



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 25, 2022 – 06:11 PM JST

PDB ID : 7VYX
Title : Crystal structure of the selenomethionine(SeMet)-derived Cas12c1 (D969A) ternary complex
Authors : Zhang, B.; Lin, J.Y.; Perculija, V.; OuYang, S.Y.
Deposited on : 2021-11-15
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.31.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

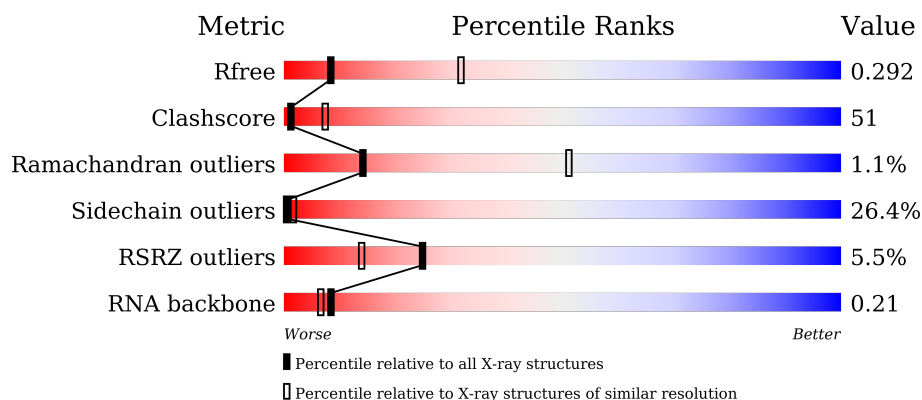
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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.



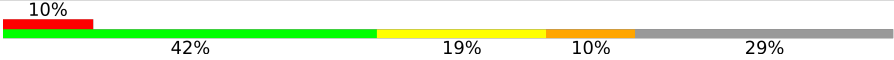



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)
RNA backbone	3102	1010 (3.50-2.90)

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	1310	<div> <div>5%</div> <div>36% 41% 15% 8%</div> </div>
1	B	1310	<div> <div>5%</div> <div>33% 42% 15% 9%</div> </div>
2	C	136	<div> <div>7%</div> <div>18% 30% 23% 5% 24%</div> </div>
2	D	136	<div> <div>5%</div> <div>16% 21% 25% 5% 33%</div> </div>

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Mol	Chain	Length	Quality of chain
3	E	31	
3	F	31	
4	G	23	
4	H	23	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 24465 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 Selenomethionine (SeMet)-labeled Cas12c1 D969A mutant.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	1211	Total	C	N	O	S	Se	0	0	0
			9533	6075	1639	1788	20	11			
1	B	1193	Total	C	N	O	S	Se	0	0	0
			9369	5977	1607	1754	20	11			

- Molecule 2 is a RNA chain called sgRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	103	Total	C	N	O	P	0	0	0
			2188	978	387	720	103			
2	D	91	Total	C	N	O	P	0	0	0
			1934	865	344	634	91			

- Molecule 3 is a DNA chain called Target DNA strand.

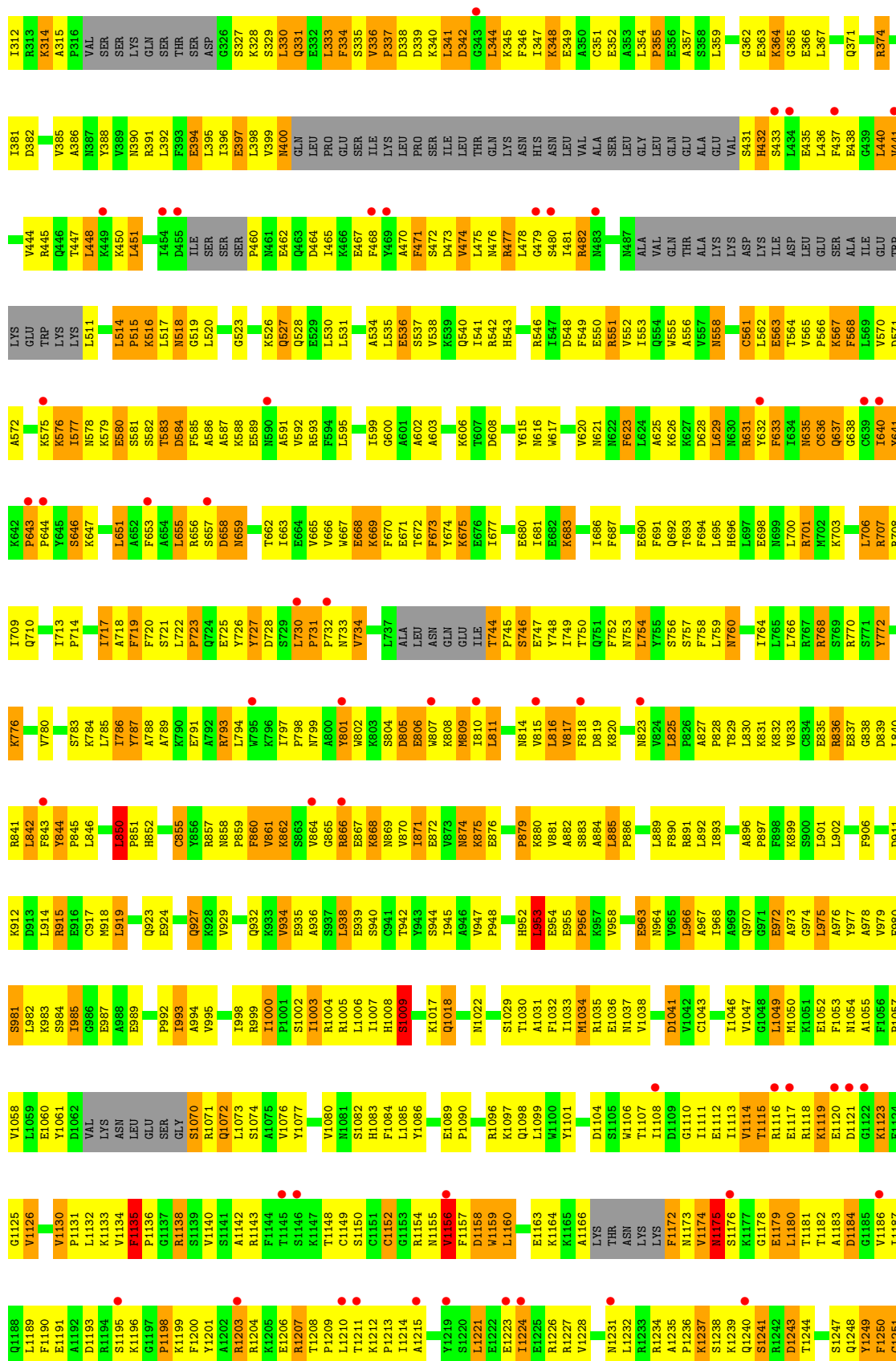
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	22	Total	C	N	O	P	0	0	0
			451	216	78	135	22			
3	F	26	Total	C	N	O	P	0	0	0
			534	256	92	160	26			

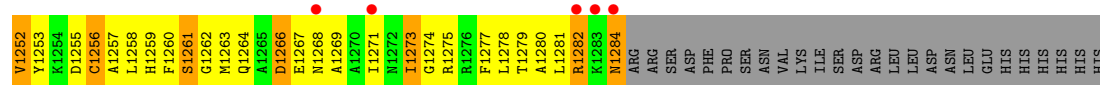
- Molecule 4 is a DNA chain called Non-target DNA strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	11	Total	C	N	O	P	0	0	0
			227	108	42	66	11			
4	H	11	Total	C	N	O	P	0	0	0
			227	108	42	66	11			

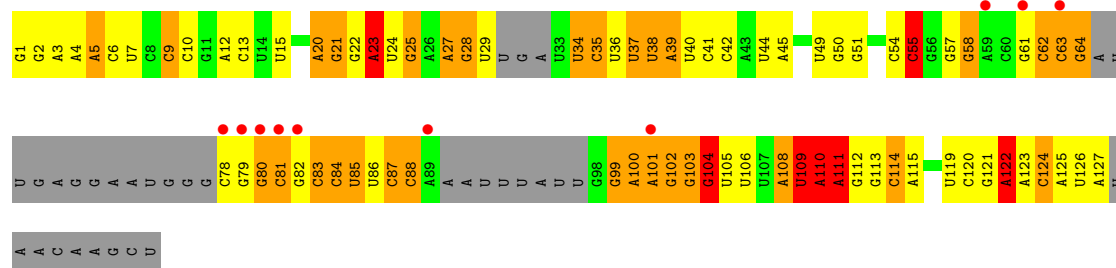
- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total 1	Zn 1	0	0
5	B	1	Total 1	Zn 1	0	0

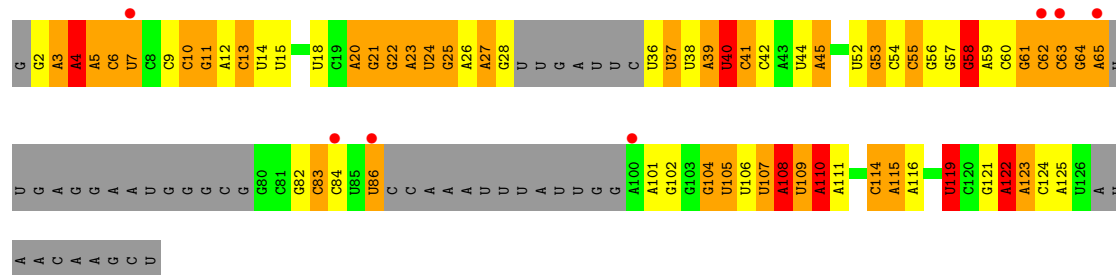




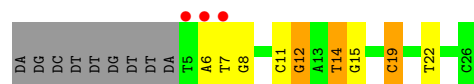
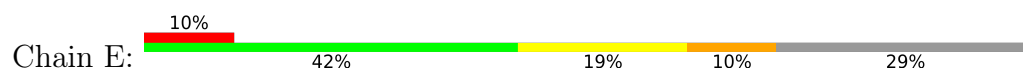
• Molecule 2: sgRNA



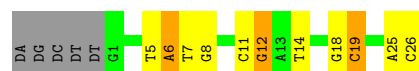
• Molecule 2: sgRNA



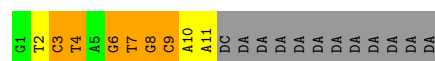
• Molecule 3: Target DNA strand



• Molecule 3: Target DNA strand



• Molecule 4: Non-target DNA strand



● Molecule 4: Non-target DNA strand



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	93.13Å 149.85Å 173.25Å 90.00° 91.59° 90.00°	Depositor
Resolution (Å)	49.73 – 3.20 49.68 – 3.20	Depositor EDS
% Data completeness (in resolution range)	79.4 (49.73-3.20) 79.4 (49.68-3.20)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.96 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.256 , 0.292 0.256 , 0.292	Depositor DCC
R_{free} test set	2973 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	53.0	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 54.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.045 for h,-k,-l	Xtriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	24465	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.86% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	1.20	8/9713 (0.1%)	0.96	31/13105 (0.2%)
1	B	1.09	4/9549 (0.0%)	0.95	34/12891 (0.3%)
2	C	0.81	11/2441 (0.5%)	0.89	6/3793 (0.2%)
2	D	0.70	6/2158 (0.3%)	0.96	9/3352 (0.3%)
3	E	0.68	0/504	1.63	9/776 (1.2%)
3	F	0.67	0/597	1.53	10/920 (1.1%)
4	G	1.25	4/254 (1.6%)	1.03	2/390 (0.5%)
4	H	0.59	0/254	0.91	0/390
All	All	1.06	33/25470 (0.1%)	0.99	101/35617 (0.3%)

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	337	PRO	N-CD	13.97	1.67	1.47
1	B	956	PRO	N-CD	10.04	1.61	1.47
1	A	515	PRO	N-CD	9.92	1.61	1.47
1	A	460	PRO	N-CD	-9.83	1.34	1.47
1	A	1190	PHE	C-N	9.49	1.55	1.34
2	C	111	A	O3'-P	-7.61	1.52	1.61
4	G	8	DG	O3'-P	-7.58	1.52	1.61
2	C	104	G	O3'-P	-7.30	1.52	1.61
2	C	113	G	O3'-P	-6.92	1.52	1.61
2	D	40	U	O3'-P	-6.70	1.53	1.61
2	C	23	A	O3'-P	-6.47	1.53	1.61
2	C	81	C	O3'-P	-6.29	1.53	1.61
2	D	4	A	O3'-P	-6.28	1.53	1.61
2	C	55	C	O3'-P	-6.23	1.53	1.61
2	C	110	A	O3'-P	-6.19	1.53	1.61
1	A	77	TYR	CE1-CZ	-6.17	1.30	1.38
2	D	39	A	O3'-P	-5.98	1.53	1.61
4	G	6	DG	O3'-P	-5.92	1.54	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	290	GLN	C-N	5.82	1.47	1.34
2	D	58	G	O3'-P	-5.71	1.54	1.61
2	C	9	C	O3'-P	-5.69	1.54	1.61
1	B	723	PRO	N-CD	-5.64	1.40	1.47
1	B	355	PRO	N-CD	-5.55	1.40	1.47
2	C	114	C	O3'-P	-5.53	1.54	1.61
1	A	1101	TYR	CE1-CZ	-5.50	1.31	1.38
1	B	77	TYR	CE1-CZ	-5.50	1.31	1.38
2	D	41	C	O3'-P	-5.47	1.54	1.61
2	C	109	U	O3'-P	-5.41	1.54	1.61
4	G	9	DC	O3'-P	-5.36	1.54	1.61
4	G	7	DT	O3'-P	-5.30	1.54	1.61
1	A	772	TYR	CE1-CZ	-5.28	1.31	1.38
2	D	11	G	O3'-P	-5.23	1.54	1.61
2	C	51	G	O3'-P	-5.15	1.54	1.61

