:B:1139:ILE:HD13	2.02	0.42
2:B:326:ASP:OD1	2:B:329:THR:OG1	2.24	0.42
2:B:654:ARG:HA	2:B:654:ARG:HD3	1.78	0.42
3:C:45:ALA:CB	3:C:170:TRP:CD1	2.97	0.42
4:E:144:ILE:HG13	4:E:145:THR:N	2.34	0.42
8:J:2:ILE:C	8:J:3:VAL:O	2.63	0.42
11:T:12:DC:HI'	11:T:13:DA:O4'	2.18	0.42
1:A:353:ILE:HD13	1:A:487:MET:CE	2.49	0.42
1:A:390:GLN:O	1:A:393:ARG:HB3	2.20	0.42
1:A:406:ILE:CD1	1:A:431:LYS:HB3	2.49	0.42
1:A:879:GLU:OE1	1:A:962:ARG:NH2	2.53	0.42
1:A:902:LEU:HG	1:A:926:GLN:HG3	2.01	0.42
1:A:1424:VAL:HG22	1:A:1436:ILE:HD11	2.01	0.42
2:B:96:TYR:HB2	2:B:129:PHE:HB2	2.01	0.42
2:B:651:LEU:CD2	2:B:710:LEU:HD11	2.50	0.42
3:C:129:ILE:HD12	3:C:129:ILE:HA	1.79	0.42
4:E:168:TYR:O	4:E:169:ARG:C	2.63	0.42
6:H:113:ALA:HA	6:H:125:LEU:O	2.20	0.42
1:A:94:GLY:O	1:A:95:PHE:CD1	2.73	0.42
1:A:152:VAL:HG12	1:A:153:PRO:N	2.35	0.42
1:A:475:THR:HG22	1:A:476:SER:N	2.35	0.42
2:B:295:GLY:H	2:B:298:LEU:HG	1.85	0.42
6:H:4:THR:CG2	6:H:5:LEU:N	2.82	0.42
9:K:42:LEU:HD13	9:K:46:ILE:CG1	2.50	0.42
11:T:6:DG:N2	12:N:10:DG:N1	2.68	0.42
12:N:12:DT:H2''	12:N:13:DA:C8	2.55	0.42
1:A:87:ALA:HB3	1:A:276:LEU:HD23	2.01	0.42
1:A:815:PHE:O	1:A:818:MET:N	2.53	0.42
1:A:1396:ALA:HA	1:A:1399:ARG:NH2	2.35	0.42
2:B:102:VAL:HG23	2:B:112:LEU:HB2	2.02	0.42
2:B:263:GLY:O	2:B:265:SER:N	2.52	0.42
2:B:431:TYR:CZ	2:B:447:ALA:HB3	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:558:LEU:HD13	2:B:580:VAL:HG11	2.01	0.42
2:B:708:GLU:O	2:B:712:PRO:CG	2.68	0.42
2:B:906:SER:HB3	2:B:946:ASN:HB2	2.01	0.42
4:E:26:ARG:O	4:E:75:MET:HE1	2.18	0.42
6:H:61:SER:O	6:H:62:SER:HB3	2.20	0.42
6:H:123:MET:HE1	6:H:142:LEU:HD13	2.02	0.42
7:I:78:CYS:SG	7:I:80:SER:CB	3.01	0.42
1:A:705:LYS:HD2	1:A:708:MET:CE	2.48	0.41
1:A:707:GLY:C	1:A:708:MET:CG	2.93	0.41
1:A:1341:ILE:HD13	1:A:1380:GLY:HA2	2.01	0.41
2:B:1095:LEU:C	2:B:1097:HIS:N	2.73	0.41
2:B:1189:ILE:HD12	2:B:1190:ASP:N	2.34	0.41
6:H:137:GLN:HG3	6:H:138:GLU:HA	2.01	0.41
8:J:14:VAL:HG12	8:J:41:LEU:HD21	2.01	0.41
1:A:35:ILE:HG22	1:A:270:LEU:HD11	2.01	0.41
2:B:101:MET:HE3	2:B:101:MET:HB2	1.88	0.41
2:B:789:MET:HE3	2:B:789:MET:HB3	1.75	0.41
2:B:980:PHE:CE2	2:B:1094:ARG:CG	2.98	0.41
2:B:1006:ILE:HG21	2:B:1087:PHE:HE2	1.85	0.41
2:B:1084:GLN:HG2	3:C:201:TRP:CH2	2.55	0.41
3:C:39:ALA:HA	3:C:164:ALA:HB3	2.02	0.41
3:C:41:ILE:HA	3:C:42:PRO:HD3	1.94	0.41
3:C:69:LEU:O	8:J:6:ARG:NH1	2.54	0.41
3:C:201:TRP:HA	3:C:202:PRO:HD3	1.87	0.41
1:A:250:ILE:HG13	1:A:251:SER:H	1.85	0.41
1:A:393:ARG:C	1:A:395:GLY:N	2.78	0.41
1:A:481:ASP:OD1	1:A:485:ASP:OD1	2.38	0.41
1:A:533:LYS:HA	1:A:533:LYS:HD2	1.84	0.41
1:A:852:TYR:O	5:F:81:THR:HG22	2.20	0.41
2:B:762:ASN:HD22	2:B:762:ASN:HA	1.55	0.41
2:B:857:ARG:O	2:B:967:ARG:HA	2.20	0.41
3:C:123:ASN:OD1	3:C:125:MET:HB3	2.20	0.41
4:E:7:ARG:O	4:E:10:SER:N	2.52	0.41
8:J:44:TYR:HA	8:J:47:ARG:HB3	2.02	0.41
11:T:9:DA:H2'	11:T:10:DA:N7	2.34	0.41
1:A:362:ASP:OD1	1:A:362:ASP:N	2.46	0.41
2:B:174:LEU:HD21	2:B:204:ILE:HD11	2.01	0.41
2:B:367:LEU:HB3	2:B:368:GLU:H	1.55	0.41
3:C:27:LEU:HA	3:C:228:PHE:CZ	2.55	0.41
3:C:52:GLU:HA	10:L:64:LEU:CD1	2.51	0.41
3:C:69:LEU:HB3	8:J:5:VAL:CG1	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:LYS:HE3	1:A:294:SER:HB3	2.01	0.41
1:A:294:SER:HA	1:A:297:GLN:HB3	2.01	0.41
1:A:455:MET:HE1	2:B:1130:PHE:CE1	2.55	0.41
1:A:831:THR:HG23	1:A:832:ALA:N	2.34	0.41
1:A:1399:ARG:NH1	1:A:1408:ILE:HD12	2.36	0.41
2:B:46:GLN:H	2:B:46:GLN:HG3	1.49	0.41
2:B:96:TYR:N	2:B:129:PHE:O	2.52	0.41
2:B:758:PHE:CE1	2:B:1044:ALA:HA	2.55	0.41
2:B:1081:LEU:HD23	2:B:1081:LEU:HA	1.71	0.41
5:F:101:ILE:HG21	5:F:120:ILE:HD12	2.03	0.41
6:H:89:LEU:HB2	6:H:91:ASP:OD2	2.20	0.41
9:K:39:ASP:HB2	9:K:40:HIS:H	1.76	0.41
9:K:87:LEU:O	9:K:90:ALA:HB3	2.20	0.41
11:T:7:DA:H2''	11:T:8:DT:C5'	2.38	0.41
11:T:15:DA:N7	11:T:16:DC:C4	2.88	0.41
1:A:259:GLU:OE1	1:A:259:GLU:HA	2.18	0.41
1:A:407:ARG:HD3	1:A:413:ILE:HD11	1.99	0.41
1:A:606:LEU:HD11	1:A:608:ILE:CD1	2.49	0.41
1:A:954:TRP:HA	1:A:955:PRO:HD2	1.85	0.41
1:A:1098:VAL:N	1:A:1099:PRO:HD2	2.36	0.41
1:A:1154:TYR:CE1	1:A:1156:PRO:HG3	2.55	0.41
2:B:216:GLU:OE1	2:B:500:THR:OG1	2.31	0.41
2:B:468:GLU:C	2:B:470:LYS:N	2.76	0.41
3:C:164:ALA:HA	3:C:167:HIS:O	2.21	0.41
4:E:46:TYR:CE1	4:E:58:MET:CG	3.03	0.41
5:F:109:VAL:O	5:F:111:LEU:HD22	2.20	0.41
7:I:111:THR:HG22	7:I:112:SER:N	2.35	0.41
9:K:12:LEU:HD12	9:K:12:LEU:N	2.34	0.41
1:A:53:LEU:C	1:A:55:ASP:N	2.78	0.41
2:B:217:ARG:HD3	2:B:407:ASP:OD2	2.21	0.41
3:C:44:LEU:HD12	3:C:160:LYS:O	2.21	0.41