All (101) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	19	DC	O5'-P-OP2	-20.37	86.26	110.70
3	F	14	DT	O5'-P-OP1	-18.06	89.03	110.70
3	F	19	DC	O5'-P-OP1	-17.79	89.36	110.70
3	E	14	DT	O5'-P-OP2	-16.98	90.33	110.70
3	E	12	DG	O5'-P-OP1	-16.18	91.14	105.70
3	F	12	DG	O5'-P-OP2	-15.98	91.31	105.70
3	F	14	DT	O5'-P-OP2	13.87	127.35	110.70
2	D	110	A	O5'-P-OP2	-13.23	93.79	105.70
3	E	14	DT	O5'-P-OP1	12.82	126.08	110.70
2	C	119	U	O5'-P-OP1	11.73	124.78	110.70
3	F	19	DC	O5'-P-OP2	11.51	124.51	110.70
2	D	108	A	O5'-P-OP1	-11.50	95.35	105.70
3	E	19	DC	O5'-P-OP1	11.43	124.41	110.70
2	C	108	A	O5'-P-OP2	-11.04	95.76	105.70
3	F	12	DG	O5'-P-OP1	10.66	123.49	110.70
3	E	12	DG	O5'-P-OP2	10.05	122.76	110.70
2	D	110	A	O5'-P-OP1	9.73	122.38	110.70
2	D	108	A	O5'-P-OP2	9.45	122.04	110.70
2	C	108	A	O5'-P-OP1	9.17	121.70	110.70
1	B	954	GLU	N-CA-C	-9.12	86.37	111.00
1	A	742	GLU	CB-CA-C	-8.90	92.59	110.40
2	D	57	G	OP1-P-OP2	-8.20	107.30	119.60
3	F	18	DG	O5'-P-OP2	-7.95	98.55	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	57	G	OP1-P-OP2	-7.86	107.81	119.60
2	D	119	U	O5'-P-OP2	7.82	120.08	110.70
3	E	6	DA	O5'-P-OP1	7.58	119.80	110.70
1	B	183	PHE	N-CA-C	7.44	131.09	111.00
3	F	6	DA	O5'-P-OP2	7.34	119.51	110.70
1	B	364	LYS	N-CA-C	-7.22	91.52	111.00
1	B	1152	CYS	CB-CA-C	-7.20	95.99	110.40
2	D	119	U	O5'-P-OP1	-7.17	99.25	105.70
1	A	487	ASN	N-CA-CB	7.06	123.31	110.60
1	A	337	PRO	CA-N-CD	-7.04	101.64	111.50
2	D	122	A	O5'-P-OP1	-6.93	99.46	105.70
1	B	1257	ALA	N-CA-CB	-6.90	100.44	110.10
4	G	4	DT	C1'-O4'-C4'	-6.83	103.27	110.10
1	B	1121	ASP	N-CA-C	6.79	129.32	111.00
1	B	919	LEU	CA-CB-CG	6.68	130.66	115.30
1	B	293	LEU	CA-CB-CG	6.66	130.62	115.30
1	A	485	ILE	CB-CA-C	-6.63	98.34	111.60
1	A	1235	ALA	N-CA-CB	-6.59	100.87	110.10
1	A	337	PRO	N-CA-CB	6.59	111.21	103.30
1	B	633	PHE	CB-CA-C	-6.56	97.27	110.40
2	D	45	A	O5'-P-OP1	6.45	118.44	110.70
2	C	119	U	O5'-P-OP2	-6.41	99.94	105.70
1	B	1256	CYS	CA-CB-SG	6.33	125.40	114.00
1	B	81	GLU	N-CA-C	6.20	127.75	111.00
1	A	953	LEU	CA-CB-CG	6.19	129.54	115.30
2	C	122	A	O5'-P-OP2	-6.17	100.14	105.70
1	B	659	ASN	N-CA-C	-6.10	94.53	111.00
1	A	515	PRO	CA-N-CD	-6.09	102.97	111.50
1	A	295	THR	N-CA-C	6.04	127.31	111.00
1	B	1255	ASP	N-CA-C	5.97	127.11	111.00
1	A	337	PRO	N-CA-C	-5.89	96.79	112.10
1	A	919	LEU	CA-CB-CG	5.88	128.82	115.30
1	B	953	LEU	N-CA-C	-5.85	95.21	111.00
1	A	81	GLU	N-CA-C	5.81	126.67	111.00
1	A	973	ALA	N-CA-CB	5.79	118.20	110.10
3	F	18	DG	O5'-P-OP1	5.77	117.63	110.70
1	B	956	PRO	CA-N-CD	-5.75	103.46	111.50
1	A	197	LYS	N-CA-C	5.71	126.43	111.00
1	B	1175	ASN	N-CA-CB	-5.70	100.35	110.60
1	A	1261	SER	N-CA-CB	-5.69	101.97	110.50
4	G	3	DC	C1'-O4'-C4'	-5.62	104.48	110.10
1	B	1072	GLN	N-CA-CB	5.56	120.61	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	6	DA	O5'-P-OP1	-5.54	100.71	105.70
1	B	1261	SER	N-CA-CB	5.54	118.81	110.50
1	B	985	ILE	CB-CA-C	-5.49	100.61	111.60
1	A	1190	PHE	O-C-N	5.48	131.47	122.70
1	B	658	ASP	CB-CA-C	-5.44	99.53	110.40
1	B	1135	PHE	C-N-CD	-5.41	108.69	120.60
1	A	76	ILE	CB-CA-C	-5.39	100.83	111.60
1	A	292	HIS	N-CA-C	5.36	125.48	111.00
1	B	850	LEU	CA-CB-CG	5.34	127.59	115.30
1	B	868	LYS	CB-CA-C	-5.33	99.74	110.40
1	B	1207	ARG	N-CA-C	5.33	125.39	111.00
1	A	1232	LEU	CA-CB-CG	5.32	127.53	115.30
1	A	1261	SER	N-CA-C	5.29	125.29	111.00
1	B	603	ALA	CB-CA-C	-5.29	102.16	110.10
1	B	868	LYS	O-C-N	5.27	131.13	122.70
1	A	1020	LEU	N-CA-CB	-5.26	99.87	110.40
1	B	868	LYS	C-N-CA	5.24	134.80	121.70
1	A	99	GLY	N-CA-C	5.21	126.12	113.10
1	A	741	GLN	CB-CA-C	-5.21	99.99	110.40
1	B	474	VAL	N-CA-C	5.21	125.06	111.00
1	B	1070	SER	CB-CA-C	-5.15	100.31	110.10
3	E	15	DG	O5'-P-OP1	5.14	116.87	110.70
1	A	511	LEU	N-CA-C	-5.14	97.12	111.00
1	A	460	PRO	CA-N-CD	5.14	118.89	111.70
1	B	731	PRO	C-N-CD	-5.14	109.30	120.60
1	A	460	PRO	N-CA-CB	-5.12	96.97	102.60
1	A	1034	MSE	CA-CB-CG	-5.11	104.61	113.30
1	B	52	LEU	CA-CB-CG	5.09	127.02	115.30
1	A	620	VAL	CB-CA-C	-5.07	101.77	111.40
1	A	341	LEU	CB-CA-C	-5.05	100.60	110.20
1	A	340	LYS	CB-CA-C	-5.05	100.30	110.40
3	E	6	DA	O5'-P-OP2	-5.05	101.16	105.70
1	A	354	LEU	CA-CB-CG	5.03	126.87	115.30
1	B	197	LYS	N-CA-C	5.03	124.57	111.00
1	B	184	ASP	N-CA-CB	5.02	119.63	110.60
1	B	1241	SER	N-CA-C	-5.01	97.46	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9533	0	9379	994	0
1	B	9369	0	9165	1088	0
2	C	2188	0	1113	138	0
2	D	1934	0	984	123	0
3	E	451	0	251	10	0
3	F	534	0	297	7	0
4	G	227	0	125	15	0
4	H	227	0	125	6	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
All	All	24465	0	21439	2321	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 51.

All (2321) 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:B:1159:TRP:CH2	1:B:1183:ALA:HB2	1.29	1.67
1:B:565:VAL:HB	1:B:708:ARG:CD	1.31	1.60
1:B:565:VAL:CB	1:B:708:ARG:HD3	1.34	1.52
1:A:444:VAL:HG21	1:A:471:PHE:CD2	1.43	1.49
1:A:1201:TYR:CE2	1:A:1209:PRO:HD2	1.48	1.47
1:B:1159:TRP:CZ3	1:B:1183:ALA:HB2	1.50	1.46
1:B:1235:ALA:HB1	1:B:1236:PRO:CD	1.29	1.46
1:B:1200:PHE:CZ	1:B:1204:ARG:HD2	1.52	1.45
1:A:1235:ALA:CB	1:A:1236:PRO:HD2	1.41	1.43
1:B:1150:SER:HB3	1:B:1268:ASN:ND2	1.35	1.40
2:D:52:U:C2'	2:D:53:G:H5''	1.50	1.38
1:A:1235:ALA:HB1	1:A:1236:PRO:CD	1.43	1.38
1:B:336:VAL:CG1	1:B:337:PRO:HD3	1.52	1.37
1:B:817:VAL:CG2	1:B:825:LEU:HD13	1.56	1.34
1:A:472:SER:CA	1:A:475:LEU:HD11	1.58	1.34
1:B:1235:ALA:CB	1:B:1236:PRO:HD2	1.25	1.33
1:B:140:PRO:CB	1:B:231:MSE:HE3	1.56	1.33