3:C:142:VAL:N	8:J:16:ASP:HB3	2.33	0.41
5:F:72:LYS:HE2	5:F:72:LYS:C	2.45	0.41
12:N:12:DT:C1'	12:N:13:DA:C8	3.04	0.41
2:B:241:ARG:HA	2:B:253:THR:HG22	2.01	0.41
3:C:18:VAL:HG22	3:C:240:VAL:HB	2.03	0.41
3:C:227:THR:HG22	3:C:229:TYR:CE1	2.56	0.41
6:H:8:ASP:HB3	6:H:10:PHE:CE1	2.56	0.41
6:H:61:SER:O	6:H:62:SER:CB	2.69	0.41
10:L:38:LEU:HD21	10:L:49:LYS:CD	2.48	0.41
11:T:8:DT:H3'	11:T:8:DT:P	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:VAL:HG22	1:A:301:ALA:HA	2.02	0.41
1:A:298:PHE:HE1	1:A:312:PRO:O	2.03	0.41
1:A:320:ARG:HA	1:A:321:PRO:HA	1.73	0.41
1:A:355:GLY:N	1:A:482:PHE:CZ	2.89	0.41
1:A:453:MET:HE2	1:A:453:MET:HB2	1.93	0.41
1:A:482:PHE:HD2	2:B:835:GLN:O	2.04	0.41
1:A:547:LEU:HB3	9:K:58:PHE:CE1	2.56	0.41
1:A:563:PRO:HD3	1:A:572:TRP:HZ2	1.85	0.41
1:A:852:TYR:CE1	1:A:1060:PRO:HB2	2.56	0.41
1:A:855:THR:HG22	1:A:857:ARG:HG2	2.03	0.41
1:A:925:LEU:HD23	1:A:925:LEU:HA	1.89	0.41
1:A:1209:MET:SD	1:A:1236:LEU:HD13	2.61	0.41
2:B:37:PHE:O	2:B:39:ARG:N	2.53	0.41
2:B:500:THR:HA	2:B:501:PRO:HD3	1.84	0.41
2:B:707:PRO:O	2:B:709:ASP:N	2.54	0.41
2:B:830:TYR:CZ	2:B:1000:PRO:HD3	2.55	0.41
2:B:996:ARG:NH2	3:C:174:ALA:O	2.53	0.41
5:F:109:VAL:HG12	5:F:110:ASP:H	1.85	0.41
5:F:154:ASP:C	5:F:155:LEU:HD23	2.46	0.41
10:L:37:LYS:HE2	10:L:37:LYS:HB3	1.91	0.41
1:A:43:GLU:CB	1:A:50:ILE:CD1	2.51	0.41
1:A:357:PRO:HG3	2:B:832:GLY:O	2.21	0.41
1:A:444:PHE:CE2	1:A:470:LEU:HD23	2.38	0.41
1:A:452:LYS:HG3	1:A:453:MET:N	2.36	0.41
1:A:563:PRO:CG	1:A:572:TRP:CZ2	3.04	0.41
1:A:1291:VAL:HA	1:A:1292:PRO:HD3	1.94	0.41
2:B:1163:CYS:C	2:B:1165:ILE:H	2.29	0.41
6:H:63:LEU:HA	6:H:90:ALA:CB	2.51	0.41
7:I:74:GLU:O	7:I:75:CYS:C	2.64	0.41
12:N:2:DT:H1'	12:N:3:DG:C5	2.56	0.41
1:A:605:MET:HA	1:A:605:MET:HE3	2.03	0.40
2:B:642:ASP:C	2:B:644:GLU:H	2.29	0.40
2:B:973:ILE:CG2	2:B:974:PRO:HD2	2.51	0.40
6:H:6:PHE:CZ	6:H:8:ASP:HB2	2.56	0.40
7:I:65:ASP:HA	7:I:66:PRO:HD3	1.90	0.40
11:T:2:DT:H1'	11:T:3:DA:O5'	2.21	0.40
1:A:249:SER:HB2	1:A:250:ILE:CG2	2.49	0.40
1:A:259:GLU:HB3	1:A:264:PHE:CE1	2.56	0.40
1:A:625:SER:HB2	1:A:626:ASN:H	1.76	0.40
3:C:141:GLY:O	3:C:142:VAL:HB	2.20	0.40
6:H:137:GLN:HE21	6:H:137:GLN:HB3	1.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:I:15:TYR:CD1	7:I:15:TYR:N	2.89	0.40
1:A:357:PRO:HD2	2:B:833:TYR:CE2	2.55	0.40
1:A:485:ASP:OD2	13:R:9:G:O2'	2.38	0.40
1:A:779:PHE:CZ	2:B:517:THR:HA	2.56	0.40
1:A:873:MET:HB2	1:A:878:ILE:HD11	2.02	0.40
2:B:123:THR:O	2:B:125:SER:N	2.55	0.40
2:B:313:MET:HE3	2:B:386:LEU:HD22	2.02	0.40
2:B:599:THR:O	2:B:603:LEU:HG	2.22	0.40
2:B:843:GLN:NE2	2:B:843:GLN:O	2.54	0.40
4:E:54:GLN:HB3	4:E:57:MET:HB3	2.03	0.40
5:F:98:ALA:O	5:F:102:SER:HB3	2.22	0.40
6:H:101:ALA:HB2	6:H:116:TYR:CE1	2.57	0.40
7:I:75:CYS:SG	7:I:103:CYS:HB2	2.61	0.40
9:K:61:TYR:HA	9:K:72:LYS:O	2.21	0.40
10:L:47:ARG:CB	10:L:54:ARG:CA	2.99	0.40
11:T:7:DA:O5'	11:T:8:DT:H71	2.21	0.40
11:T:9:DA:C2'	11:T:10:DA:C8	3.04	0.40
12:N:7:DA:OP2	12:N:7:DA:H8	2.04	0.40
1:A:1153:TYR:CE2	1:A:1163:ILE:HD11	2.56	0.40
2:B:228:LYS:HE2	2:B:228:LYS:HB3	1.90	0.40
2:B:432:MET:HE2	2:B:432:MET:HB2	1.90	0.40
2:B:745:PRO:HB2	2:B:1047:PHE:CD2	2.57	0.40
2:B:841:MET:HE1	2:B:980:PHE:CE2	2.56	0.40
3:C:11:ARG:HE	3:C:21:ILE:HD11	1.87	0.40
3:C:262:LEU:HD11	9:K:87:LEU:HD23	2.03	0.40
4:E:14:ARG:NH1	4:E:141:VAL:HG12	2.37	0.40
4:E:20:LYS:HD2	4:E:34:GLU:HG2	2.02	0.40
4:E:29:PHE:C	4:E:30:ILE:HD12	2.46	0.40
1:A:443:LEU:HD23	1:A:443:LEU:HA	1.84	0.40
1:A:981:LEU:HD22	1:A:1038:THR:CA	2.51	0.40
1:A:1111:MET:HE3	1:A:1111:MET:HB2	1.78	0.40
1:A:1143:LEU:O	1:A:1146:VAL:HG23	2.22	0.40
2:B:213:ILE:N	2:B:479:VAL:O	2.49	0.40
2:B:426:LYS:HE2	2:B:430:ARG:HH12	1.86	0.40
3:C:82:TYR:O	3:C:85:ASP:HB2	2.20	0.40
3:C:127:ARG:HE	3:C:127:ARG:HB2	1.73	0.40
6:H:108:SER:O	6:H:110:ASP:N	2.55	0.40
7:I:75:CYS:HA	7:I:76:PRO:HD3	1.75	0.40
9:K:22:ASP:HA	9:K:23:PRO:HD3	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	
1	A	1379/1733 (80%)	1169 (85%)	177 (13%)	33 (2%)	4	24
2	B	1085/1224 (89%)	927 (85%)	135 (12%)	23 (2%)	5	26
3	C	264/318 (83%)	228 (86%)	35 (13%)	1 (0%)	30	60
4	E	212/215 (99%)	183 (86%)	25 (12%)	4 (2%)	6	28
5	F	82/155 (53%)	72 (88%)	10 (12%)	0	100	100
6	H	129/146 (88%)	106 (82%)	16 (12%)	7 (5%)	1	10
7	I	117/122 (96%)	98 (84%)	17 (14%)	2 (2%)	7	30
8	J	63/70 (90%)	56 (89%)	6 (10%)	1 (2%)	7	31
9	K	112/120 (93%)	106 (95%)	6 (5%)	0	100	100
10	L	42/70 (60%)	28 (67%)	11 (26%)	3 (7%)	1	6
All	All	3485/4173 (84%)	2973 (85%)	438 (13%)	74 (2%)	5	26

All (74) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	286	HIS
1	A	321	PRO
1	A	593	GLU
1	A	1393	ASN
2	B	230	ALA
2	B	266	ALA
2	B	367	LEU
2	B	711	GLU
2	B	1046	PRO
6	H	62	SER
6	H	140	ALA
7	I	33	SER
10	L	38	LEU
10	L	55	ILE

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Mol	Chain	Res	Type
1	A	40	THR
1	A	65	LEU
1	A	79	GLY
1	A	93	VAL
1	A	142	CYS
1	A	250	ILE
1	A	307	ASP
1	A	311	GLN
1	A	331	GLY
1	A	1234	GLU
2	B	65	GLU
2	B	124	TYR
2	B	275	TYR
2	B	780	VAL
2	B	864	LYS
4	E	36	GLU
6	H	87	ARG
7	I	9	ASP
10	L	45	ALA
1	A	87	ALA
1	A	214	ILE
1	A	609	ASP
1	A	1123	GLY
2	B	476	ARG
2	B	865	LYS
3	C	142	VAL
4	E	86	PRO
6	H	133	ASN
1	A	111	GLY
1	A	130	ASP
1	A	248	PRO
1	A	1093	LYS
2	B	466	TRP
2	B	648	HIS
2	B	901	PRO
4	E	125	PRO
8	J	3	VAL
1	A	45	GLN
1	A	224	PHE
1	A	453	MET
1	A	922	ASP
1	A	958	VAL