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:336:VAL:HG13	1:B:337:PRO:CD	1.60	1.31
1:B:817:VAL:HG23	1:B:825:LEU:CD1	1.58	1.29
1:B:444:VAL:HG21	1:B:471:PHE:CD2	1.68	1.29
4:G:6:DG:C2'	4:G:7:DT:H5'	1.64	1.28
2:D:52:U:H2'	2:D:53:G:C5'	1.63	1.27
1:A:564:THR:HB	1:A:567:LYS:CB	1.62	1.27
1:B:140:PRO:HB3	1:B:231:MSE:CE	1.66	1.26
1:B:257:VAL:CG1	1:B:258:ASP:OD1	1.84	1.25
1:B:312:ILE:O	1:B:348:LYS:HD3	1.33	1.24
1:B:836:ARG:HG3	1:B:843:PHE:CZ	1.73	1.23
1:A:444:VAL:HG21	1:A:471:PHE:CE2	1.72	1.22
1:B:1159:TRP:CZ3	1:B:1183:ALA:CB	2.23	1.21
1:A:1159:TRP:CZ2	1:A:1183:ALA:HB2	1.74	1.21
1:B:1159:TRP:CH2	1:B:1183:ALA:CB	2.23	1.20
1:B:967:ALA:HA	1:B:1058:VAL:CG2	1.72	1.20
1:B:312:ILE:HG21	1:B:351:CYS:SG	1.83	1.19
1:B:722:LEU:HD12	1:B:723:PRO:CD	1.73	1.19
1:A:444:VAL:CG2	1:A:471:PHE:CD2	2.26	1.18
1:B:1237:LYS:HD2	2:D:105:U:OP1	1.39	1.18
1:B:257:VAL:HG13	1:B:258:ASP:OD1	1.00	1.18
1:A:564:THR:HB	1:A:567:LYS:HB2	1.19	1.17
1:B:722:LEU:CD1	1:B:723:PRO:HD2	1.75	1.16
1:A:472:SER:HA	1:A:475:LEU:CD1	1.74	1.16
1:A:809:MSE:SE	1:A:810:ILE:HD12	1.96	1.15
1:A:839:ASP:O	1:A:842:LEU:HD22	1.43	1.15
1:A:850:LEU:HD23	1:A:851:PRO:HD2	1.28	1.15
1:B:1134:VAL:HB	1:B:1136:PRO:O	1.43	1.15
1:B:1173:ASN:O	1:B:1180:LEU:HD21	1.45	1.15
1:B:479:GLY:O	1:B:482:ARG:HG2	1.46	1.15
1:B:260:GLU:HB2	1:B:263:VAL:CG2	1.77	1.14
1:A:1207:ARG:NE	1:A:1236:PRO:HG2	1.61	1.14
1:B:963:GLU:O	1:B:982:LEU:HB2	1.44	1.14
1:A:1112:GLU:HB2	1:A:1130:VAL:O	1.46	1.13
1:B:396:ILE:HG23	1:B:448:LEU:HD11	1.29	1.13
1:B:1107:THR:HG22	1:B:1133:LYS:HG2	1.23	1.13
1:A:809:MSE:SE	1:A:810:ILE:CD1	2.46	1.12
1:B:315:ALA:O	1:B:348:LYS:HE2	1.48	1.12
1:B:437:PHE:O	1:B:441:VAL:HG12	1.48	1.12
1:A:731:PRO:CB	1:A:732:PRO:HD2	1.71	1.11
1:B:731:PRO:CB	1:B:732:PRO:HD2	1.76	1.11
1:A:21:ARG:NH1	1:A:953:LEU:HA	1.66	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:643:PRO:HB2	1:B:644:PRO:CD	1.82	1.10
1:B:766:LEU:HD22	1:B:934:VAL:HG21	1.31	1.10
1:A:1251:CYS:HB3	1:A:1256:CYS:SG	1.79	1.09
1:A:865:GLY:HA3	1:A:883:SER:OG	1.53	1.09
1:B:329:SER:HB2	1:B:334:PHE:CD2	1.86	1.09
1:B:102:ILE:HG23	1:B:295:THR:CG2	1.81	1.08
1:B:621:ASN:HB2	1:B:623:PHE:CE1	1.87	1.08
1:B:885:LEU:HD12	1:B:886:PRO:HD2	1.30	1.08
2:C:62:C:H5''	2:C:62:C:H6	1.17	1.08
1:A:975:LEU:CD2	1:A:998:ILE:HG13	1.83	1.08
1:B:564:THR:HG22	1:B:566:PRO:HD2	1.29	1.08
1:B:257:VAL:CG2	1:B:346:PHE:HB2	1.84	1.07
2:C:80:G:H5'	2:C:80:G:H8	1.13	1.07
1:A:564:THR:CB	1:A:567:LYS:HB2	1.83	1.07
1:A:1146:SER:HB2	1:A:1233:ARG:HH21	1.20	1.07
1:B:76:ILE:HD11	1:B:359:LEU:HD11	1.31	1.07
1:B:621:ASN:HB2	1:B:623:PHE:HE1	0.96	1.07
1:B:396:ILE:CG2	1:B:448:LEU:HD11	1.85	1.07
1:B:1200:PHE:CZ	1:B:1204:ARG:CD	2.38	1.07
1:A:1201:TYR:CE2	1:A:1209:PRO:CD	2.37	1.06
1:B:980:PHE:CE2	1:B:1274:GLY:HA3	1.90	1.06
1:B:980:PHE:CE1	1:B:992:PRO:HB3	1.91	1.06
1:B:52:LEU:CD2	1:B:948:PRO:HB3	1.86	1.06
1:B:140:PRO:CB	1:B:231:MSE:CE	2.27	1.06
1:B:980:PHE:HE2	1:B:1274:GLY:HA3	1.16	1.06
2:C:88:C:H6	2:C:88:C:H5'	1.18	1.06
1:A:21:ARG:NH1	1:A:953:LEU:HB3	1.70	1.05
1:A:336:VAL:HG13	1:A:337:PRO:HD3	1.30	1.05
1:A:444:VAL:CG2	1:A:471:PHE:HD2	1.66	1.05
1:A:636:CYS:O	1:A:637:GLN:HG2	1.56	1.05
4:G:6:DG:H2''	4:G:7:DT:H5'	1.08	1.05
1:A:21:ARG:HH12	1:A:953:LEU:HA	0.93	1.05
1:A:21:ARG:HH11	1:A:953:LEU:HB3	1.12	1.05
1:B:727:TYR:CD2	1:B:758:PHE:HE2	1.74	1.05
1:B:786:ILE:HG21	1:B:889:LEU:CD1	1.84	1.05
1:B:126:GLN:HG2	1:B:225:PHE:CE1	1.91	1.05
1:A:1108:ILE:HG13	1:A:1132:LEU:CD2	1.86	1.05
1:B:197:LYS:HD3	1:B:214:LEU:HD12	1.37	1.04
1:B:727:TYR:HD2	1:B:758:PHE:CE2	1.75	1.04
1:A:731:PRO:HB2	1:A:732:PRO:HD2	1.09	1.04
1:B:329:SER:HB2	1:B:334:PHE:CE2	1.92	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:THR:O	1:A:163:ILE:HD12	1.57	1.04
1:B:49:LEU:HD13	1:B:953:LEU:CD1	1.88	1.04
1:B:468:PHE:HE1	1:B:514:LEU:CD1	1.70	1.04
1:B:1115:THR:HG21	1:B:1130:VAL:CG2	1.88	1.04
1:B:1224:ILE:O	1:B:1228:VAL:HG23	1.55	1.03
1:A:1200:PHE:O	1:A:1203:ARG:HB2	1.57	1.03
1:B:621:ASN:CB	1:B:623:PHE:HE1	1.71	1.03
1:B:286:VAL:O	1:B:290:GLN:HG3	1.55	1.03
1:A:441:VAL:CG2	1:A:445:ARG:HH11	1.69	1.03
1:A:1130:VAL:HG12	1:A:1131:PRO:HD2	1.40	1.03
1:B:120:ASN:OD1	1:B:140:PRO:HG2	1.59	1.03
1:B:744:THR:HA	1:B:747:GLU:OE2	1.58	1.02
1:A:185:SER:O	1:A:189:LYS:HD2	1.59	1.02
1:A:720:PHE:HB2	1:A:751:GLN:OE1	1.58	1.02
1:B:564:THR:CG2	1:B:566:PRO:HD2	1.88	1.02
1:B:836:ARG:HG3	1:B:843:PHE:CE2	1.94	1.01
1:A:1232:LEU:HD13	1:A:1249:TYR:HD2	1.24	1.01
1:A:1207:ARG:NE	1:A:1236:PRO:CG	2.24	1.01
1:B:29:THR:HG22	1:B:1104:ASP:OD1	1.59	1.01
2:D:52:U:H2'	2:D:53:G:H5''	1.01	1.01
1:B:1259:HIS:HD2	1:B:1260:PHE:CE1	1.79	1.01
1:A:336:VAL:CG1	1:A:337:PRO:HD3	1.90	1.00
1:B:140:PRO:HB3	1:B:231:MSE:HE3	1.18	1.00
1:A:1225:GLU:O	1:A:1229:ARG:HG2	1.61	1.00
1:B:865:GLY:H	1:B:885:LEU:HD22	1.23	1.00
4:G:6:DG:H2''	4:G:7:DT:C5'	1.90	1.00
1:A:472:SER:O	1:A:475:LEU:HD12	1.58	1.00
1:B:468:PHE:HE1	1:B:514:LEU:HD13	1.25	1.00
1:B:257:VAL:HG21	1:B:346:PHE:HB2	1.44	0.99
1:A:396:ILE:HA	1:A:448:LEU:HD12	1.43	0.99
1:B:643:PRO:HB2	1:B:644:PRO:HD2	1.02	0.99
1:A:471:PHE:CE1	1:A:475:LEU:HD23	1.98	0.99
1:A:1242:ARG:NH1	2:C:106:U:H4'	1.78	0.99
1:A:1046:ILE:O	1:A:1050:MSE:HG3	1.62	0.98
1:B:1070:SER:HB2	1:B:1073:LEU:HB3	1.44	0.98
1:B:531:LEU:HD21	1:B:927:GLN:HE22	1.28	0.98
2:D:2:G:H8	2:D:2:G:H5''	1.27	0.98
1:B:703:LYS:HE2	1:B:753:ASN:HD21	1.29	0.98
1:A:76:ILE:HD11	1:A:359:LEU:HD11	1.44	0.98
1:A:1107:THR:HG22	1:A:1133:LYS:HG2	1.45	0.98
1:A:1201:TYR:CD2	1:A:1208:THR:HA	1.99	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:52:LEU:HD21	1:B:948:PRO:HB3	1.46	0.98
2:C:38:U:HO2'	2:C:39:A:H8	1.11	0.98
1:B:432:HIS:O	1:B:435:GLU:HG2	1.64	0.97
1:A:564:THR:HB	1:A:567:LYS:HB3	1.42	0.97
1:B:396:ILE:HG22	1:B:448:LEU:HD21	1.43	0.97
1:B:159:THR:O	1:B:163:ILE:HG13	1.64	0.97
1:B:1150:SER:HB3	1:B:1268:ASN:HD22	0.83	0.97
1:B:173:ARG:CG	1:B:183:PHE:HE2	1.77	0.97
1:B:643:PRO:CB	1:B:644:PRO:HD2	1.95	0.97
1:B:1175:ASN:OD1	1:B:1175:ASN:N	1.95	0.96
1:B:967:ALA:HA	1:B:1058:VAL:HG23	1.44	0.96
1:A:479:GLY:O	1:A:482:ARG:HB3	1.65	0.96
1:A:1159:TRP:CZ2	1:A:1183:ALA:CB	2.48	0.95
1:B:1200:PHE:CE1	1:B:1204:ARG:HD2	2.00	0.95
1:B:71:ASP:O	1:B:75:GLN:HG3	1.66	0.95
1:B:140:PRO:HB2	1:B:231:MSE:HE3	1.46	0.95
1:A:616:ASN:O	1:A:620:VAL:HG23	1.67	0.95
1:A:1201:TYR:HD2	1:A:1208:THR:HA	1.32	0.94
1:B:1150:SER:CB	1:B:1268:ASN:HD22	1.77	0.94
1:B:1150:SER:CB	1:B:1268:ASN:ND2	2.30	0.94
1:B:102:ILE:HG23	1:B:295:THR:HG21	1.48	0.94
1:A:260:GLU:O	1:A:264:MSE:HG3	1.66	0.94
1:A:1173:ASN:O	1:A:1173:ASN:ND2	2.01	0.94
1:A:1250:PHE:HB3	1:A:1258:LEU:O	1.67	0.94
1:B:691:PHE:HE1	1:B:695:LEU:HD11	1.31	0.94
1:A:1159:TRP:HZ2	1:A:1183:ALA:HB2	1.20	0.94
1:B:722:LEU:HD12	1:B:723:PRO:HD2	0.94	0.94
1:B:1046:ILE:HG21	1:B:1084:PHE:CE2	2.02	0.94
1:A:1207:ARG:CD	1:A:1236:PRO:HG2	1.97	0.93
1:A:36:ARG:O	1:A:40:SER:HB3	1.68	0.93
1:B:665:VAL:O	1:B:668:GLU:HG3	1.66	0.93
1:B:786:ILE:HG21	1:B:889:LEU:HD11	1.50	0.93
1:A:1175:ASN:O	1:A:1215:ALA:HB1	1.68	0.93
1:A:1146:SER:CB	1:A:1233:ARG:HH21	1.81	0.93
1:A:1226:ARG:CZ	1:A:1226:ARG:HB3	1.95	0.93
1:B:468:PHE:CE1	1:B:514:LEU:CD1	2.51	0.93
1:B:1275:ARG:O	1:B:1279:THR:HG23	1.66	0.93
1:B:985:ILE:O	1:B:985:ILE:HG22	1.66	0.93
1:B:1115:THR:CG2	1:B:1130:VAL:CG2	2.47	0.93
1:B:964:ASN:O	1:B:1055:ALA:HB1	1.69	0.93
1:B:1207:ARG:HD2	1:B:1236:PRO:HG2	1.50	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1251:CYS:SG	1:B:1256:CYS:HB3	2.08	0.92
1:B:257:VAL:HG13	1:B:258:ASP:CG	1.89	0.92
1:B:836:ARG:HG3	1:B:843:PHE:HZ	1.26	0.92
1:A:691:PHE:CE1	1:A:695:LEU:HD11	2.05	0.92
1:B:144:GLU:HG3	1:B:232:ILE:HG12	1.52	0.92
1:B:727:TYR:HD2	1:B:758:PHE:HE2	0.92	0.92
1:A:312:ILE:HG13	1:A:328:LYS:HE3	1.48	0.92
1:B:396:ILE:HG22	1:B:448:LEU:CD2	1.99	0.92
1:B:1259:HIS:CD2	1:B:1260:PHE:CE1	2.57	0.92
1:B:866:ARG:H	1:B:866:ARG:HE	1.15	0.92
1:A:1201:TYR:HE2	1:A:1209:PRO:HD2	1.13	0.91
1:B:730:LEU:HD12	1:B:730:LEU:H	1.35	0.91
1:B:1108:ILE:HG12	1:B:1132:LEU:HD23	1.49	0.91
1:A:444:VAL:HG21	1:A:471:PHE:HD2	1.11	0.91
1:A:584:ASP:O	1:A:588:LYS:HD3	1.69	0.91
1:A:438:GLU:HA	1:A:441:VAL:CG1	2.01	0.91
1:A:966:LEU:HD12	1:A:1055:ALA:HB3	1.52	0.91
1:B:257:VAL:CG2	1:B:346:PHE:CB	2.48	0.91
1:B:396:ILE:HA	1:B:448:LEU:HD21	1.50	0.91
1:B:701:ARG:HG2	1:B:701:ARG:HH11	1.34	0.91
1:B:731:PRO:HB3	1:B:732:PRO:HD2	1.51	0.91
1:A:336:VAL:HG13	1:A:337:PRO:CD	2.01	0.91
2:C:102:G:H5''	2:C:102:G:H8	1.36	0.91
1:A:1177:LYS:O	1:A:1213:PRO:HB3	1.71	0.90
1:B:49:LEU:HD13	1:B:953:LEU:HD12	1.51	0.90
1:B:477:ARG:HH11	1:B:477:ARG:HG3	1.35	0.90
1:B:482:ARG:HG3	1:B:482:ARG:HH11	1.34	0.90
1:A:975:LEU:HD22	1:A:998:ILE:HG13	1.53	0.90
2:C:80:G:H5'	2:C:80:G:C8	2.05	0.90
1:B:974:GLY:HA2	1:B:1000:ILE:HB	1.52	0.90
1:B:669:LYS:O	1:B:672:THR:CG2	2.20	0.90
2:C:101:A:H8	2:C:101:A:H5''	1.37	0.90
1:B:669:LYS:O	1:B:672:THR:HG22	1.72	0.90
1:A:395:LEU:O	1:A:398:LEU:HB2	1.71	0.90
1:B:444:VAL:HG21	1:B:471:PHE:HD2	1.05	0.90
1:B:1108:ILE:CG1	1:B:1132:LEU:HD23	2.01	0.90
1:A:59:LEU:CD2	1:A:892:LEU:HD12	2.01	0.89
1:A:1175:ASN:O	1:A:1215:ALA:CB	2.20	0.89
1:B:1117:GLU:O	1:B:1125:GLY:HA3	1.72	0.89
1:A:1225:GLU:O	1:A:1229:ARG:CG	2.20	0.89
1:B:102:ILE:CG2	1:B:295:THR:CG2	2.50	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:731:PRO:CB	1:B:732:PRO:CD	2.49	0.89
1:B:565:VAL:HG12	1:B:566:PRO:HD3	1.51	0.89
1:A:21:ARG:HH12	1:A:953:LEU:CA	1.84	0.89
1:A:850:LEU:CD2	1:A:851:PRO:HD2	2.02	0.89
1:A:1250:PHE:HD2	1:A:1262:GLY:HA2	1.37	0.89
1:A:871:ILE:HD11	1:A:906:PHE:CZ	2.07	0.89
1:B:140:PRO:HG3	1:B:231:MSE:HE1	1.52	0.89
1:A:438:GLU:HA	1:A:441:VAL:HG12	1.53	0.89
1:B:745:PRO:HD2	1:B:747:GLU:OE2	1.71	0.89
2:C:124:C:H42	3:E:8:DG:H1	1.21	0.89
1:B:538:VAL:HG13	1:B:759:LEU:HD12	1.54	0.88