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Mol	Chain	Res	Type
1	A	1361	SER
1	A	1392	SER
2	B	408	LEU
2	B	469	GLN
1	A	923	LEU
1	A	1156	PRO
2	B	462	ALA
2	B	708	GLU
6	H	43	ASN
6	H	81	PRO
6	H	109	LYS
4	E	118	PRO
2	B	731	VAL
2	B	1103	ILE
1	A	312	PRO
1	A	600	PRO
2	B	167	ILE
2	B	593	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	
1	A	1216/1520 (80%)	1014 (83%)	202 (17%)	2	11
2	B	957/1061 (90%)	786 (82%)	171 (18%)	2	8
3	C	234/274 (85%)	195 (83%)	39 (17%)	2	11
4	E	196/197 (100%)	166 (85%)	30 (15%)	3	13
5	F	74/137 (54%)	59 (80%)	15 (20%)	1	6
6	H	117/128 (91%)	99 (85%)	18 (15%)	2	12
7	I	113/116 (97%)	90 (80%)	23 (20%)	1	6
8	J	60/65 (92%)	49 (82%)	11 (18%)	2	7
9	K	99/102 (97%)	86 (87%)	13 (13%)	4	17
10	L	39/57 (68%)	29 (74%)	10 (26%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3105/3657 (85%)	2573 (83%)	532 (17%)	2 10

All (532) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	ARG
1	A	13	THR
1	A	18	GLN
1	A	22	PHE
1	A	30	ILE
1	A	34	LYS
1	A	57	ARG
1	A	65	LEU
1	A	93	VAL
1	A	98	LYS
1	A	126	LEU
1	A	132	LYS
1	A	144	THR
1	A	146	MET
1	A	148	CYS
1	A	154	SER
1	A	161	LEU
1	A	163	SER
1	A	169	ASN
1	A	179	LEU
1	A	208	LEU
1	A	216	VAL
1	A	222	LEU
1	A	226	GLU
1	A	227	VAL
1	A	235	ILE
1	A	251	SER
1	A	252	PHE
1	A	254	GLU
1	A	259	GLU
1	A	270	LEU
1	A	271	LYS
1	A	274	ILE
1	A	287	HIS
1	A	289	ILE
1	A	297	GLN
1	A	315	LEU

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Mol	Chain	Res	Type
1	A	316	GLN
1	A	320	ARG
1	A	322	VAL
1	A	323	LYS
1	A	329	LEU
1	A	330	LYS
1	A	332	LYS
1	A	333	GLU
1	A	335	ARG
1	A	337	ARG
1	A	359	LEU
1	A	373	THR
1	A	375	THR
1	A	381	THR
1	A	383	TYR
1	A	404	TYR
1	A	415	LEU
1	A	417	TYR
1	A	419	LYS
1	A	427	GLN
1	A	436	ILE
1	A	443	LEU
1	A	451	HIS
1	A	452	LYS
1	A	454	SER
1	A	469	ARG
1	A	470	LEU
1	A	472	LEU
1	A	474	VAL
1	A	475	THR
1	A	476	SER
1	A	481	ASP
1	A	485	ASP
1	A	493	GLN
1	A	496	GLU
1	A	497	THR
1	A	504	LEU
1	A	509	LEU
1	A	512	VAL
1	A	513	SER
1	A	517	ASN
1	A	532	ARG

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Mol	Chain	Res	Type
1	A	550	LEU
1	A	567	LYS
1	A	569	LYS
1	A	577	ILE
1	A	588	LEU
1	A	596	THR
1	A	605	MET
1	A	612	ILE
1	A	618	GLU
1	A	621	THR
1	A	625	SER
1	A	629	LEU
1	A	637	LYS
1	A	666	ILE
1	A	702	LEU
1	A	709	THR
1	A	710	LEU
1	A	732	LEU
1	A	740	LEU
1	A	752	LYS
1	A	754	SER
1	A	758	ILE
1	A	764	CYS
1	A	765	VAL
1	A	768	GLN
1	A	774	ARG
1	A	783	THR
1	A	788	SER
1	A	797	LYS
1	A	801	GLU
1	A	821	ARG
1	A	829	VAL
1	A	838	GLN
1	A	839	ARG
1	A	879	GLU
1	A	881	GLN
1	A	886	ILE
1	A	896	ARG
1	A	913	LEU
1	A	914	GLU
1	A	917	SER
1	A	919	ILE

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Mol	Chain	Res	Type
1	A	922	ASP
1	A	926	GLN
1	A	936	LEU
1	A	941	LYS
1	A	949	ASP
1	A	961	ARG
1	A	970	THR
1	A	976	THR
1	A	977	LYS
1	A	980	ASP
1	A	981	LEU
1	A	982	THR
1	A	995	GLU
1	A	996	ASN
1	A	1000	LEU
1	A	1001	ARG
1	A	1017	LEU
1	A	1029	ARG
1	A	1033	GLN
1	A	1036	ARG
1	A	1037	LEU
1	A	1063	MET
1	A	1064	VAL
1	A	1067	LEU
1	A	1081	LEU
1	A	1092	LYS
1	A	1093	LYS
1	A	1095	THR
1	A	1109	LYS
1	A	1111	MET
1	A	1116	LEU
1	A	1128	GLN
1	A	1135	ARG
1	A	1142	THR
1	A	1146	VAL
1	A	1165	GLU
1	A	1172	LEU
1	A	1187	GLN
1	A	1205	LYS
1	A	1206	ASP
1	A	1208	THR
1	A	1223	ASP

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Mol	Chain	Res	Type
1	A	1227	ILE
1	A	1237	ILE
1	A	1240	CYS
1	A	1243	VAL
1	A	1257	ASP
1	A	1262	LYS
1	A	1264	GLU
1	A	1267	MET
1	A	1269	GLU
1	A	1276	VAL
1	A	1288	ASP
1	A	1291	VAL
1	A	1295	THR
1	A	1297	GLU
1	A	1299	VAL
1	A	1300	LYS
1	A	1322	ILE
1	A	1325	THR
1	A	1333	ILE
1	A	1350	LYS
1	A	1351	GLU
1	A	1354	ASN
1	A	1359	ASP
1	A	1366	ARG
1	A	1374	VAL
1	A	1376	THR
1	A	1383	SER
1	A	1384	VAL
1	A	1386	ARG
1	A	1405	THR
1	A	1406	VAL
1	A	1407	GLU
1	A	1425	SER
1	A	1426	GLU
1	A	1438	THR
1	A	1442	ASP
1	A	1443	VAL
1	A	1444	MET
1	A	1445	ILE
2	B	20	ASP
2	B	28	GLU
2	B	46	GLN

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Mol	Chain	Res	Type
2	B	63	ILE
2	B	65	GLU
2	B	97	VAL
2	B	98	THR
2	B	103	ASN
2	B	104	GLU
2	B	108	VAL
2	B	109	THR
2	B	128	LEU
2	B	130	VAL
2	B	134	LYS
2	B	165	VAL
2	B	167	ILE
2	B	175	ARG
2	B	176	SER
2	B	183	GLU
2	B	194	GLU
2	B	217	ARG
2	B	222	ILE
2	B	225	VAL
2	B	242	SER
2	B	244	LEU
2	B	248	SER
2	B	249	ARG
2	B	250	PHE
2	B	251	ILE
2	B	268	THR
2	B	276	ILE
2	B	277	LYS
2	B	283	VAL
2	B	305	VAL
2	B	315	LYS
2	B	319	GLU
2	B	323	VAL
2	B	328	GLU
2	B	334	ILE
2	B	346	GLU
2	B	361	LEU
2	B	365	THR
2	B	368	GLU
2	B	387	LEU
2	B	393	LYS

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Mol	Chain	Res	Type
2	B	394	ASP
2	B	398	ARG
2	B	412	LEU
2	B	416	LEU
2	B	424	LEU
2	B	425	THR
2	B	426	LYS
2	B	428	ILE
2	B	432	MET
2	B	448	ILE
2	B	453	ILE
2	B	454	THR
2	B	461	LEU
2	B	465	ASN
2	B	466	TRP
2	B	470	LYS
2	B	473	MET
2	B	475	SER
2	B	481	GLN
2	B	482	VAL
2	B	483	LEU
2	B	487	THR
2	B	498	THR
2	B	513	GLN
2	B	527	THR
2	B	542	MET
2	B	549	THR
2	B	552	MET
2	B	556	THR
2	B	563	MET
2	B	567	GLU
2	B	570	VAL
2	B	578	THR
2	B	598	GLU
2	B	604	ARG
2	B	619	ILE
2	B	637	LEU
2	B	649	LYS
2	B	653	VAL
2	B	655	LYS
2	B	658	ILE
2	B	680	THR

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Mol	Chain	Res	Type
2	B	690	VAL
2	B	705	MET
2	B	714	GLU
2	B	730	ARG
2	B	732	SER
2	B	734	HIS
2	B	751	VAL
2	B	754	SER
2	B	755	ILE
2	B	762	ASN
2	B	780	VAL
2	B	786	ASN
2	B	788	ARG
2	B	795	ILE
2	B	810	GLU
2	B	822	ASN
2	B	825	VAL
2	B	827	ILE
2	B	844	SER
2	B	857	ARG
2	B	864	LYS
2	B	865	LYS
2	B	866	TYR
2	B	878	GLN
2	B	879	ARG
2	B	880	THR
2	B	883	LEU
2	B	933	SER
2	B	935	ARG
2	B	943	SER
2	B	953	LEU
2	B	955	THR
2	B	957	ASN
2	B	963	PHE
2	B	970	THR
2	B	971	THR
2	B	973	ILE
2	B	976	ILE
2	B	983	ARG
2	B	987	LYS
2	B	992	ILE
2	B	996	ARG

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Mol	Chain	Res	Type
2	B	997	GLU
2	B	999	MET
2	B	1002	THR
2	B	1004	GLU
2	B	1007	VAL
2	B	1010	LEU
2	B	1019	SER
2	B	1021	MET
2	B	1028	GLU
2	B	1030	LEU
2	B	1055	ILE
2	B	1057	LYS
2	B	1065	GLN
2	B	1066	SER
2	B	1072	MET
2	B	1077	THR
2	B	1082	MET
2	B	1103	ILE
2	B	1113	VAL
2	B	1119	VAL
2	B	1122	ARG
2	B	1124	ARG
2	B	1147	LEU
2	B	1150	ARG
2	B	1151	LEU
2	B	1159	ARG
2	B	1160	VAL
2	B	1163	CYS
2	B	1171	VAL
2	B	1174	LYS
2	B	1176	ASN
2	B	1182	CYS
2	B	1183	LYS
2	B	1185	CYS
2	B	1188	LYS
2	B	1189	ILE
2	B	1191	ILE
2	B	1194	ILE
2	B	1202	LEU
2	B	1205	GLN
2	B	1212	ILE
2	B	1220	ARG

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Mol	Chain	Res	Type
3	C	4	GLU
3	C	11	ARG
3	C	15	LYS
3	C	18	VAL
3	C	22	LEU
3	C	23	SER
3	C	25	VAL
3	C	26	ASP
3	C	41	ILE
3	C	43	THR
3	C	53	THR
3	C	56	THR
3	C	57	VAL
3	C	77	ILE
3	C	79	GLN
3	C	80	LEU
3	C	89	GLU
3	C	99	LEU
3	C	100	THR
3	C	102	GLN
3	C	106	GLU
3	C	120	ILE
3	C	129	ILE
3	C	137	LYS
3	C	140	ASN
3	C	149	LYS
3	C	151	GLN
3	C	154	LYS
3	C	188	HIS
3	C	189	THR
3	C	197	SER
3	C	222	LYS
3	C	226	ASP
3	C	240	VAL
3	C	244	VAL
3	C	253	LYS
3	C	259	LEU
3	C	267	GLN
3	C	268	ASP
4	E	3	GLN
4	E	4	GLU
4	E	9	ILE

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Mol	Chain	Res	Type
4	E	11	ARG
4	E	14	ARG
4	E	30	ILE
4	E	31	THR
4	E	40	GLU
4	E	43	LYS
4	E	54	GLN
4	E	57	MET
4	E	78	LEU
4	E	81	GLU
4	E	90	VAL
4	E	92	THR
4	E	94	LYS
4	E	98	ILE
4	E	123	LEU
4	E	127	ILE
4	E	131	THR
4	E	134	THR
4	E	150	VAL
4	E	162	ARG
4	E	165	LEU
4	E	169	ARG
4	E	179	GLN
4	E	196	VAL
4	E	201	LYS
4	E	204	THR
4	E	215	MET
5	F	72	LYS
5	F	74	ILE
5	F	79	ARG
5	F	82	THR
5	F	93	ILE
5	F	102	SER
5	F	109	VAL
5	F	111	LEU
5	F	112	GLU
5	F	114	GLU
5	F	119	ARG
5	F	133	VAL
5	F	142	SER
5	F	149	GLU
5	F	155	LEU