1:B:1173:ASN:O	1:B:1180:LEU:CD2	2.21	0.88
1:A:477:ARG:HH11	1:A:477:ARG:HG3	1.37	0.88
2:D:52:U:C2'	2:D:53:G:C5'	2.37	0.88
1:A:1111:ILE:CG2	1:A:1281:LEU:HD23	2.03	0.88
1:A:53:LYS:HB2	1:A:951:TYR:HE1	1.38	0.88
1:A:1163:GLU:N	1:A:1163:GLU:OE1	2.06	0.88
1:A:1043:CYS:O	1:A:1047:VAL:HG23	1.72	0.88
2:C:62:C:H5''	2:C:62:C:C6	2.08	0.88
1:B:1269:ALA:O	1:B:1273:ILE:HG12	1.74	0.88
1:B:568:PHE:O	1:B:572:ALA:HB2	1.73	0.88
1:A:621:ASN:CB	1:A:623:PHE:HE1	1.86	0.88
1:A:636:CYS:O	1:A:637:GLN:CG	2.21	0.88
1:B:1089:GLU:OE2	1:B:1089:GLU:N	2.07	0.88
1:A:1226:ARG:HB3	1:A:1226:ARG:NH1	1.89	0.87
1:B:59:LEU:HD23	1:B:892:LEU:HD12	1.56	0.87
1:B:396:ILE:CG2	1:B:448:LEU:HD21	2.04	0.87
1:B:1201:TYR:CE1	1:B:1209:PRO:HD2	2.09	0.87
1:A:1089:GLU:N	1:A:1089:GLU:OE2	2.08	0.87
1:A:1277:PHE:CE2	1:A:1281:LEU:HD11	2.09	0.87
1:A:28:ASP:OD2	1:A:1107:THR:HG23	1.73	0.87
1:B:158:TRP:NE1	1:B:199:ASP:HA	1.90	0.87
1:B:638:GLY:HA3	1:B:653:PHE:HE2	1.39	0.87
1:B:793:ARG:C	1:B:794:LEU:HD23	1.94	0.87
1:A:706:LEU:HD12	1:A:748:TYR:HD2	1.37	0.87
2:D:21:G:H2'	2:D:22:G:H5'	1.57	0.87
1:A:801:TYR:CD1	2:C:23:A:H1'	2.10	0.86
1:B:120:ASN:OD1	1:B:140:PRO:CG	2.22	0.86
1:A:396:ILE:HA	1:A:448:LEU:CD1	2.05	0.86
1:A:599:ILE:HG22	1:A:700:LEU:CD2	2.05	0.86
1:B:396:ILE:HG22	1:B:448:LEU:CG	2.04	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1191:GLU:HG2	1:B:1214:ILE:HB	1.56	0.86
1:B:9:HIS:HD2	2:D:109:U:C2	1.94	0.86
1:A:487:ASN:O	1:A:487:ASN:ND2	2.08	0.86
1:A:814:ASN:O	1:A:814:ASN:ND2	2.07	0.86
1:B:1173:ASN:O	1:B:1174:VAL:HG13	1.75	0.86
1:B:625:ALA:HB3	1:B:628:ASP:OD2	1.75	0.86
1:B:399:VAL:HG11	1:B:445:ARG:HG2	1.58	0.86
1:B:1140:VAL:HG21	1:B:1273:ILE:CG2	2.05	0.86
1:A:59:LEU:HD23	1:A:892:LEU:HD12	1.55	0.86
1:A:44:ASP:N	1:A:44:ASP:OD1	2.08	0.85
1:A:128:LYS:O	1:A:132:GLY:HA2	1.76	0.85
1:A:454:ILE:HG22	1:A:454:ILE:O	1.76	0.85
1:B:691:PHE:CE1	1:B:695:LEU:HD11	2.11	0.85
1:B:998:ILE:HG22	1:B:999:ARG:N	1.92	0.85
1:B:565:VAL:CG1	1:B:566:PRO:HD3	2.06	0.85
1:A:731:PRO:CB	1:A:732:PRO:CD	2.53	0.85
1:A:963:GLU:O	1:A:982:LEU:HB2	1.75	0.85
1:B:708:ARG:HH11	1:B:708:ARG:HG3	1.42	0.85
1:A:341:LEU:O	1:A:341:LEU:HD23	1.75	0.85
1:B:76:ILE:HD11	1:B:359:LEU:CD1	2.07	0.85
1:B:173:ARG:HD3	1:B:183:PHE:CE2	2.10	0.85
1:B:885:LEU:HD12	1:B:886:PRO:CD	2.06	0.85
1:A:441:VAL:CG2	1:A:445:ARG:NH1	2.39	0.84
1:B:1158:ASP:OD1	1:B:1158:ASP:N	2.08	0.84
1:A:441:VAL:HG22	1:A:445:ARG:HH11	1.41	0.84
1:A:471:PHE:CE1	1:A:475:LEU:CD2	2.60	0.84
1:A:731:PRO:HB2	1:A:732:PRO:CD	2.01	0.84
1:B:995:VAL:HG12	1:B:1267:GLU:OE2	1.78	0.84
1:B:595:LEU:O	1:B:595:LEU:HD13	1.77	0.84
1:B:61:VAL:HG23	1:B:890:PHE:CE1	2.13	0.84
1:A:1146:SER:CB	1:A:1233:ARG:NH2	2.40	0.84
1:B:371:GLN:O	1:B:374:ARG:HG2	1.77	0.84
1:B:479:GLY:O	1:B:482:ARG:CG	2.26	0.84
1:A:1250:PHE:CD2	1:A:1262:GLY:HA2	2.13	0.84
1:B:329:SER:CB	1:B:334:PHE:CD2	2.61	0.84
1:B:850:LEU:HD22	1:B:851:PRO:HD2	1.58	0.84
1:B:1160:LEU:O	1:B:1160:LEU:HD22	1.77	0.84
1:B:1191:GLU:CG	1:B:1214:ILE:HB	2.08	0.84
1:B:723:PRO:HB2	1:B:726:TYR:CD2	2.12	0.84
1:A:817:VAL:O	1:A:825:LEU:HD12	1.77	0.83
1:A:1232:LEU:HD13	1:A:1249:TYR:CD2	2.12	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:621:ASN:CB	1:B:623:PHE:CE1	2.54	0.83
1:B:391:ARG:HD3	1:B:516:LYS:O	1.77	0.83
1:A:315:ALA:O	1:A:348:LYS:HE3	1.77	0.83
1:A:437:PHE:O	1:A:441:VAL:HG12	1.78	0.83
1:A:472:SER:CA	1:A:475:LEU:CD1	2.45	0.83
1:B:260:GLU:HB2	1:B:263:VAL:HG21	1.57	0.83
1:B:672:THR:O	1:B:675:LYS:HB2	1.79	0.83
1:A:53:LYS:HB2	1:A:951:TYR:CE1	2.13	0.83
1:B:924:GLU:HG2	1:B:939:GLU:HB3	1.59	0.83
1:A:21:ARG:NH1	1:A:953:LEU:CA	2.42	0.82
1:B:816:LEU:HA	1:B:829:THR:HG23	1.60	0.82
1:B:1110:GLY:C	1:B:1111:ILE:HD13	1.99	0.82
1:B:534:ALA:O	1:B:538:VAL:HG23	1.78	0.82
1:A:151:ARG:HG2	1:A:151:ARG:HH11	1.42	0.82
1:B:464:ASP:HA	1:B:467:GLU:HG3	1.60	0.82
1:B:564:THR:HG22	1:B:566:PRO:CD	2.09	0.82
1:B:1279:THR:O	1:B:1282:ARG:HD3	1.79	0.82
2:C:88:C:H5'	2:C:88:C:C6	2.10	0.82
1:A:759:LEU:HD12	1:A:759:LEU:O	1.80	0.82
1:B:1116:ARG:HA	1:B:1126:VAL:O	1.77	0.82
1:A:472:SER:O	1:A:475:LEU:CD1	2.28	0.82
1:A:680:GLU:HG3	1:A:683:LYS:CE	2.10	0.82
1:A:730:LEU:HD23	1:A:734:VAL:O	1.78	0.82
1:A:827:ALA:HB3	1:A:828:PRO:HD3	1.60	0.82
1:A:839:ASP:O	1:A:842:LEU:CD2	2.26	0.82
1:A:1220:SER:HB3	1:A:1223:GLU:HG3	1.59	0.82
1:B:766:LEU:CD2	1:B:934:VAL:HG21	2.09	0.82
1:A:21:ARG:NH1	1:A:953:LEU:CB	2.42	0.82
1:B:260:GLU:CB	1:B:263:VAL:CG2	2.56	0.82
1:B:228:VAL:HG12	1:B:232:ILE:HD12	1.61	0.82
1:B:707:ARG:HH11	1:B:749:ILE:HD13	1.44	0.82
1:B:1214:ILE:HG23	1:B:1214:ILE:O	1.80	0.82
1:A:669:LYS:O	1:A:672:THR:CG2	2.27	0.81
1:A:1108:ILE:HG13	1:A:1132:LEU:HD23	1.62	0.81
2:D:23:A:H5''	2:D:23:A:H8	1.44	0.81
1:A:36:ARG:O	1:A:40:SER:CB	2.29	0.81
1:A:542:ARG:O	1:A:545:GLN:HB2	1.81	0.81
1:A:1201:TYR:CD2	1:A:1209:PRO:HD2	2.14	0.81
1:B:312:ILE:CG2	1:B:351:CYS:SG	2.68	0.81
1:B:1115:THR:CG2	1:B:1130:VAL:HG23	2.09	0.81
1:B:565:VAL:N	1:B:566:PRO:CD	2.43	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:306:LYS:HB2	1:A:371:GLN:OE1	1.81	0.81
2:D:21:G:C2'	2:D:22:G:H5'	2.11	0.81
1:B:158:TRP:HE1	1:B:199:ASP:HA	1.45	0.81
1:A:485:ILE:HG12	1:A:485:ILE:O	1.80	0.81
1:A:1242:ARG:HH11	2:C:106:U:H4'	1.41	0.81
1:A:720:PHE:CE1	1:A:755:TYR:CE1	2.68	0.81
1:B:731:PRO:HB2	1:B:732:PRO:HD2	1.63	0.81
1:B:126:GLN:CG	1:B:225:PHE:CE1	2.64	0.80
1:B:397:GLU:O	1:B:397:GLU:HG3	1.79	0.80
1:A:1234:ARG:HD2	1:A:1250:PHE:CE1	2.17	0.80
1:A:312:ILE:HG21	1:A:351:CYS:SG	2.22	0.80
1:A:606:LYS:HD3	1:A:693:THR:OG1	1.81	0.80
1:A:1201:TYR:HE2	1:A:1209:PRO:CD	1.87	0.80
1:B:1207:ARG:CD	1:B:1236:PRO:HG2	2.10	0.80
1:B:1235:ALA:HB1	1:B:1236:PRO:HD3	1.59	0.80
1:B:264:MSE:N	1:B:265:PRO:CD	2.45	0.80
1:A:833:VAL:HG13	1:A:843:PHE:CD2	2.16	0.80
1:B:562:LEU:HD12	1:B:562:LEU:O	1.82	0.80
1:B:1159:TRP:CZ2	1:B:1183:ALA:HB2	2.11	0.80
1:A:553:ILE:O	1:A:557:VAL:HG23	1.81	0.80
1:A:565:VAL:HB	1:A:566:PRO:HD3	1.63	0.80
1:B:444:VAL:CG2	1:B:471:PHE:HD2	1.93	0.80
1:B:659:ASN:OD1	1:B:659:ASN:O	2.00	0.80
1:B:964:ASN:O	1:B:1055:ALA:CB	2.28	0.80
1:B:1232:LEU:HD22	1:B:1249:TYR:CE2	2.17	0.80
1:A:471:PHE:O	1:A:475:LEU:HG	1.80	0.79
1:A:1146:SER:HB3	1:A:1233:ARG:NH2	1.98	0.79
1:B:651:LEU:H	1:B:651:LEU:HD22	1.46	0.79
1:A:850:LEU:HD23	1:A:851:PRO:CD	2.12	0.79
1:A:1018:GLN:HG3	1:A:1018:GLN:O	1.82	0.79
1:B:966:LEU:O	1:B:1058:VAL:HG22	1.82	0.79
1:A:37:ARG:HH22	1:A:954:GLU:HB3	1.45	0.79
1:A:865:GLY:H	1:A:885:LEU:HD11	1.45	0.79
1:A:669:LYS:O	1:A:672:THR:HG22	1.81	0.79
1:B:102:ILE:HG23	1:B:295:THR:HG22	1.61	0.79
1:A:436:LEU:HD23	1:A:436:LEU:O	1.82	0.79
1:A:686:ILE:HD12	1:A:686:ILE:H	1.46	0.79
1:A:595:LEU:O	1:A:599:ILE:HG12	1.83	0.79
1:B:468:PHE:CE1	1:B:514:LEU:HD13	2.15	0.79
1:B:432:HIS:HD2	1:B:435:GLU:OE1	1.65	0.78
2:C:88:C:H6	2:C:88:C:C5'	1.94	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1151:CYS:SG	1:A:1258:LEU:HD21	2.22	0.78
1:B:49:LEU:HD13	1:B:953:LEU:HD11	1.64	0.78
1:A:1251:CYS:CB	1:A:1256:CYS:SG	2.69	0.78
1:A:82:THR:HG22	1:A:522:GLY:O	1.82	0.78
1:A:556:ALA:HB1	1:A:562:LEU:HD11	1.65	0.78
1:A:875:LYS:O	1:A:913:ASP:HB2	1.83	0.78
2:C:38:U:H2'	2:C:39:A:C8	2.17	0.78
2:D:2:G:H5''	2:D:2:G:C8	2.14	0.78
1:A:472:SER:HA	1:A:475:LEU:HD11	0.80	0.78
1:A:100:PHE:O	1:A:101:ARG:NE	2.16	0.78
1:A:1232:LEU:O	1:A:1249:TYR:HA	1.83	0.78
1:B:707:ARG:HH11	1:B:749:ILE:CD1	1.97	0.78
1:A:1191:GLU:OE1	1:A:1191:GLU:HA	1.82	0.78
1:A:32:LYS:HD3	1:A:36:ARG:NH1	1.99	0.77
1:A:1130:VAL:HG12	1:A:1131:PRO:CD	2.13	0.77
1:B:166:VAL:O	1:B:170:GLU:HG2	1.83	0.77
1:B:638:GLY:HA3	1:B:653:PHE:CE2	2.19	0.77
1:B:1115:THR:HG21	1:B:1130:VAL:HG21	1.65	0.77
1:B:1191:GLU:HG2	1:B:1214:ILE:CB	2.13	0.77
1:B:1237:LYS:HG2	1:B:1238:SER:H	1.48	0.77
2:C:62:C:OP1	2:C:62:C:H4'	1.83	0.77
1:B:257:VAL:CG2	1:B:346:PHE:CG	2.67	0.77
1:B:260:GLU:CB	1:B:263:VAL:HG22	2.15	0.77
1:B:568:PHE:O	1:B:572:ALA:CB	2.32	0.77
1:A:479:GLY:O	1:A:482:ARG:CB	2.32	0.77
1:A:730:LEU:HD22	1:A:731:PRO:O	1.84	0.77
1:B:90:TYR:CE1	1:B:264:MSE:SE	2.87	0.77
2:D:52:U:O2'	2:D:53:G:H5''	1.85	0.77
1:A:636:CYS:O	1:A:637:GLN:OE1	2.02	0.77
1:B:636:CYS:O	1:B:637:GLN:OE1	2.02	0.77
1:B:825:LEU:H	1:B:825:LEU:HD12	1.48	0.77
1:B:1046:ILE:HG21	1:B:1084:PHE:HE2	1.46	0.77
1:B:72:ARG:NH1	1:B:359:LEU:HD23	1.98	0.77
1:A:1164:LYS:HD3	1:A:1221:LEU:HD21	1.66	0.77
1:B:260:GLU:HB2	1:B:263:VAL:HG22	1.65	0.77
1:B:329:SER:HB2	1:B:334:PHE:CG	2.19	0.77
1:B:817:VAL:HG23	1:B:825:LEU:HD13	0.80	0.77
1:B:269:ILE:HG21	1:B:388:TYR:CE2	2.20	0.77
1:A:1138:ARG:HG2	1:A:1138:ARG:HH11	1.49	0.77
1:B:865:GLY:N	1:B:885:LEU:HD22	2.00	0.77
2:C:102:G:H5''	2:C:102:G:C8	2.19	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:621:ASN:HB3	1:A:623:PHE:HE1	1.48	0.76
1:B:139:ILE:HB	1:B:140:PRO:HD2	1.66	0.76
1:B:396:ILE:CG2	1:B:448:LEU:CD1	2.63	0.76
2:C:84:C:H6	2:C:84:C:H5''	1.50	0.76
2:D:52:U:H2'	2:D:53:G:H5'	1.65	0.76
1:A:810:ILE:HG22	1:A:816:LEU:HD11	1.67	0.76
1:A:185:SER:O	1:A:189:LYS:CD	2.33	0.76
1:A:1258:LEU:HD22	1:A:1263:MSE:HG3	1.66	0.76
1:A:1174:VAL:HG13	1:A:1178:GLY:HA2	1.66	0.76
1:A:1193:ASP:HA	1:A:1212:LYS:CB	2.16	0.76
1:A:1234:ARG:HD2	1:A:1250:PHE:CZ	2.20	0.76
2:D:23:A:H8	2:D:23:A:C5'	1.99	0.76
1:A:71:ASP:O	1:A:75:GLN:HG3	1.85	0.76
1:B:538:VAL:HG13	1:B:759:LEU:CD1	2.15	0.76
1:B:827:ALA:N	1:B:828:PRO:CD	2.49	0.76
1:A:438:GLU:CA	1:A:441:VAL:HG12	2.16	0.75
1:B:9:HIS:CD2	2:D:109:U:C2	2.75	0.75
1:B:97:LEU:HD11	1:B:267:MSE:HB3	1.68	0.75
1:B:257:VAL:HG22	1:B:346:PHE:CG	2.20	0.75
4:H:6:DG:H2''	4:H:7:DT:H5'	1.69	0.75
1:A:1207:ARG:HE	1:A:1236:PRO:HG2	1.50	0.75
1:B:1174:VAL:HG12	1:B:1180:LEU:HD23	1.67	0.75
1:B:482:ARG:HG3	1:B:482:ARG:NH1	1.99	0.75
1:B:703:LYS:HE2	1:B:753:ASN:ND2	2.02	0.75
1:B:786:ILE:HG21	1:B:889:LEU:HD13	1.64	0.75