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Mol	Chain	Res	Type
6	H	19	ARG
6	H	21	ASN
6	H	34	ASP
6	H	58	THR
6	H	78	SER
6	H	88	SER
6	H	89	LEU
6	H	97	MET
6	H	103	LYS
6	H	109	LYS
6	H	124	ARG
6	H	125	LEU
6	H	130	ARG
6	H	136	LYS
6	H	137	GLN
6	H	143	LEU
6	H	145	ARG
6	H	146	ARG
7	I	2	THR
7	I	3	THR
7	I	8	ARG
7	I	14	LEU
7	I	15	TYR
7	I	22	ASN
7	I	28	GLU
7	I	29	CYS
7	I	50	THR
7	I	55	THR
7	I	71	SER
7	I	77	LYS
7	I	81	ARG
7	I	84	VAL
7	I	89	GLN
7	I	90	GLN
7	I	91	ARG
7	I	95	THR
7	I	98	VAL
7	I	107	SER
7	I	116	ASN
7	I	117	LYS
7	I	118	ARG
8	J	6	ARG

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Mol	Chain	Res	Type
8	J	9	SER
8	J	22	LEU
8	J	28	ASP
8	J	29	GLU
8	J	31	ASP
8	J	46	CYS
8	J	48	ARG
8	J	49	MET
8	J	59	LYS
8	J	64	ASN
9	K	1	MET
9	K	6	ARG
9	K	18	LYS
9	K	20	LYS
9	K	26	LYS
9	K	41	THR
9	K	42	LEU
9	K	47	ARG
9	K	77	THR
9	K	101	LEU
9	K	103	THR
9	K	106	GLU
9	K	107	THR
10	L	34	CYS
10	L	38	LEU
10	L	42	ARG
10	L	46	VAL
10	L	47	ARG
10	L	49	LYS
10	L	50	ASP
10	L	51	CYS
10	L	54	ARG
10	L	63	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	80	HIS
1	A	256	GLN
1	A	297	GLN
1	A	306	ASN

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Mol	Chain	Res	Type
1	A	316	GLN
1	A	339	ASN
1	A	399	HIS
1	A	425	GLN
1	A	435	HIS
1	A	445	ASN
1	A	479	ASN
1	A	493	GLN
1	A	517	ASN
1	A	700	ASN
1	A	903	ASN
1	A	972	HIS
1	A	1033	GLN
2	B	52	ASN
2	B	395	GLN
2	B	449	ASN
2	B	465	ASN
2	B	531	GLN
2	B	590	HIS
2	B	686	ASN
2	B	734	HIS
2	B	762	ASN
2	B	776	GLN
2	B	842	ASN
2	B	843	GLN
2	B	878	GLN
2	B	1015	HIS
2	B	1025	HIS
2	B	1084	GLN
2	B	1117	GLN
2	B	1141	HIS
2	B	1193	GLN
2	B	1195	HIS
3	C	65	HIS
3	C	167	HIS
3	C	203	GLN
3	C	231	ASN
4	E	54	GLN
4	E	146	HIS
4	E	179	GLN
6	H	134	ASN
6	H	137	GLN

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Mol	Chain	Res	Type
7	I	60	GLN
7	I	83	ASN
7	I	108	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	R	8/9 (88%)	2 (25%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
13	R	2	U
13	R	9	G

There are no RNA pucker outliers to report.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
11	1CC	T	19	11	20,23,24	1.19	2 (10%)	25,33,36	1.40	3 (12%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	1CC	T	19	11	-	0/11/25/26	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	T	19	1CC	C2-N1	-2.32	1.35	1.40
11	T	19	1CC	C5-C4	2.02	1.47	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	T	19	1CC	O2-C2-N3	-2.65	118.15	122.33
11	T	19	1CC	C5-C6-N1	-2.60	119.28	123.06
11	T	19	1CC	C2'-C1'-N1	-2.46	107.67	113.81

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	T	19	1CC	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 10 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
16	G2P	T	101	15	30,34,34	1.77	7 (23%)	46,54,54	1.38	6 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	G2P	T	101	15	-	4/19/38/38	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	T	101	G2P	PB-O2B	4.40	1.61	1.51
16	T	101	G2P	PA-O2A	4.23	1.61	1.51
16	T	101	G2P	PG-O2G	3.74	1.62	1.50
16	T	101	G2P	PB-O3B	3.01	1.61	1.58
16	T	101	G2P	PB-O1B	-2.47	1.50	1.56
16	T	101	G2P	C2-N1	2.15	1.42	1.37
16	T	101	G2P	O4'-C1'	2.08	1.46	1.42

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	T	101	G2P	C2'-C1'-N9	3.48	122.94	113.25
16	T	101	G2P	O1G-PG-O3B	3.03	114.81	104.64
16	T	101	G2P	O4'-C1'-N9	2.60	114.25	108.36
16	T	101	G2P	O6-C6-N1	2.21	124.27	120.11
16	T	101	G2P	C2-N1-C6	-2.18	121.15	125.11
16	T	101	G2P	O2B-PB-C3A	-2.13	103.44	109.05

There are no chirality outliers.

All (4) torsion outliers are listed below:

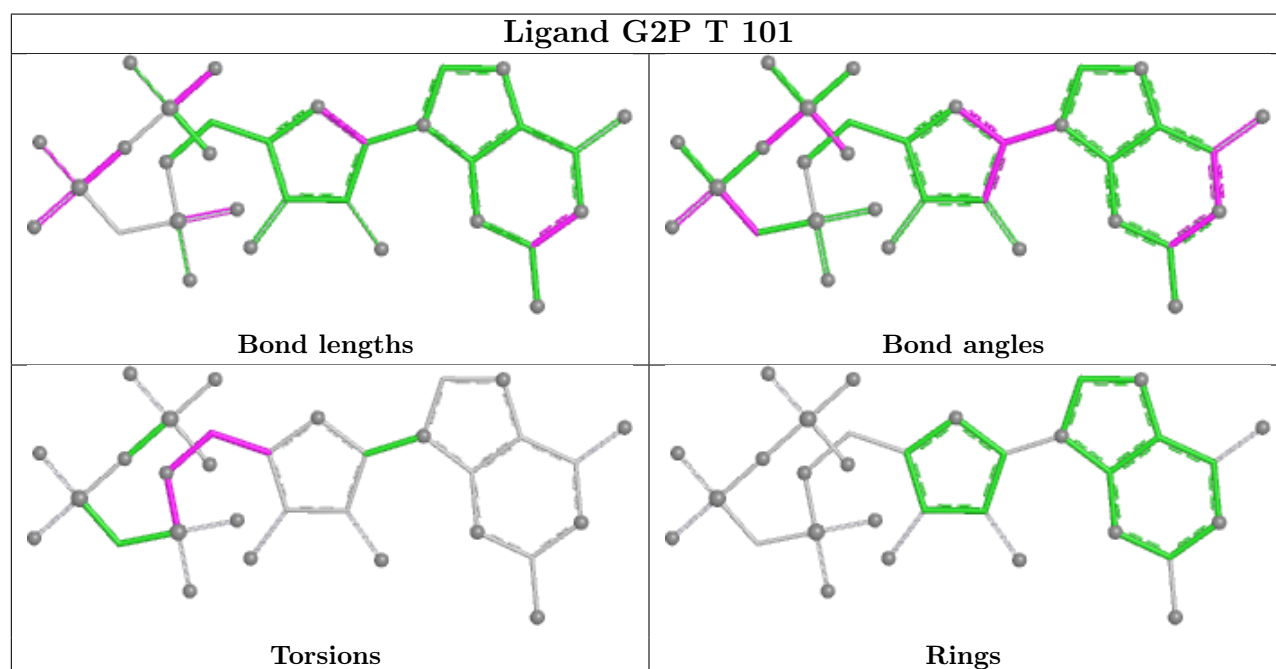
Mol	Chain	Res	Type	Atoms
16	T	101	G2P	O4'-C4'-C5'-O5'
16	T	101	G2P	C5'-O5'-PA-O1A
16	T	101	G2P	C3'-C4'-C5'-O5'
16	T	101	G2P	C4'-C5'-O5'-PA

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	T	101	G2P	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1393/1733 (80%)	0.33	56 (4%) 42 28	45, 88, 191, 305	0
2	B	1103/1224 (90%)	0.21	44 (3%) 42 28	42, 79, 153, 277	0
3	C	266/318 (83%)	-0.03	3 (1%) 78 60	50, 79, 117, 170	0
4	E	214/215 (99%)	0.35	5 (2%) 61 42	63, 114, 201, 236	0
5	F	84/155 (54%)	0.11	1 (1%) 76 58	65, 93, 138, 182	0
6	H	133/146 (91%)	0.75	11 (8%) 17 13	75, 116, 207, 288	0
7	I	119/122 (97%)	0.46	3 (2%) 58 39	58, 97, 139, 186	0
8	J	65/70 (92%)	0.12	2 (3%) 51 35	56, 74, 113, 131	0
9	K	114/120 (95%)	0.02	2 (1%) 67 49	54, 86, 115, 164	0
10	L	44/70 (62%)	1.37	13 (29%) 1 1	73, 158, 247, 292	0
11	T	28/29 (96%)	0.45	1 (3%) 46 31	60, 286, 368, 372	0
12	N	14/14 (100%)	0.81	0 100 100	247, 290, 330, 344	0
13	R	9/9 (100%)	-0.58	0 100 100	54, 66, 111, 116	0
All	All	3586/4225 (84%)	0.28	141 (3%) 43 29	42, 87, 187, 372	0

All (141) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	335	GLY	5.4
1	A	141	LEU	5.4
1	A	568	PRO	5.3
6	H	139	ASN	5.1
1	A	1081	LEU	5.1
2	B	472	ALA	4.5
1	A	65	LEU	4.4
10	L	27	LEU	4.4
2	B	711	GLU	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	253	ASN	4.3
1	A	314	ALA	4.0
1	A	76	GLU	4.0
2	B	478	GLY	3.9
10	L	46	VAL	3.7
1	A	598	LEU	3.6
6	H	63	LEU	3.6
2	B	881	ASN	3.6
1	A	151	ASP	3.5
1	A	309	ALA	3.5
1	A	1038	THR	3.5
1	A	161	LEU	3.4
10	L	65	VAL	3.4
2	B	250	PHE	3.4
1	A	1174	PHE	3.3
2	B	883	LEU	3.3
7	I	4	PHE	3.3
2	B	715	ALA	3.3
1	A	1176	LEU	3.2
1	A	315	LEU	3.2
2	B	502	ILE	3.2
1	A	179	LEU	3.2
2	B	479	VAL	3.1
1	A	323	LYS	3.1
2	B	509	ALA	3.1
2	B	275	TYR	3.1
1	A	885	THR	3.1
2	B	637	LEU	3.0
2	B	736	THR	3.0
2	B	446	LEU	2.9
11	T	18	DA	2.9
10	L	32	ALA	2.9
1	A	592	ASP	2.9
1	A	49	LYS	2.9
6	H	60	ALA	2.9
1	A	1280	GLU	2.9
2	B	713	ALA	2.8
2	B	467	GLY	2.8
4	E	95	THR	2.8
5	F	72	LYS	2.7
1	A	78	PRO	2.7
1	A	54	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	38	PRO	2.7
1	A	596	THR	2.7
1	A	541	ILE	2.7
10	L	39	SER	2.7
2	B	919	SER	2.6
1	A	79	GLY	2.6
1	A	162	VAL	2.6
8	J	44	TYR	2.6
1	A	397	ASN	2.6
1	A	248	PRO	2.6
2	B	636	PRO	2.6
2	B	706	GLN	2.6
2	B	471	LYS	2.6
10	L	53	HIS	2.5
10	L	35	SER	2.5
1	A	59	GLY	2.5
6	H	136	LYS	2.5
4	E	83	CYS	2.5
2	B	251	ILE	2.5
1	A	56	PRO	2.5
1	A	231	PRO	2.5
6	H	2	SER	2.5
1	A	1330	ASN	2.5
1	A	589	GLN	2.5
2	B	1221	SER	2.5
9	K	41	THR	2.5
1	A	50	ILE	2.4
1	A	135	PHE	2.4
10	L	28	LYS	2.4
2	B	466	TRP	2.4
1	A	322	VAL	2.4
3	C	175	ALA	2.4
4	E	94	LYS	2.4
1	A	40	THR	2.4
1	A	250	ILE	2.4
1	A	572	TRP	2.4
1	A	399	HIS	2.3
10	L	41	SER	2.3
6	H	146	ARG	2.3
10	L	30	ILE	2.3
2	B	866	TYR	2.3
2	B	643	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	254	GLU	2.3
2	B	1042	GLY	2.3
1	A	252	PHE	2.3
1	A	310	GLY	2.3
2	B	869	SER	2.3
1	A	423	ASP	2.3
4	E	88	VAL	2.3
10	L	55	ILE	2.3
2	B	737	THR	2.2
1	A	154	SER	2.2
2	B	476	ARG	2.2
2	B	262	GLU	2.2
1	A	91	PHE	2.2
2	B	1180	PHE	2.2
1	A	308	ILE	2.2
2	B	243	ALA	2.2
2	B	644	GLU	2.2
2	B	709	ASP	2.2
1	A	1445	ILE	2.2
2	B	646	LEU	2.2
1	A	567	LYS	2.2
6	H	134	ASN	2.2
4	E	118	PRO	2.2
2	B	1100	ASP	2.2
9	K	39	ASP	2.2
2	B	115	GLN	2.1
7	I	2	THR	2.1
1	A	163	SER	2.1
2	B	252	SER	2.1
1	A	1405	THR	2.1
8	J	5	VAL	2.1
1	A	115	LEU	2.1
3	C	159	ALA	2.1
6	H	82	PRO	2.1
6	H	138	GLU	2.1
2	B	734	HIS	2.1
2	B	935	ARG	2.1
3	C	26	ASP	2.1
10	L	29	TYR	2.1
1	A	844	ALA	2.1
1	A	168	GLY	2.1
2	B	731	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
2	B	475	SER	2.0
6	H	130	ARG	2.0
7	I	74	GLU	2.0
6	H	135	LEU	2.0
10	L	45	ALA	2.0
2	B	816	GLU	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
11	1CC	T	19	22/23	0.91	0.08	71,87,132,144	0