1:A:730:LEU:CD2	1:A:734:VAL:O	2.35	0.75
1:B:976:ALA:HB2	1:B:1266:ASP:HB2	1.66	0.75
1:A:250:THR:OG1	1:A:253:ALA:HB2	1.87	0.75
1:A:547:ILE:O	1:A:551:ARG:HD3	1.86	0.75
1:A:662:THR:HG22	1:A:665:VAL:HG23	1.69	0.75
1:B:396:ILE:CA	1:B:448:LEU:HD21	2.17	0.75
1:A:312:ILE:CG1	1:A:328:LYS:HE3	2.16	0.75
1:B:1237:LYS:CD	2:D:105:U:OP1	2.30	0.75
1:A:599:ILE:CG2	1:A:700:LEU:HD21	2.17	0.74
1:B:120:ASN:OD1	1:B:140:PRO:HD2	1.87	0.74
1:A:306:LYS:HG2	1:A:306:LYS:O	1.88	0.74
2:D:86:U:H6	2:D:86:U:C5'	2.00	0.74
1:B:470:ALA:O	1:B:474:VAL:HG23	1.86	0.74
1:B:552:VAL:O	1:B:555:TRP:HB3	1.87	0.74
1:B:1191:GLU:HG2	1:B:1214:ILE:CG2	2.18	0.74
1:B:1235:ALA:CB	1:B:1236:PRO:CD	2.08	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:122:A:H2'	2:C:123:A:C8	2.22	0.74
1:A:621:ASN:HB2	1:A:623:PHE:HE1	1.53	0.74
1:A:691:PHE:HE1	1:A:695:LEU:HD11	1.53	0.74
1:A:730:LEU:H	1:A:730:LEU:HD13	1.53	0.74
1:B:975:LEU:HD23	1:B:975:LEU:O	1.87	0.74
1:A:313:ARG:NH1	1:A:351:CYS:O	2.20	0.74
1:A:663:ILE:HD12	1:A:663:ILE:O	1.88	0.74
1:A:842:LEU:HD13	1:A:842:LEU:N	2.03	0.74
1:B:185:SER:O	1:B:189:LYS:HD2	1.88	0.74
1:B:1107:THR:HG22	1:B:1133:LYS:CG	2.13	0.73
2:D:18:U:H4'	2:D:110:A:OP1	1.87	0.73
1:A:720:PHE:CE1	1:A:755:TYR:HE1	2.06	0.73
1:B:1060:GLU:HB2	1:B:1142:ALA:HB2	1.69	0.73
2:C:78:C:H2'	2:C:79:G:H8	1.53	0.73
1:B:432:HIS:O	1:B:435:GLU:CG	2.36	0.73
1:A:76:ILE:HD11	1:A:359:LEU:CD1	2.18	0.73
1:A:686:ILE:HD12	1:A:686:ILE:N	2.03	0.73
2:C:62:C:H6	2:C:62:C:C5'	1.98	0.73
1:B:144:GLU:O	1:B:148:LYS:HB2	1.89	0.73
1:B:998:ILE:CG2	1:B:999:ARG:H	2.02	0.73
1:A:954:GLU:OE1	1:A:954:GLU:HA	1.85	0.73
1:A:662:THR:HG22	1:A:665:VAL:CG2	2.19	0.73
1:A:703:LYS:HE2	1:A:753:ASN:OD1	1.88	0.73
1:A:363:GLU:O	1:A:364:LYS:HG2	1.89	0.73
1:A:723:PRO:HB2	1:A:726:TYR:CD2	2.24	0.73
1:B:197:LYS:HD3	1:B:214:LEU:CD1	2.17	0.73
1:B:511:LEU:HD12	1:B:511:LEU:N	2.03	0.73
1:B:1073:LEU:HD11	1:B:1077:TYR:CE2	2.24	0.73
1:A:102:ILE:HG23	1:A:295:THR:CG2	2.19	0.72
1:A:1207:ARG:CZ	1:A:1236:PRO:HG3	2.19	0.72
1:B:140:PRO:CG	1:B:231:MSE:HE1	2.18	0.72
1:A:548:ASP:HB3	1:A:748:TYR:OH	1.87	0.72
1:A:817:VAL:CG1	1:A:832:LYS:HE3	2.19	0.72
1:B:269:ILE:HG21	1:B:388:TYR:HE2	1.52	0.72
1:B:766:LEU:HD22	1:B:934:VAL:CG2	2.15	0.72
1:B:788:ALA:HA	1:B:870:VAL:HG11	1.69	0.72
1:A:52:LEU:CD2	1:A:948:PRO:HB3	2.20	0.72
1:A:294:THR:HG21	1:A:378:ALA:HA	1.71	0.72
1:A:434:LEU:HD23	1:A:434:LEU:O	1.87	0.72
1:A:564:THR:HG22	1:A:566:PRO:HD2	1.71	0.72
1:A:1226:ARG:HH11	1:A:1226:ARG:H	1.38	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:836:ARG:CG	1:B:843:PHE:CE2	2.71	0.72
1:A:21:ARG:NH2	1:A:911:ASP:OD1	2.23	0.72
1:A:706:LEU:CD1	1:A:748:TYR:HD2	2.03	0.72
1:B:677:ILE:HD12	1:B:694:PHE:HD1	1.55	0.72
1:B:806:GLU:O	1:B:809:MSE:HB3	1.90	0.72
1:B:1043:CYS:O	1:B:1047:VAL:HG23	1.89	0.72
2:D:52:U:C3'	2:D:53:G:H5''	2.18	0.72
1:A:528:GLN:NE2	1:A:936:ALA:H	1.87	0.72
1:A:875:LYS:NZ	3:E:19:DC:OP2	2.22	0.72
1:A:938:LEU:N	1:A:938:LEU:HD12	2.04	0.72
1:A:312:ILE:HG13	1:A:328:LYS:CE	2.19	0.72
1:B:173:ARG:CD	1:B:183:PHE:CE2	2.72	0.72
1:B:801:TYR:O	1:B:807:TRP:HB3	1.90	0.72
1:B:842:LEU:HD13	1:B:842:LEU:N	2.05	0.72
2:D:4:A:C5'	2:D:4:A:H8	2.03	0.72
1:A:454:ILE:O	1:A:454:ILE:CG2	2.37	0.72
4:G:6:DG:H2'	4:G:7:DT:H5'	1.71	0.72
1:B:120:ASN:OD1	1:B:140:PRO:CD	2.38	0.72
1:B:260:GLU:O	1:B:263:VAL:HG23	1.89	0.72
1:B:363:GLU:O	1:B:364:LYS:HB3	1.88	0.72
1:B:516:LYS:HB2	2:D:121:G:OP1	1.90	0.72
1:B:568:PHE:CE2	1:B:707:ARG:HG2	2.25	0.72
1:B:814:ASN:O	1:B:814:ASN:ND2	2.23	0.72
1:B:1096:ARG:NH2	1:B:1135:PHE:HB3	2.05	0.71
2:C:101:A:H5''	2:C:101:A:C8	2.23	0.71
2:D:2:G:H8	2:D:2:G:C5'	2.01	0.71
1:A:317:VAL:HG21	1:A:341:LEU:HD21	1.71	0.71
1:A:1108:ILE:CG1	1:A:1132:LEU:HD23	2.18	0.71
1:B:855:CYS:HB3	1:B:890:PHE:O	1.90	0.71
1:B:1072:GLN:O	1:B:1076:VAL:HG13	1.90	0.71
1:A:606:LYS:CD	1:A:693:THR:OG1	2.38	0.71
1:A:636:CYS:C	1:A:637:GLN:HG2	2.10	0.71
1:A:801:TYR:OH	2:C:22:G:N3	2.23	0.71
1:A:1242:ARG:HH11	2:C:106:U:C4'	2.03	0.71
1:B:998:ILE:CG2	1:B:999:ARG:N	2.52	0.71
1:B:130:ILE:HD12	1:B:225:PHE:CZ	2.26	0.71
1:B:593:ARG:HB2	1:B:641:TYR:HB2	1.70	0.71
1:A:151:ARG:HH11	1:A:151:ARG:CG	2.04	0.71
1:B:602:ALA:O	1:B:606:LYS:HE3	1.91	0.71
1:A:680:GLU:O	1:A:683:LYS:HG2	1.90	0.71
1:B:173:ARG:CG	1:B:183:PHE:CE2	2.69	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:998:ILE:HG22	1:B:999:ARG:H	1.55	0.71
1:B:59:LEU:CD2	1:B:892:LEU:HD12	2.21	0.71
1:A:286:VAL:HG13	1:A:386:ALA:HA	1.72	0.71
1:B:477:ARG:HG3	1:B:477:ARG:NH1	2.06	0.71
2:D:27:A:OP1	2:D:27:A:H4'	1.90	0.71
1:A:165:ARG:HG2	1:A:165:ARG:HH11	1.56	0.70
1:A:400:ASN:HD22	1:A:400:ASN:N	1.89	0.70
1:A:1200:PHE:O	1:A:1203:ARG:CB	2.37	0.70
1:B:974:GLY:HA2	1:B:1000:ILE:CB	2.21	0.70
1:B:980:PHE:CE1	1:B:992:PRO:CB	2.72	0.70
2:D:10:C:H3'	2:D:10:C:C6	2.26	0.70
1:A:549:PHE:HE1	1:A:706:LEU:HD23	1.55	0.70
1:A:1111:ILE:CG2	1:A:1281:LEU:CD2	2.68	0.70
1:B:342:ASP:OD1	1:B:342:ASP:N	2.17	0.70
1:B:432:HIS:CD2	1:B:435:GLU:OE1	2.43	0.70
1:B:632:TYR:CE2	1:B:633:PHE:HE1	2.09	0.70
1:A:964:ASN:OD1	1:A:964:ASN:N	2.22	0.70
1:A:1174:VAL:CG1	1:A:1178:GLY:HA2	2.21	0.70
1:B:1138:ARG:HG2	1:B:1138:ARG:HH11	1.55	0.70
1:B:1150:SER:HB3	1:B:1268:ASN:HD21	1.53	0.70
1:A:95:LEU:HD13	1:A:304:PHE:CZ	2.26	0.70
1:A:226:ASP:OD1	1:A:226:ASP:N	2.18	0.70
1:B:651:LEU:HD22	1:B:651:LEU:N	2.04	0.70
1:B:686:ILE:N	1:B:686:ILE:HD12	2.07	0.70
1:B:980:PHE:HD1	1:B:992:PRO:HA	1.55	0.70
1:B:1237:LYS:HD2	2:D:105:U:P	2.31	0.70
1:B:632:TYR:CD2	1:B:633:PHE:CE1	2.78	0.70
1:B:798:PRO:O	1:B:801:TYR:HB2	1.90	0.70
1:A:556:ALA:CB	1:A:562:LEU:HD11	2.21	0.70
1:A:730:LEU:H	1:A:730:LEU:CD1	2.04	0.70
1:A:1119:LYS:HD3	1:A:1119:LYS:C	2.11	0.70
1:A:1235:ALA:HB1	1:A:1236:PRO:HD3	1.69	0.70
1:A:706:LEU:HD12	1:A:748:TYR:CD2	2.26	0.70
1:A:1158:ASP:OD1	1:A:1158:ASP:N	2.21	0.70
1:B:49:LEU:CD1	1:B:953:LEU:HD12	2.21	0.70
2:C:85:U:H4'	2:C:85:U:OP1	1.91	0.70
1:B:628:ASP:HB3	1:B:653:PHE:CD1	2.27	0.70
1:A:102:ILE:HG23	1:A:295:THR:HG22	1.74	0.70
1:A:477:ARG:HG3	1:A:477:ARG:NH1	2.02	0.70
1:B:140:PRO:CG	1:B:231:MSE:CE	2.70	0.70
1:A:662:THR:CG2	1:A:665:VAL:HG23	2.22	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:216:ASP:OD1	1:B:227:SER:HA	1.91	0.70
1:B:238:ARG:NH1	1:B:238:ARG:HB3	2.06	0.70
1:B:707:ARG:CD	1:B:749:ILE:CD1	2.70	0.70
1:B:748:TYR:O	1:B:752:PHE:N	2.25	0.70
1:B:862:LYS:HD3	1:B:862:LYS:N	2.07	0.69
1:B:980:PHE:CD1	1:B:992:PRO:HA	2.27	0.69
1:A:1204:ARG:HD3	2:C:84:C:O2'	1.92	0.69
1:A:1207:ARG:HD2	1:A:1236:PRO:HG2	1.72	0.69
1:B:885:LEU:CD1	1:B:886:PRO:HD2	2.18	0.69
1:B:29:THR:CG2	1:B:1104:ASP:OD1	2.37	0.69
1:B:263:VAL:C	1:B:265:PRO:HD2	2.11	0.69
1:B:264:MSE:HE1	1:B:346:PHE:HZ	1.57	0.69
1:B:531:LEU:HD21	1:B:927:GLN:NE2	2.07	0.69
1:B:1140:VAL:HG21	1:B:1273:ILE:HG23	1.74	0.69
1:A:354:LEU:CD1	1:A:370:TYR:CE2	2.75	0.69
2:C:36:U:H2'	2:C:37:U:H6	1.57	0.69
1:A:128:LYS:O	1:A:132:GLY:CA	2.41	0.69
1:A:599:ILE:CG2	1:A:700:LEU:CD2	2.70	0.69
1:A:1266:ASP:N	1:A:1266:ASP:OD1	2.25	0.69
1:B:537:SER:O	1:B:541:ILE:HG13	1.92	0.69
1:B:551:ARG:NH1	1:B:719:PHE:HE1	1.90	0.69
1:A:371:GLN:O	1:A:374:ARG:HG2	1.92	0.69
1:A:740:ASN:HD22	1:A:740:ASN:N	1.91	0.69
1:B:637:GLN:OE1	1:B:637:GLN:HA	1.92	0.69
1:B:825:LEU:HD12	1:B:825:LEU:N	2.06	0.69
1:B:980:PHE:HE1	1:B:992:PRO:HB3	1.52	0.69
1:A:43:ALA:HB1	1:A:48:GLU:OE2	1.93	0.69
1:A:312:ILE:CG2	1:A:351:CYS:SG	2.81	0.69
1:A:472:SER:C	1:A:475:LEU:CD1	2.60	0.69
1:A:975:LEU:O	1:A:975:LEU:HD23	1.93	0.69
1:B:447:THR:CG2	1:B:464:ASP:HB2	2.23	0.69
1:B:1174:VAL:HB	1:B:1178:GLY:HA2	1.75	0.69
1:A:962:PHE:CD2	1:A:1056:PHE:HB3	2.28	0.69
1:B:264:MSE:CE	1:B:346:PHE:HZ	2.06	0.69
1:B:1073:LEU:CD1	1:B:1077:TYR:CE2	2.76	0.69
1:A:456:ILE:HD13	1:A:456:ILE:N	2.07	0.68
1:B:701:ARG:HG2	1:B:701:ARG:NH1	2.07	0.68
1:B:985:ILE:O	1:B:985:ILE:CG2	2.41	0.68
1:A:92:LEU:HD13	1:A:293:LEU:HD12	1.74	0.68
1:A:1207:ARG:NE	1:A:1236:PRO:HG3	2.07	0.68
1:B:329:SER:CB	1:B:334:PHE:CE2	2.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1152:CYS:SG	1:B:1256:CYS:HB2	2.24	0.68
1:A:36:ARG:O	1:A:40:SER:N	2.25	0.68
1:B:871:ILE:HD11	1:B:906:PHE:CZ	2.28	0.68
1:B:1232:LEU:O	1:B:1249:TYR:HA	1.93	0.68
2:C:37:U:C6	2:C:37:U:H5''	2.28	0.68
1:A:722:LEU:HD23	1:A:723:PRO:HD2	1.76	0.68
1:B:173:ARG:HG2	1:B:183:PHE:HE2	1.58	0.68
1:A:59:LEU:CD2	1:A:892:LEU:CD1	2.71	0.68
1:B:260:GLU:HG3	1:B:462:GLU:HG3	1.74	0.68
1:A:345:LYS:O	1:A:349:GLU:HG3	1.93	0.68
1:A:594:PHE:HD1	1:A:641:TYR:CE2	2.12	0.68
1:B:173:ARG:CD	1:B:183:PHE:HE2	2.04	0.68
1:A:549:PHE:CE1	1:A:706:LEU:HD23	2.28	0.68
1:A:556:ALA:HB1	1:A:562:LEU:CD1	2.22	0.68
1:A:1204:ARG:HB3	2:C:84:C:O2'	1.93	0.68
1:B:100:PHE:O	1:B:101:ARG:HD3	1.94	0.68
1:B:264:MSE:N	1:B:265:PRO:HD2	2.08	0.68
2:C:38:U:O2'	2:C:39:A:H8	1.75	0.68
1:B:329:SER:HB2	1:B:334:PHE:CZ	2.28	0.68
1:B:623:PHE:H	1:B:623:PHE:HD1	1.40	0.68
1:B:970:GLN:OE1	1:B:1077:TYR:HE1	1.76	0.68
2:D:60:C:O5'	2:D:60:C:H6	1.76	0.68
1:A:783:SER:OG	1:A:874:ASN:ND2	2.26	0.68
1:B:527:GLN:OE1	1:B:527:GLN:N	2.27	0.68
1:B:666:VAL:HA	1:B:669:LYS:HB2	1.75	0.68
1:B:1149:CYS:HB2	1:B:1152:CYS:HB3	1.65	0.68
2:D:4:A:H8	2:D:4:A:H5''	1.59	0.68
1:A:680:GLU:HG3	1:A:683:LYS:HE2	1.76	0.67
1:A:1112:GLU:O	1:A:1283:LYS:CB	2.41	0.67
2:C:10:C:H3'	2:C:10:C:C6	2.29	0.67
1:A:1111:ILE:HG22	1:A:1281:LEU:HD23	1.74	0.67
1:B:830:LEU:O	1:B:833:VAL:HG22	1.94	0.67
1:B:871:ILE:HD11	1:B:906:PHE:CE2	2.29	0.67
1:A:545:GLN:HG2	1:A:755:TYR:CD2	2.29	0.67
1:B:1232:LEU:HD22	1:B:1249:TYR:HE2	1.57	0.67
1:A:509:LYS:HD3	1:A:510:LYS:O	1.94	0.67
1:A:1157:PHE:O	1:A:1160:LEU:HB3	1.93	0.67
1:A:1277:PHE:CE2	1:A:1281:LEU:CD1	2.75	0.67
1:A:938:LEU:HD12	1:A:938:LEU:H	1.59	0.67
2:C:80:G:H8	2:C:80:G:C5'	2.02	0.67
1:B:793:ARG:O	1:B:794:LEU:HD23	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1110:GLY:O	1:B:1284:ASN:C	2.33	0.67