6.3 Carbohydrates [i](#)

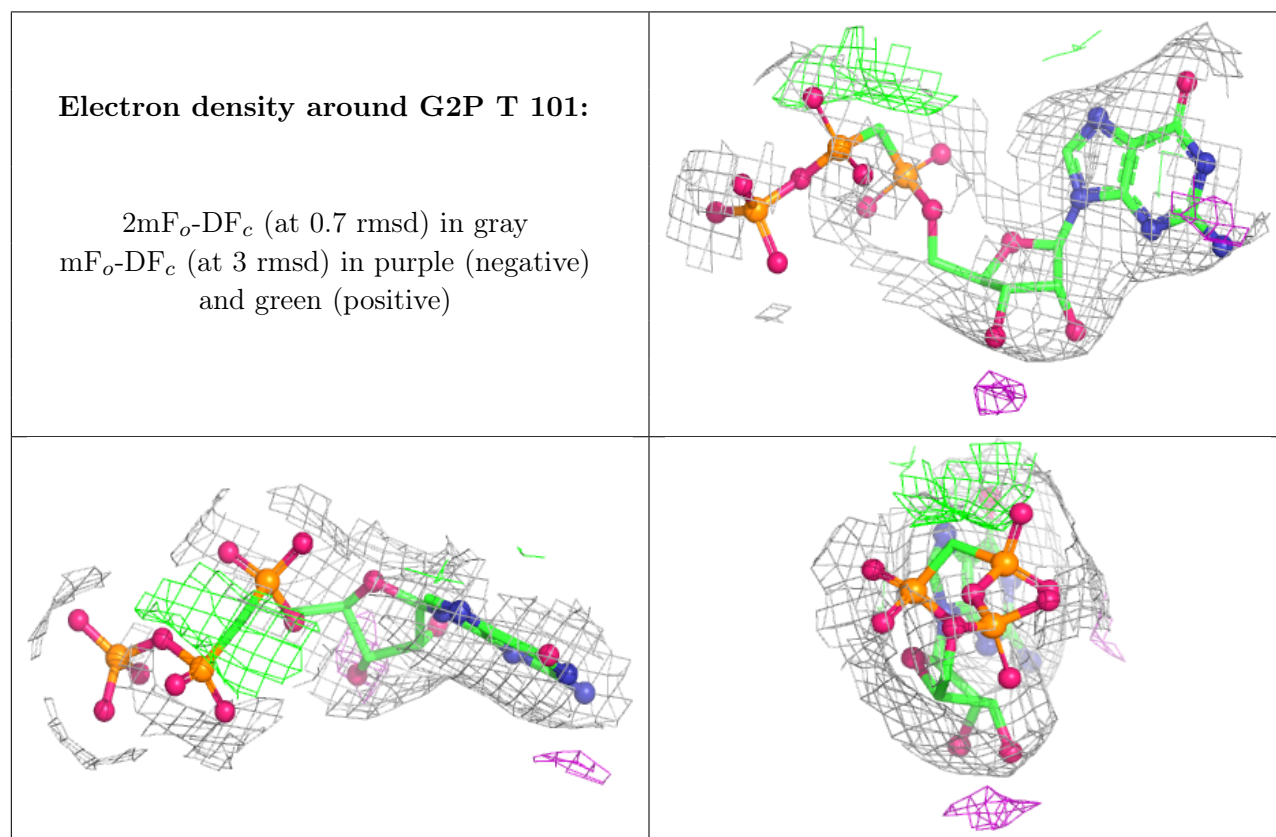
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
15	MG	A	1804	1/1	0.82	0.10	87,87,87,87	0
16	G2P	T	101	32/32	0.88	0.09	59,73,127,131	0
14	ZN	L	101	1/1	0.91	0.10	172,172,172,172	0
14	ZN	A	1801	1/1	0.92	0.07	266,266,266,266	0
14	ZN	A	1802	1/1	0.96	0.06	136,136,136,136	0
14	ZN	I	202	1/1	0.97	0.05	93,93,93,93	0
14	ZN	J	101	1/1	0.99	0.04	92,92,92,92	0
14	ZN	C	401	1/1	0.99	0.03	107,107,107,107	0
15	MG	A	1803	1/1	0.99	0.03	42,42,42,42	0
14	ZN	I	201	1/1	0.99	0.03	104,104,104,104	0
14	ZN	B	1301	1/1	0.99	0.03	123,123,123,123	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.