2:C:38:U:O2'	2:C:39:A:C8	2.47	0.67
1:A:801:TYR:CE1	2:C:23:A:H1'	2.30	0.67
1:B:1193:ASP:CG	1:B:1211:THR:HG22	2.15	0.67
1:B:866:ARG:HE	1:B:866:ARG:N	1.90	0.67
1:B:917:CYS:SG	1:B:947:VAL:HG12	2.34	0.67
4:G:3:DC:H2'	4:G:4:DT:C6	2.28	0.67
1:A:932:GLN:OE1	1:A:932:GLN:HA	1.95	0.67
1:A:984:SER:HB2	1:A:989:GLU:CG	2.25	0.67
1:B:257:VAL:HG23	1:B:346:PHE:CD2	2.29	0.67
1:B:794:LEU:HD23	1:B:794:LEU:N	2.07	0.67
1:B:1138:ARG:HH11	1:B:1138:ARG:CG	2.07	0.67
1:A:396:ILE:O	1:A:400:ASN:ND2	2.28	0.67
1:A:1226:ARG:HA	1:A:1229:ARG:HG3	1.77	0.67
1:A:232:ILE:O	1:A:236:ASP:HB2	1.94	0.66
1:A:809:MSE:SE	1:A:810:ILE:HD13	2.44	0.66
1:A:975:LEU:HD23	1:A:975:LEU:C	2.16	0.66
1:B:159:THR:O	1:B:163:ILE:CG1	2.42	0.66
1:B:399:VAL:HG11	1:B:445:ARG:CG	2.25	0.66
1:B:801:TYR:O	1:B:807:TRP:CB	2.43	0.66
1:B:776:LYS:HD3	2:D:116:A:O2'	1.94	0.66
1:A:90:TYR:HH	1:A:346:PHE:HE1	1.42	0.66
1:A:730:LEU:HD23	1:A:734:VAL:HB	1.76	0.66
1:B:643:PRO:HG2	1:B:647:LYS:H	1.60	0.66
1:B:60:GLU:OE1	1:B:891:ARG:NH1	2.29	0.66
1:B:568:PHE:HE2	1:B:707:ARG:HG2	1.59	0.66
1:A:151:ARG:NH2	1:A:170:GLU:OE2	2.25	0.66
1:A:241:LEU:HD12	1:A:331:GLN:O	1.96	0.66
1:A:400:ASN:HD22	1:A:400:ASN:H	1.44	0.66
1:A:549:PHE:CE1	1:A:706:LEU:CD2	2.79	0.66
1:A:865:GLY:N	1:A:885:LEU:HD11	2.10	0.66
1:B:330:LEU:C	1:B:330:LEU:HD12	2.16	0.66
1:B:1073:LEU:HG	1:B:1077:TYR:CE2	2.31	0.66
2:D:54:C:O5'	2:D:54:C:H6	1.77	0.66
1:A:1281:LEU:O	1:A:1283:LYS:N	2.23	0.66
1:B:551:ARG:HH12	1:B:719:PHE:HE1	1.38	0.66
1:B:816:LEU:H	1:B:816:LEU:HD12	1.60	0.66
1:A:37:ARG:O	1:A:41:GLY:N	2.26	0.66
1:B:662:THR:HG22	1:B:665:VAL:HG23	1.77	0.66
1:B:258:ASP:OD1	1:B:258:ASP:N	2.28	0.66
1:B:857:ARG:O	1:B:859:PRO:HD3	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1031:ALA:HB3	3:F:11:DC:OP2	1.94	0.66
1:B:98:SER:OG	1:B:347:ILE:HD11	1.94	0.66
1:B:99:GLY:O	1:B:249:PHE:HD1	1.79	0.66
1:B:1160:LEU:HD22	1:B:1160:LEU:C	2.15	0.66
1:B:1175:ASN:O	1:B:1215:ALA:CB	2.43	0.66
1:A:294:THR:C	1:A:295:THR:HG23	2.16	0.66
1:B:1224:ILE:O	1:B:1228:VAL:CG2	2.38	0.66
2:D:25:G:H5''	2:D:25:G:C8	2.31	0.66
1:A:354:LEU:HD11	1:A:370:TYR:CE2	2.31	0.65
1:A:1004:ARG:HD2	1:A:1008:HIS:ND1	2.10	0.65
1:B:1070:SER:HB2	1:B:1073:LEU:CB	2.23	0.65
2:D:36:U:H3'	2:D:36:U:H6	1.62	0.65
1:B:632:TYR:CE2	1:B:633:PHE:CE1	2.83	0.65
1:B:1076:VAL:O	1:B:1080:VAL:HG23	1.97	0.65
1:B:1108:ILE:CG1	1:B:1132:LEU:CD2	2.74	0.65
1:B:1207:ARG:NE	1:B:1236:PRO:HG2	2.11	0.65
1:B:583:THR:O	1:B:584:ASP:C	2.33	0.65
1:B:1191:GLU:CG	1:B:1214:ILE:CB	2.73	0.65
1:B:707:ARG:CD	1:B:749:ILE:HD11	2.26	0.65
1:B:447:THR:HG21	1:B:464:ASP:HB2	1.78	0.65
1:B:565:VAL:N	1:B:566:PRO:HD3	2.12	0.65
1:B:1072:GLN:O	1:B:1076:VAL:CG1	2.44	0.65
1:A:444:VAL:HG22	1:A:471:PHE:HD2	1.60	0.65
1:A:706:LEU:CD1	1:A:748:TYR:CD2	2.80	0.65
1:A:1224:ILE:N	1:A:1224:ILE:CD1	2.59	0.65
1:B:1275:ARG:O	1:B:1279:THR:CG2	2.43	0.65
2:C:104:G:H2'	2:C:104:G:N3	2.12	0.65
1:A:397:GLU:HG3	1:A:397:GLU:O	1.96	0.65
1:B:788:ALA:HA	1:B:870:VAL:CG1	2.26	0.65
1:A:106:SER:CB	4:G:7:DT:OP1	2.45	0.65
1:A:669:LYS:O	1:A:672:THR:HG23	1.97	0.65
1:A:621:ASN:HB3	1:A:623:PHE:CE1	2.32	0.65
1:A:810:ILE:CG2	1:A:816:LEU:HD11	2.26	0.65
1:A:1000:ILE:HD11	1:A:1045:LYS:HG3	1.79	0.65
1:B:593:ARG:CB	1:B:641:TYR:HB2	2.27	0.65
1:A:730:LEU:HD13	1:A:730:LEU:O	1.97	0.64
1:A:990:THR:O	1:A:1275:ARG:NH2	2.30	0.64
1:A:1175:ASN:O	1:A:1215:ALA:HB2	1.98	0.64
1:B:52:LEU:HD21	1:B:948:PRO:CB	2.24	0.64
1:B:616:ASN:O	1:B:620:VAL:HG23	1.96	0.64
1:B:839:ASP:HB3	1:B:842:LEU:HD21	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:485:ILE:O	1:A:485:ILE:CG1	2.44	0.64
1:B:615:TYR:HD2	1:B:633:PHE:HD2	1.44	0.64
1:B:1004:ARG:NH2	1:B:1243:ASP:HA	2.12	0.64
2:D:4:A:H2'	2:D:5:A:O4'	1.97	0.64
1:A:463:GLN:N	1:A:463:GLN:OE1	2.30	0.64
1:A:471:PHE:CZ	1:A:475:LEU:HD23	2.32	0.64
1:B:140:PRO:HG3	1:B:231:MSE:CE	2.26	0.64
1:B:669:LYS:O	1:B:672:THR:HG23	1.97	0.64
1:A:564:THR:H	1:A:567:LYS:HE2	1.63	0.64
1:A:730:LEU:HD22	1:A:730:LEU:O	1.97	0.64
1:A:1162:THR:HG22	1:A:1163:GLU:OE1	1.97	0.64
1:B:1207:ARG:CZ	1:B:1236:PRO:HG3	2.28	0.64
1:B:1266:ASP:OD1	1:B:1266:ASP:N	2.26	0.64
2:C:1:G:O6	2:C:109:U:H5	1.80	0.64
1:A:680:GLU:HG3	1:A:683:LYS:HE3	1.79	0.64
1:A:1281:LEU:C	1:A:1283:LYS:N	2.49	0.64
1:B:1123:LYS:CE	1:B:1123:LYS:HA	2.28	0.64
1:A:27:SER:HA	1:A:1106:TRP:CD1	2.33	0.64
1:A:564:THR:CG2	1:A:567:LYS:HB2	2.27	0.64
1:A:1057:PRO:HD2	1:A:1136:PRO:O	1.97	0.64
1:B:228:VAL:CG1	1:B:232:ILE:HD12	2.28	0.64
1:A:1072:GLN:OE1	1:A:1072:GLN:HA	1.96	0.64
1:B:1003:ILE:HD13	1:B:1073:LEU:CD1	2.27	0.64
2:D:86:U:H6	2:D:86:U:O5'	1.80	0.64
1:A:112:PHE:CE2	1:A:250:THR:HG22	2.33	0.64
1:B:329:SER:HA	1:B:334:PHE:HB3	1.80	0.64
1:B:1073:LEU:HD11	1:B:1077:TYR:CZ	2.33	0.64
2:C:3:A:C2	2:C:4:A:C4	2.86	0.64
1:A:21:ARG:HH11	1:A:953:LEU:CB	2.00	0.64
1:A:550:GLU:O	1:A:553:ILE:HG13	1.97	0.64
1:B:595:LEU:HD13	1:B:595:LEU:C	2.16	0.64
1:B:686:ILE:HD12	1:B:686:ILE:H	1.59	0.64
2:C:124:C:N4	3:E:8:DG:H1	1.91	0.64
1:B:363:GLU:O	1:B:364:LYS:C	2.36	0.64
1:B:817:VAL:CG2	1:B:825:LEU:CD1	2.39	0.64
1:B:1221:LEU:O	1:B:1224:ILE:HB	1.98	0.64
1:A:546:ARG:HG3	1:A:546:ARG:HH21	1.63	0.63
1:A:865:GLY:N	1:A:885:LEU:CD1	2.60	0.63
1:A:295:THR:OG1	1:A:295:THR:O	2.16	0.63
1:A:817:VAL:HG21	1:A:828:PRO:HB2	1.79	0.63
1:B:59:LEU:HD13	1:B:890:PHE:HD2	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:SER:O	1:A:192:GLN:HB2	1.97	0.63
1:B:257:VAL:CB	1:B:258:ASP:OD1	2.46	0.63
1:B:666:VAL:O	1:B:670:PHE:N	2.24	0.63
1:B:1034:MSE:O	1:B:1038:VAL:HG23	1.98	0.63
1:B:1152:CYS:N	1:B:1256:CYS:SG	2.71	0.63
2:D:23:A:H3'	2:D:23:A:C8	2.32	0.63
1:A:812:ASP:OD1	1:A:812:ASP:N	2.31	0.63
1:B:162:ASN:O	1:B:166:VAL:HG13	1.97	0.63
1:B:448:LEU:O	1:B:448:LEU:HD12	1.99	0.63
4:H:3:DC:H2'	4:H:4:DT:C6	2.34	0.63
1:A:336:VAL:CG1	1:A:337:PRO:CD	2.67	0.63
1:B:28:ASP:OD2	1:B:1107:THR:HG23	1.99	0.63
1:B:242:PRO:HG3	1:B:331:GLN:HG2	1.80	0.63
1:B:440:LEU:N	1:B:440:LEU:HD23	2.14	0.63
1:B:677:ILE:HD12	1:B:694:PHE:CD1	2.33	0.63
1:A:805:ASP:OD1	1:A:805:ASP:N	2.29	0.63
1:B:707:ARG:NH1	1:B:749:ILE:CD1	2.61	0.63
1:B:836:ARG:CB	1:B:843:PHE:HE2	2.11	0.63
1:B:1279:THR:O	1:B:1282:ARG:CD	2.47	0.63
1:A:470:ALA:O	1:A:473:ASP:CB	2.47	0.63
1:B:286:VAL:O	1:B:290:GLN:CG	2.41	0.63
1:B:865:GLY:H	1:B:885:LEU:CD2	2.06	0.63
1:B:869:ASN:HB2	1:B:884:ALA:H	1.62	0.63
1:B:768:ARG:O	1:B:927:GLN:HG3	1.99	0.62
1:B:827:ALA:N	1:B:828:PRO:HD3	2.13	0.62
1:A:581:SER:HB3	1:A:586:ALA:HB3	1.81	0.62
1:B:44:ASP:OD1	1:B:44:ASP:N	2.27	0.62
1:A:260:GLU:HB2	1:A:263:VAL:HG22	1.80	0.62
1:A:1204:ARG:O	1:A:1205:LYS:CB	2.45	0.62
1:B:100:PHE:C	1:B:101:ARG:HD3	2.19	0.62
1:B:1018:GLN:H	1:B:1018:GLN:CD	2.01	0.62
1:B:1227:ARG:O	1:B:1231:ASN:ND2	2.32	0.62
1:A:398:LEU:CD1	1:A:514:LEU:HD22	2.30	0.62
1:A:1281:LEU:C	1:A:1283:LYS:H	2.00	0.62
1:B:973:ALA:HB2	1:B:1004:ARG:HH21	1.64	0.62
1:B:52:LEU:HD23	1:B:948:PRO:HB3	1.78	0.62
1:B:135:VAL:HG12	1:B:138:PHE:HB2	1.80	0.62
1:B:707:ARG:HD3	1:B:749:ILE:CD1	2.28	0.62
1:A:593:ARG:HB3	1:A:641:TYR:HB2	1.81	0.62
1:A:686:ILE:H	1:A:686:ILE:CD1	2.13	0.62
1:A:1056:PHE:CD1	1:A:1134:VAL:HG11	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:PHE:CE2	1:A:183:PHE:HE1	2.18	0.62
1:A:528:GLN:HE22	1:A:935:GLU:HA	1.65	0.62
1:A:599:ILE:HG22	1:A:700:LEU:HD22	1.80	0.62
1:A:990:THR:OG1	1:A:1275:ARG:NH2	2.33	0.62
1:B:1113:ILE:HG13	1:B:1281:LEU:HD23	1.80	0.62
1:A:472:SER:C	1:A:475:LEU:HD12	2.20	0.62
1:A:984:SER:HB2	1:A:989:GLU:HG3	1.81	0.62
1:B:102:ILE:CG2	1:B:295:THR:HG21	2.24	0.62
1:B:970:GLN:OE1	1:B:1077:TYR:CE1	2.52	0.62
1:A:563:GLU:HG2	1:A:567:LYS:CE	2.29	0.62
1:B:90:TYR:HE1	1:B:264:MSE:SE	2.33	0.62
1:B:993:ILE:HD13	1:B:993:ILE:N	2.14	0.62
1:B:1130:VAL:HG12	1:B:1131:PRO:HD3	1.80	0.62
1:B:995:VAL:CG1	1:B:1267:GLU:OE2	2.47	0.62
1:A:92:LEU:HD13	1:A:293:LEU:CD1	2.29	0.61
1:A:328:LYS:HB2	1:A:328:LYS:HZ3	1.63	0.61
1:B:708:ARG:HH11	1:B:708:ARG:CG	2.10	0.61
1:B:967:ALA:HA	1:B:1058:VAL:HG22	1.76	0.61
1:A:98:SER:O	1:A:98:SER:OG	2.15	0.61
1:A:472:SER:C	1:A:475:LEU:HD11	2.18	0.61
1:A:546:ARG:HH21	1:A:546:ARG:CG	2.13	0.61
1:A:1242:ARG:HD2	2:C:106:U:H5''	1.81	0.61
1:B:386:ALA:O	1:B:390:ASN:HB2	2.01	0.61
1:B:691:PHE:CE1	1:B:695:LEU:CD1	2.82	0.61
1:B:862:LYS:HB2	1:B:864:VAL:HG13	1.82	0.61
1:B:953:LEU:HD22	1:B:1101:TYR:HB3	1.80	0.61
1:A:165:ARG:HG2	1:A:165:ARG:NH1	2.13	0.61
1:A:596:LEU:HD11	1:A:623:PHE:HD2	1.64	0.61
1:B:336:VAL:CB	1:B:337:PRO:HD3	2.25	0.61
1:A:37:ARG:NH2	1:A:954:GLU:HB3	2.16	0.61
1:B:631:ARG:HA	1:B:635:ASN:HB2	1.83	0.61
2:C:99:G:H5''	2:C:99:G:H8	1.66	0.61
1:A:32:LYS:CD	1:A:36:ARG:NH1	2.63	0.61
1:A:461:ASN:O	1:A:465:ILE:HD12	1.99	0.61
1:A:691:PHE:CD1	1:A:695:LEU:HD11	2.34	0.61
1:B:168:ASN:HD22	1:B:173:ARG:HB2	1.65	0.61
2:D:83:C:O5'	2:D:83:C:H6	1.83	0.61
1:A:549:PHE:CD1	1:A:706:LEU:HD21	2.36	0.61
1:A:815:VAL:O	1:A:832:LYS:HG3	2.00	0.61
1:A:985:ILE:HG23	1:A:985:ILE:O	1.99	0.61
1:A:1227:ARG:O	1:A:1231:ASN:HB2	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:207:LYS:HD3	1:B:210:GLU:OE2	2.00	0.61
1:B:972:GLU:HG3	1:B:1007:ILE:CD1	2.30	0.61
1:B:1140:VAL:HG21	1:B:1273:ILE:HG22	1.82	0.61
1:A:90:TYR:OH	1:A:346:PHE:HE1	1.84	0.61
1:A:989:GLU:O	1:A:991:LYS:N	2.32	0.61
1:B:226:ASP:N	1:B:226:ASP:OD1	2.33	0.61
1:B:315:ALA:O	1:B:348:LYS:CE	2.38	0.61
1:A:545:GLN:HA	1:A:755:TYR:CE2	2.36	0.61
1:B:1058:VAL:HG23	1:B:1058:VAL:O	1.99	0.61
2:D:23:A:H5''	2:D:23:A:C8	2.32	0.61
1:A:52:LEU:HD23	1:A:948:PRO:HB3	1.81	0.61
1:A:83:ILE:HG21	1:A:520:LEU:HD13	1.82	0.61
1:A:966:LEU:CD1	1:A:1055:ALA:HB3	2.29	0.61
1:B:570:VAL:CG2	1:B:663:ILE:HG12	2.31	0.61
1:B:643:PRO:CB	1:B:644:PRO:CD	2.60	0.61
1:B:974:GLY:HA2	1:B:1000:ILE:CG1	2.30	0.61
1:B:1187:ILE:HB	1:B:1252:VAL:HB	1.83	0.61
1:B:8:LEU:O	1:B:8:LEU:HD23	2.01	0.61
1:B:768:ARG:O	1:B:927:GLN:CG	2.49	0.61
1:A:768:ARG:O	1:A:927:GLN:CG	2.49	0.60
1:A:866:ARG:NH2	1:A:869:ASN:HD21	1.99	0.60
1:A:1204:ARG:HB2	1:A:1206:GLU:HG3	1.83	0.60
1:A:1234:ARG:CD	1:A:1250:PHE:CE1	2.84	0.60
1:A:1234:ARG:N	1:A:1248:GLN:O	2.34	0.60
1:B:576:LYS:O	1:B:577:ILE:HD13	2.01	0.60
1:B:691:PHE:HE1	1:B:695:LEU:CD1	2.09	0.60
1:A:29:THR:HG22	1:A:1104:ASP:OD1	2.01	0.60
2:C:1:G:O6	2:C:109:U:C5	2.54	0.60
2:D:6:C:O5'	2:D:6:C:H6	1.83	0.60
2:D:23:A:C8	2:D:23:A:C3'	2.85	0.60
1:A:176:SER:HB2	1:A:179:SER:HB3	1.82	0.60
1:A:658:ASP:O	1:A:660:LYS:HE3	2.00	0.60
1:A:1114:VAL:HG22	1:A:1129:ILE:HG22	1.83	0.60
1:A:1159:TRP:CH2	1:A:1183:ALA:HB2	2.32	0.60
1:B:850:LEU:HD22	1:B:851:PRO:CD	2.28	0.60
2:C:63:C:C5'	2:C:63:C:H6	2.13	0.60
2:C:84:C:H42	2:C:102:G:H1	1.49	0.60
1:B:1156:VAL:HG23	1:B:1156:VAL:O	2.00	0.60
1:B:1251:CYS:HB3	1:B:1258:LEU:HB2	1.82	0.60
1:A:565:VAL:N	1:A:566:PRO:HD2	2.16	0.60
1:B:966:LEU:HD11	1:B:1049:LEU:HB3	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:ALA:HB3	1:A:184:ASP:HB2	1.83	0.60
1:A:319:SER:O	1:A:319:SER:OG	2.13	0.60
1:B:593:ARG:NH2	1:B:640:ILE:O	2.35	0.60
1:B:1235:ALA:HB3	1:B:1236:PRO:HD2	1.64	0.60
1:B:1237:LYS:CG	1:B:1238:SER:N	2.64	0.60
1:A:707:ARG:HD2	1:A:749:ILE:HG13	1.83	0.60
1:A:806:GLU:O	1:A:810:ILE:HD13	2.00	0.60
1:B:723:PRO:HB2	1:B:726:TYR:HD2	1.64	0.60
2:C:101:A:C8	2:C:101:A:C5'	2.85	0.60
1:A:483:ASN:ND2	1:A:483:ASN:H	1.98	0.60
1:B:966:LEU:O	1:B:1057:PRO:HA	2.01	0.60
1:B:1111:ILE:HD13	1:B:1111:ILE:N	2.14	0.60
1:B:1240:GLN:HG3	1:B:1240:GLN:O	2.02	0.60
2:D:25:G:C8	2:D:25:G:C5'	2.85	0.60
1:A:391:ARG:HH21	1:A:391:ARG:CG	2.14	0.60
1:A:841:ARG:HH21	1:A:841:ARG:CG	2.14	0.60
1:A:1081:ASN:ND2	1:A:1085:LEU:HD11	2.17	0.60
1:A:1207:ARG:HE	1:A:1236:PRO:CG	2.10	0.60
1:B:98:SER:CB	1:B:347:ILE:HD11	2.31	0.60
1:B:399:VAL:CG1	1:B:445:ARG:HG2	2.30	0.60
1:B:899:LYS:O	1:B:902:LEU:HB2	2.02	0.60
1:B:1050:MSE:O	1:B:1054:ASN:N	2.35	0.60
1:B:1130:VAL:HG12	1:B:1131:PRO:CD	2.31	0.60
1:A:966:LEU:HD12	1:A:1055:ALA:CB	2.29	0.60
1:A:1108:ILE:HG13	1:A:1132:LEU:HD21	1.79	0.60
1:B:1173:ASN:O	1:B:1174:VAL:CG1	2.48	0.60
1:B:1259:HIS:CD2	1:B:1260:PHE:CD1	2.90	0.60
1:A:1071:ARG:NE	1:A:1071:ARG:O	2.34	0.59
1:A:1277:PHE:HE2	1:A:1281:LEU:HD11	1.64	0.59
1:B:21:ARG:O	1:B:24:ALA:HB3	2.01	0.59
1:B:450:LYS:CB	1:B:460:PRO:HG3	2.32	0.59
1:A:106:SER:HB3	4:G:7:DT:OP1	2.02	0.59
1:A:915:ARG:HD2	1:A:950:ARG:HB2	1.84	0.59
1:B:328:LYS:HE3	1:B:344:LEU:CD2	2.32	0.59
1:B:1237:LYS:HG2	1:B:1238:SER:N	2.16	0.59
1:A:260:GLU:HG3	1:A:462:GLU:HG3	1.85	0.59
1:A:1004:ARG:O	1:A:1008:HIS:HB2	2.02	0.59
1:B:60:GLU:OE1	1:B:891:ARG:NE	2.35	0.59
1:B:447:THR:O	1:B:451:LEU:HD12	2.02	0.59
1:B:889:LEU:N	1:B:889:LEU:HD23	2.18	0.59
2:D:10:C:C6	2:D:10:C:C3'	2.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:ASP:OD2	1:A:1107:THR:CG2	2.48	0.59
1:A:102:ILE:HG12	1:A:295:THR:HG21	1.83	0.59
1:B:63:GLU:N	1:B:63:GLU:OE2	2.34	0.59
1:B:1110:GLY:O	1:B:1111:ILE:HD13	2.00	0.59
2:D:4:A:C5'	2:D:4:A:C8	2.85	0.59
1:A:436:LEU:CD2	1:A:440:LEU:HD22	2.33	0.59
1:A:786:ILE:CG2	1:A:870:VAL:HG21	2.33	0.59
1:B:468:PHE:CE1	1:B:514:LEU:HD12	2.37	0.59
2:D:61:G:C5'	2:D:61:G:C8	2.85	0.59
1:A:621:ASN:HB2	1:A:623:PHE:CE1	2.36	0.59
1:B:144:GLU:HG3	1:B:232:ILE:CG1	2.31	0.59
1:B:964:ASN:HB2	1:B:1055:ALA:HB2	1.85	0.59
2:C:38:U:C2'	2:C:39:A:C8	2.84	0.59
1:A:470:ALA:O	1:A:473:ASP:HB3	2.03	0.59
1:A:917:CYS:SG	1:A:947:VAL:HG12	2.43	0.59
1:B:551:ARG:NH1	1:B:719:PHE:CE1	2.64	0.59
1:B:589:GLU:O	1:B:593:ARG:HG3	2.03	0.59
1:B:1256:CYS:SG	1:B:1258:LEU:HD12	2.42	0.59
2:C:63:C:C5'	2:C:63:C:C6	2.86	0.59
1:A:32:LYS:CG	1:A:36:ARG:HH11	2.16	0.59
1:B:924:GLU:HG2	1:B:939:GLU:CB	2.33	0.59
1:B:565:VAL:CG2	1:B:708:ARG:HD3	2.25	0.59
2:C:10:C:C6	2:C:10:C:C3'	2.86	0.59
1:A:32:LYS:CD	1:A:36:ARG:HH11	2.16	0.59
1:A:61:VAL:HG21	1:A:67:LEU:HD11	1.83	0.59
1:A:70:PHE:O	1:A:74:SER:N	2.32	0.59
1:A:910:LEU:N	1:A:910:LEU:HD23	2.18	0.59
1:B:707:ARG:NH1	1:B:749:ILE:HD13	2.17	0.59
1:A:85:LYS:HA	1:A:90:TYR:CD2	2.38	0.58
1:A:444:VAL:CG2	1:A:471:PHE:CE2	2.67	0.58
1:A:608:ASP:CG	1:A:611:SER:OG	2.42	0.58
1:A:1220:SER:HB3	1:A:1223:GLU:CG	2.31	0.58
1:B:1191:GLU:HG2	1:B:1214:ILE:HG21	1.84	0.58
2:C:122:A:O2'	2:C:123:A:O4'	2.08	0.58
2:D:65:A:C8	2:D:65:A:H3'	2.38	0.58
1:A:578:ASN:ND2	1:A:578:ASN:O	2.36	0.58
1:A:636:CYS:O	1:A:637:GLN:CD	2.41	0.58
1:A:642:LYS:O	1:A:642:LYS:HD2	2.03	0.58
1:B:396:ILE:HG22	1:B:448:LEU:HG	1.82	0.58
1:B:432:HIS:HD2	1:B:435:GLU:CD	2.06	0.58
1:B:707:ARG:HD3	1:B:749:ILE:HD11	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1223:GLU:O	1:B:1227:ARG:CG	2.51	0.58
2:D:61:G:H8	2:D:61:G:O5'	1.86	0.58
2:D:101:A:H8	2:D:101:A:O5'	1.85	0.58
1:A:723:PRO:HB2	1:A:726:TYR:HD2	1.67	0.58
1:B:817:VAL:HG11	1:B:828:PRO:HB2	1.85	0.58
1:B:381:ILE:O	1:B:385:VAL:HG23	2.03	0.58
1:B:804:SER:O	1:B:808:LYS:HG3	2.04	0.58
1:B:947:VAL:HG23	1:B:947:VAL:O	2.01	0.58
1:A:398:LEU:HD13	1:A:514:LEU:CD2	2.34	0.58
1:B:270:ALA:HA	1:B:451:LEU:O	2.03	0.58
2:C:1:G:C6	2:C:109:U:C5	2.91	0.58
2:D:86:U:C5'	2:D:86:U:C6	2.85	0.58
1:A:28:ASP:CG	1:A:1107:THR:HG23	2.23	0.58
1:A:938:LEU:H	1:A:938:LEU:CD1	2.17	0.58
2:C:38:U:O5'	2:C:38:U:H6	1.87	0.58
2:D:36:U:H2'	2:D:37:U:H6	1.68	0.58
1:B:707:ARG:HD2	1:B:749:ILE:CD1	2.34	0.58
1:A:215:LEU:HD23	1:A:219:LEU:HD12	1.86	0.58
1:A:1149:CYS:SG	1:A:1152:CYS:N	2.74	0.58
1:B:238:ARG:CB	1:B:238:ARG:HH11	2.16	0.58
1:B:257:VAL:HG22	1:B:258:ASP:OD1	2.03	0.58
1:B:564:THR:HG23	1:B:566:PRO:HD2	1.84	0.58
1:B:623:PHE:N	1:B:623:PHE:CD1	2.72	0.58
1:B:1199:LYS:O	1:B:1203:ARG:HG3	2.04	0.58
1:A:1138:ARG:HH11	1:A:1138:ARG:CG	2.10	0.58
1:B:665:VAL:HG12	1:B:669:LYS:HD2	1.86	0.58
1:A:193:GLU:HB3	1:A:218:MSE:HE3	1.85	0.58
1:A:748:TYR:O	1:A:752:PHE:HB2	2.04	0.58
1:B:860:PHE:N	1:B:860:PHE:CD1	2.72	0.58
1:B:1237:LYS:CG	1:B:1238:SER:H	2.17	0.58
1:A:662:THR:HG23	1:A:665:VAL:H	1.69	0.57
1:A:1201:TYR:HD2	1:A:1208:THR:CA	2.12	0.57
1:B:807:TRP:CE3	1:B:810:ILE:HG13	2.39	0.57
1:A:804:SER:HB3	2:C:23:A:O3'	2.04	0.57
1:A:1016:LYS:CB	1:A:1028:ASP:OD2	2.52	0.57
1:B:330:LEU:HD12	1:B:330:LEU:O	2.04	0.57
1:B:608:ASP:OD2	1:B:690:GLU:HA	2.04	0.57
1:A:264:MSE:N	1:A:265:PRO:CD	2.66	0.57
1:A:296:THR:HG22	1:A:296:THR:O	2.02	0.57
1:A:827:ALA:N	1:A:828:PRO:CD	2.67	0.57
1:B:531:LEU:CD2	1:B:927:GLN:HE22	2.09	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:ILE:O	1:A:312:ILE:HG23	2.04	0.57
1:A:363:GLU:HB2	1:A:857:ARG:HH11	1.69	0.57
1:A:1187:ILE:HG13	1:A:1187:ILE:O	2.04	0.57
1:A:1246:GLN:OE1	1:A:1246:GLN:N	2.37	0.57
1:A:480:SER:HA	1:A:483:ASN:HD22	1.69	0.57
1:A:947:VAL:O	1:A:947:VAL:HG23	2.03	0.57
1:A:1225:GLU:O	1:A:1229:ARG:HG3	2.01	0.57
1:A:1233:ARG:NH1	1:A:1265:ALA:HB1	2.19	0.57
1:B:168:ASN:HD22	1:B:173:ARG:CB	2.17	0.57
1:B:1107:THR:CG2	1:B:1133:LYS:HG2	2.16	0.57
1:B:1250:PHE:N	1:B:1250:PHE:HD1	2.02	0.57
1:A:117:CYS:SG	1:A:235:SER:HA	2.44	0.57
1:B:76:ILE:CD1	1:B:359:LEU:HD11	2.20	0.57
1:B:707:ARG:HD2	1:B:749:ILE:HD11	1.85	0.57
1:B:1149:CYS:HA	1:B:1249:TYR:OH	2.04	0.57
2:C:100:A:H2'	2:C:101:A:H5''	1.87	0.57
1:B:296:THR:O	1:B:296:THR:HG22	2.04	0.57
1:B:827:ALA:O	1:B:830:LEU:HB3	2.05	0.57
1:B:836:ARG:C	1:B:836:ARG:HD3	2.24	0.57
1:B:1236:PRO:HB2	1:B:1238:SER:O	2.04	0.57
1:A:294:THR:CG2	1:A:378:ALA:HA	2.35	0.57
1:A:976:ALA:HB2	1:A:1266:ASP:HB2	1.87	0.57
1:B:328:LYS:HZ3	1:B:348:LYS:HG2	1.69	0.57
1:A:336:VAL:HG12	1:A:337:PRO:HD3	1.83	0.57
1:B:730:LEU:HD12	1:B:730:LEU:N	2.05	0.57
1:B:1115:THR:HG22	1:B:1130:VAL:HG23	1.84	0.57
1:B:1149:CYS:SG	1:B:1251:CYS:HB2	2.45	0.57
1:B:1223:GLU:O	1:B:1227:ARG:HG3	2.05	0.57
1:B:1264:GLN:HB2	1:B:1267:GLU:HG3	1.86	0.57
2:C:10:C:O5'	2:C:10:C:H6	1.87	0.57
1:A:760:ASN:O	1:A:764:ILE:HG13	2.05	0.57
1:A:1150:SER:H	1:A:1268:ASN:HD21	1.52	0.57
1:A:1235:ALA:HB1	1:A:1236:PRO:HD2	0.62	0.57
1:B:228:VAL:HA	1:B:231:MSE:HG3	1.87	0.57
1:B:518:ASN:OD1	1:B:518:ASN:N	2.24	0.57
1:B:686:ILE:H	1:B:686:ILE:CD1	2.17	0.57
1:B:786:ILE:CD1	1:B:872:GLU:HG3	2.34	0.57
1:A:438:GLU:HA	1:A:441:VAL:HG11	1.85	0.56
1:A:564:THR:HG22	1:A:566:PRO:CD	2.34	0.56
1:A:963:GLU:HB2	1:A:964:ASN:OD1	2.05	0.56
1:A:1221:LEU:HD12	1:A:1221:LEU:O	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:117:CYS:SG	1:B:234:ASP:CG	2.83	0.56
1:B:825:LEU:O	1:B:828:PRO:HD2	2.05	0.56
1:B:840:LEU:O	1:B:842:LEU:N	2.38	0.56
1:A:1264:GLN:HB2	1:A:1267:GLU:HG3	1.85	0.56
1:B:680:GLU:O	1:B:683:LYS:HG3	2.04	0.56
2:C:38:U:O2'	2:C:39:A:O5'	2.23	0.56
2:D:25:G:C5'	2:D:25:G:H8	2.18	0.56
2:D:41:C:H2'	2:D:42:C:C6	2.40	0.56
1:A:94:ALA:O	1:A:98:SER:HB3	2.05	0.56
1:A:596:LEU:HB3	1:A:640:ILE:HD13	1.87	0.56
1:A:623:PHE:N	1:A:623:PHE:CD1	2.72	0.56
1:A:1145:THR:O	1:A:1272:ASN:OD1	2.23	0.56
1:A:1223:GLU:O	1:A:1227:ARG:HG2	2.05	0.56
1:B:167:LEU:O	1:B:171:PHE:HD2	1.89	0.56
1:B:312:ILE:CG2	1:B:351:CYS:CB	2.82	0.56
1:B:631:ARG:HG2	1:B:653:PHE:HZ	1.69	0.56
1:B:868:LYS:HA	1:B:883:SER:HB2	1.87	0.56
1:A:599:ILE:HG23	1:A:700:LEU:HD21	1.86	0.56
1:A:831:LYS:O	1:A:835:GLU:HG3	2.05	0.56
1:B:126:GLN:NE2	1:B:224:PRO:HG2	2.20	0.56
1:B:154:ASN:N	1:B:154:ASN:HD22	2.03	0.56
1:B:966:LEU:HD11	1:B:1049:LEU:CB	2.36	0.56
1:B:1250:PHE:N	1:B:1250:PHE:CD1	2.74	0.56
1:A:48:GLU:HB3	1:A:954:GLU:HG3	1.87	0.56
1:A:63:GLU:HA	1:A:63:GLU:OE1	2.04	0.56
1:A:885:LEU:HB3	1:A:886:PRO:HD2	1.88	0.56
1:A:962:PHE:HD2	1:A:1056:PHE:HB3	1.70	0.56
1:B:564:THR:HG22	1:B:567:LYS:H	1.69	0.56
1:B:621:ASN:HB3	1:B:623:PHE:CE1	2.37	0.56
1:B:662:THR:OG1	1:B:663:ILE:N	2.36	0.56
1:B:1214:ILE:O	1:B:1214:ILE:CG2	2.53	0.56
1:A:227:SER:O	1:A:231:MSE:HG3	2.05	0.56
1:A:396:ILE:CA	1:A:448:LEU:CD1	2.80	0.56
1:B:257:VAL:CG2	1:B:258:ASP:OD1	2.54	0.56
2:D:52:U:C3'	2:D:53:G:C5'	2.81	0.56
1:A:354:LEU:HD11	1:A:370:TYR:CZ	2.41	0.56
1:B:112:PHE:CE1	1:B:250:THR:CG2	2.88	0.56
1:B:1258:LEU:HD22	1:B:1263:MSE:HB2	1.87	0.56
1:A:327:SER:C	1:A:329:SER:H	2.10	0.56
1:A:608:ASP:OD2	1:A:611:SER:OG	2.23	0.56
1:A:1111:ILE:HG21	1:A:1281:LEU:CD2	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:655:LEU:N	1:B:655:LEU:HD23	2.21	0.56
1:B:708:ARG:HG3	1:B:708:ARG:O	2.06	0.56
2:D:23:A:C5'	2:D:23:A:C8	2.85	0.56
1:A:667:TRP:O	1:A:671:GLU:HB2	2.06	0.56
1:A:851:PRO:HA	2:C:42:C:O3'	2.06	0.56
1:A:1041:ASP:N	1:A:1041:ASP:OD1	2.36	0.56
1:B:646:SER:O	1:B:646:SER:OG	2.21	0.56
1:B:1172:PHE:N	1:B:1172:PHE:HD1	2.04	0.56
1:B:1175:ASN:O	1:B:1215:ALA:HB2	2.06	0.56
1:A:263:VAL:HA	1:A:266:TYR:HD2	1.71	0.56
1:A:1146:SER:HB3	1:A:1233:ARG:HH22	1.70	0.56
1:A:1201:TYR:CE2	1:A:1208:THR:HA	2.40	0.56
1:B:257:VAL:HG23	1:B:346:PHE:CB	2.35	0.56
1:B:816:LEU:CA	1:B:829:THR:HG23	2.35	0.56
2:C:102:G:C8	2:C:102:G:C5'	2.88	0.56
1:A:8:LEU:HD21	1:A:1052:GLU:OE2	2.06	0.55
1:A:545:GLN:CG	1:A:755:TYR:HD2	2.19	0.55
1:A:548:ASP:OD1	1:A:551:ARG:NH1	2.39	0.55
1:A:604:ARG:HG3	1:A:604:ARG:O	2.05	0.55
1:A:621:ASN:CB	1:A:623:PHE:CE1	2.78	0.55
1:A:1224:ILE:N	1:A:1224:ILE:HD13	2.20	0.55
1:A:850:LEU:CD2	1:A:851:PRO:CD	2.80	0.55
1:A:1114:VAL:HG13	1:A:1127:GLU:HG3	1.88	0.55
1:B:1191:GLU:HG3	1:B:1214:ILE:HG12	1.88	0.55
2:D:63:C:C6	2:D:63:C:H5''	2.41	0.55
1:A:273:LEU:O	1:A:276:TYR:HB3	2.05	0.55
1:A:436:LEU:HD23	1:A:436:LEU:C	2.27	0.55
1:A:1000:ILE:HG22	1:A:1000:ILE:O	2.04	0.55
1:B:260:GLU:HB3	1:B:263:VAL:HG22	1.87	0.55
1:B:591:ALA:O	1:B:592:VAL:C	2.42	0.55
1:B:1073:LEU:CG	1:B:1077:TYR:CE2	2.90	0.55
2:D:2:G:C8	2:D:2:G:C5'	2.84	0.55
1:A:193:GLU:CB	1:A:218:MSE:CE	2.84	0.55
1:A:1005:ARG:NH2	2:C:50:G:O5'	2.38	0.55
1:A:564:THR:OG1	1:A:567:LYS:HD3	2.05	0.55
1:A:604:ARG:NH2	1:A:632:TYR:CE1	2.74	0.55
1:B:95:LEU:HD13	1:B:304:PHE:CZ	2.41	0.55
1:B:680:GLU:O	1:B:683:LYS:CG	2.54	0.55
1:B:1114:VAL:O	1:B:1114:VAL:HG12	2.06	0.55
2:C:25:G:C8	2:C:25:G:H5''	2.41	0.55
2:C:54:C:O5'	2:C:54:C:H6	1.90	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:623:PHE:HD1	1:A:623:PHE:H	1.54	0.55
1:B:257:VAL:HG22	1:B:346:PHE:HB2	1.85	0.55
1:B:744:THR:O	1:B:744:THR:OG1	2.15	0.55
1:B:980:PHE:CD1	1:B:992:PRO:CA	2.89	0.55
1:B:1159:TRP:CZ3	1:B:1183:ALA:HB3	2.35	0.55
1:A:567:LYS:HG2	1:A:571:ASP:OD1	2.07	0.55
1:A:786:ILE:HD13	1:A:872:GLU:HB2	1.87	0.55
1:A:1112:GLU:HB3	1:A:1131:PRO:HA	1.89	0.55
1:A:1132:LEU:HD13	1:A:1281:LEU:HD21	1.88	0.55
1:A:1201:TYR:CE2	1:A:1209:PRO:CG	2.89	0.55
1:A:1234:ARG:CD	1:A:1250:PHE:HE1	2.20	0.55
2:D:12:A:H2'	2:D:13:C:C6	2.41	0.55
1:A:49:LEU:HD21	1:A:1102:GLY:O	2.07	0.55
1:A:396:ILE:HG22	1:A:448:LEU:HB3	1.88	0.55
1:A:864:VAL:N	1:A:885:LEU:HD13	2.21	0.55
1:A:1222:GLU:O	1:A:1225:GLU:HB3	2.07	0.55
1:A:1280:ALA:C	1:A:1282:ARG:H	2.09	0.55
1:B:362:GLY:O	1:B:365:GLY:HA2	2.07	0.55
1:B:719:PHE:CD1	1:B:719:PHE:N	2.73	0.55
1:B:734:VAL:HG22	1:B:734:VAL:O	2.07	0.55
1:B:974:GLY:HA2	1:B:1000:ILE:HG13	1.88	0.55
1:B:167:LEU:O	1:B:171:PHE:CD2	2.60	0.55
1:B:565:VAL:CG1	1:B:566:PRO:CD	2.84	0.55
1:B:1060:GLU:HG2	1:B:1060:GLU:O	2.06	0.55
1:A:122:GLN:O	1:A:125:SER:HB2	2.07	0.54
1:A:193:GLU:CB	1:A:218:MSE:HE1	2.36	0.54
1:A:1056:PHE:HB2	1:A:1136:PRO:O	2.07	0.54
1:A:1071:ARG:NH2	2:C:124:C:O2'	2.40	0.54
1:A:1159:TRP:CH2	1:A:1183:ALA:CB	2.89	0.54
1:A:1242:ARG:NH1	2:C:106:U:C4'	2.60	0.54
1:B:98:SER:HB3	1:B:347:ILE:HD11	1.89	0.54
1:B:799:ASN:HA	1:B:802:TRP:CZ3	2.42	0.54
1:B:806:GLU:O	1:B:810:ILE:HG12	2.07	0.54
1:B:1269:ALA:O	1:B:1273:ILE:CG1	2.50	0.54
1:A:547:ILE:O	1:A:551:ARG:CD	2.55	0.54
1:B:1117:GLU:O	1:B:1125:GLY:CA	2.53	0.54
2:C:110:A:H8	2:C:110:A:H5''	1.73	0.54
2:D:64:G:H8	2:D:64:G:O5'	1.89	0.54
1:A:82:THR:O	1:A:87:SER:CB	2.55	0.54
1:B:257:VAL:CG2	1:B:346:PHE:CD2	2.89	0.54
1:A:730:LEU:CD2	1:A:731:PRO:O	2.54	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1235:ALA:CB	1:A:1236:PRO:CD	2.20	0.54
1:B:295:THR:O	1:B:295:THR:OG1	2.20	0.54
1:B:553:ILE:O	1:B:556:ALA:N	2.41	0.54
1:B:628:ASP:HB3	1:B:653:PHE:CE1	2.42	0.54
1:B:568:PHE:CD1	1:B:572:ALA:HB2	2.41	0.54
1:B:727:TYR:CD2	1:B:758:PHE:CE2	2.63	0.54
2:D:37:U:C6	2:D:37:U:H5''	2.43	0.54
1:A:128:LYS:O	1:A:132:GLY:N	2.40	0.54
1:A:565:VAL:HB	1:A:566:PRO:CD	2.34	0.54
1:A:924:GLU:HG2	1:A:939:GLU:HB3	1.89	0.54
1:A:1221:LEU:HD12	1:A:1221:LEU:C	2.28	0.54
1:B:945:ILE:HG23	1:B:945:ILE:O	2.07	0.54
1:A:806:GLU:O	1:A:809:MSE:HB3	2.07	0.54
1:B:479:GLY:HA2	1:B:482:ARG:HD3	1.89	0.54
1:B:967:ALA:HA	1:B:1058:VAL:HG21	1.81	0.54
1:A:469:TYR:O	1:A:472:SER:CB	2.55	0.54
1:A:1240:GLN:NE2	2:C:104:G:H21	2.06	0.54
1:A:1251:CYS:O	1:A:1256:CYS:SG	2.64	0.54
1:B:727:TYR:HB2	1:B:758:PHE:CE2	2.43	0.54
1:B:786:ILE:HD11	1:B:857:ARG:HE	1.71	0.54
1:B:980:PHE:HE1	1:B:992:PRO:CB	2.18	0.54
1:B:987:GLU:OE2	1:B:987:GLU:N	2.35	0.54
1:B:1106:TRP:O	1:B:1134:VAL:HG22	2.08	0.54
2:C:85:U:O2	2:C:85:U:H2'	2.07	0.54
2:D:23:A:C8	2:D:23:A:C4'	2.91	0.54
1:A:334:PHE:CE2	1:A:341:LEU:HD12	2.42	0.54
1:A:736:PHE:N	1:A:736:PHE:CD1	2.73	0.54
1:A:1004:ARG:HD2	1:A:1008:HIS:CE1	2.43	0.54
1:A:1035:ARG:NH1	3:E:11:DC:OP1	2.41	0.54
1:A:1242:ARG:NH1	2:C:106:U:O3'	2.41	0.54
1:B:396:ILE:HA	1:B:448:LEU:CD2	2.31	0.54
1:B:984:SER:O	1:B:984:SER:OG	2.22	0.54
1:B:1172:PHE:N	1:B:1172:PHE:CD1	2.72	0.54
2:C:37:U:H6	2:C:37:U:H5''	1.69	0.54
2:C:63:C:C6	2:C:63:C:H5''	2.43	0.54
1:A:90:TYR:CE1	1:A:264:MSE:SE	3.11	0.54
1:A:90:TYR:HE1	1:A:264:MSE:SE	2.40	0.54
1:A:100:PHE:O	1:A:101:ARG:CD	2.55	0.54
1:B:394:GLU:O	1:B:398:LEU:HB2	2.08	0.54
1:B:815:VAL:HG11	1:B:836:ARG:HG2	1.90	0.54
1:A:32:LYS:HD3	1:A:36:ARG:HH12	1.71	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:623:PHE:N	1:A:623:PHE:HD1	2.06	0.53
1:B:193:GLU:OE2	1:B:196:ARG:NH2	2.39	0.53
1:B:1003:ILE:HD12	1:B:1077:TYR:OH	2.08	0.53
1:A:29:THR:O	1:A:32:LYS:HB3	2.09	0.53
1:B:538:VAL:CG1	1:B:759:LEU:CD1	2.86	0.53
1:A:841:ARG:HH21	1:A:841:ARG:HG2	1.73	0.53
1:A:945:ILE:HG23	1:A:945:ILE:O	2.06	0.53
1:A:1269:ALA:O	1:A:1273:ILE:CG1	2.56	0.53
2:C:103:G:H8	2:C:103:G:O5'	1.91	0.53
1:A:138:PHE:CE2	1:A:183:PHE:CE1	2.95	0.53
1:A:200:SER:O	1:A:204:VAL:HG23	2.09	0.53
1:A:294:THR:O	1:A:295:THR:HG23	2.09	0.53
1:A:608:ASP:OD1	1:A:611:SER:N	2.35	0.53
1:A:1226:ARG:NH1	1:A:1226:ARG:H	2.05	0.53
1:B:53:LYS:HB3	2:D:114:C:H5''	1.90	0.53
1:B:149:LYS:HG2	1:B:150:GLY:N	2.24	0.53
1:B:787:TYR:O	1:B:787:TYR:HD1	1.92	0.53
1:A:871:ILE:CD1	1:A:906:PHE:CZ	2.86	0.53
1:B:867:GLU:O	1:B:883:SER:HB2	2.08	0.53
1:B:1193:ASP:CB	1:B:1211:THR:HG22	2.39	0.53
1:A:259:ILE:HG22	1:A:264:MSE:HG2	1.89	0.53
1:A:1172:PHE:O	1:A:1218:SER:HA	2.08	0.53
1:B:72:ARG:HH11	1:B:359:LEU:HD23	1.74	0.53
1:B:187:LEU:O	1:B:191:SER:OG	2.23	0.53
1:B:842:LEU:N	1:B:842:LEU:CD1	2.72	0.53
1:B:975:LEU:HD21	1:B:998:ILE:HD13	1.90	0.53
1:B:1108:ILE:HG13	1:B:1132:LEU:CD2	2.38	0.53
2:C:123:A:H8	2:C:123:A:O5'	1.91	0.53
2:D:55:C:OP2	2:D:55:C:H6	1.91	0.53
1:A:23:ILE:HA	1:A:26:LEU:HD12	1.90	0.53
1:A:89:SER:O	1:A:93:PHE:CD2	2.62	0.53
1:A:450:LYS:HB3	1:A:460:PRO:HG3	1.91	0.53
1:A:810:ILE:HD13	1:A:810:ILE:N	2.24	0.53
1:A:1086:TYR:CD1	1:A:1086:TYR:C	2.82	0.53
1:A:1112:GLU:CB	1:A:1130:VAL:O	2.38	0.53
1:B:718:ALA:HB1	1:B:748:TYR:CE1	2.44	0.53
1:A:71:ASP:N	1:A:71:ASP:OD1	2.41	0.53
1:A:462:GLU:HA	1:A:465:ILE:HD13	1.91	0.53
1:A:690:GLU:OE1	1:A:690:GLU:N	2.40	0.53
1:B:294:THR:HG21	1:B:382:ASP:OD1	2.09	0.53
1:B:809:MSE:C	1:B:809:MSE:SE	2.98	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:816:LEU:HD12	1:B:816:LEU:N	2.22	0.53
1:B:1196:LYS:CB	1:B:1201:TYR:CE2	2.92	0.53
1:A:1079:ALA:O	1:A:1082:SER:HB2	2.08	0.53
1:B:468:PHE:CE2	1:B:517:LEU:HD13	2.44	0.53
1:B:804:SER:OG	1:B:807:TRP:HB2	2.09	0.53
1:B:1191:GLU:HG3	1:B:1214:ILE:CG1	2.39	0.53
2:D:62:C:C6	2:D:62:C:H5''	2.44	0.53
1:A:932:GLN:HG3	1:A:932:GLN:O	2.08	0.52
1:B:107:SER:O	1:B:111:THR:HG23	2.10	0.52
1:B:680:GLU:HG3	1:B:683:LYS:HE3	1.90	0.52
1:A:112:PHE:HE2	1:A:250:THR:HG22	1.74	0.52
1:A:545:GLN:HA	1:A:755:TYR:CD2	2.44	0.52
1:A:641:TYR:CD1	1:A:641:TYR:C	2.83	0.52
1:A:984:SER:HB2	1:A:989:GLU:HG2	1.92	0.52
1:B:60:GLU:O	1:B:60:GLU:HG2	2.08	0.52
1:B:431:SER:O	1:B:431:SER:OG	2.22	0.52
1:B:440:LEU:N	1:B:440:LEU:CD2	2.72	0.52
1:B:669:LYS:C	1:B:672:THR:HG22	2.30	0.52
1:B:784:LYS:HG2	1:B:874:ASN:OD1	2.08	0.52
2:C:88:C:C6	2:C:88:C:C4'	2.92	0.52
1:A:398:LEU:HD12	1:A:514:LEU:HD22	1.91	0.52
1:A:1240:GLN:HG3	1:A:1240:GLN:O	2.10	0.52
1:B:173:ARG:HG3	1:B:183:PHE:HE2	1.70	0.52
1:B:706:LEU:N	1:B:706:LEU:CD2	2.73	0.52
1:A:313:ARG:NH1	1:A:354:LEU:O	2.42	0.52
1:A:391:ARG:NH2	1:A:391:ARG:HG2	2.25	0.52
1:B:396:ILE:HD12	1:B:397:GLU:N	2.23	0.52
1:A:562:LEU:HD13	1:A:562:LEU:N	2.24	0.52
1:B:21:ARG:HH12	1:B:912:LYS:HZ2	1.57	0.52
1:B:665:VAL:O	1:B:668:GLU:CG	2.49	0.52
1:B:708:ARG:HG3	1:B:708:ARG:NH1	2.21	0.52
1:B:1180:LEU:HD13	1:B:1181:THR:H	1.74	0.52
1:A:793:ARG:O	1:A:793:ARG:HG3	2.07	0.52
1:A:994:ALA:C	1:A:995:VAL:HG23	2.30	0.52
1:A:1149:CYS:SG	1:A:1150:SER:N	2.82	0.52
1:B:471:PHE:O	1:B:474:VAL:HB	2.10	0.52
1:B:706:LEU:N	1:B:706:LEU:HD23	2.25	0.52
1:B:1060:GLU:CB	1:B:1142:ALA:HB2	2.38	0.52
1:A:851:PRO:HG3	2:C:42:C:C5'	2.40	0.52
1:A:911:ASP:OD1	1:A:911:ASP:O	2.27	0.52
1:A:993:ILE:N	1:A:993:ILE:CD1	2.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:60:GLU:HB2	1:B:893:ILE:HD11	1.92	0.52
1:B:99:GLY:O	1:B:249:PHE:CD1	2.61	0.52
1:B:126:GLN:HE22	1:B:224:PRO:HG2	1.73	0.52
1:B:327:SER:O	1:B:330:LEU:HB3	2.09	0.52
1:A:565:VAL:CB	1:A:566:PRO:CD	2.88	0.52
1:A:615:TYR:HD1	1:A:633:PHE:CD2	2.28	0.52
1:A:976:ALA:CB	1:A:1266:ASP:HB2	2.40	0.52
1:A:979:VAL:O	1:A:993:ILE:N	2.41	0.52
1:A:1150:SER:HB3	1:A:1268:ASN:HD22	1.74	0.52
1:B:117:CYS:SG	1:B:234:ASP:OD2	2.68	0.52
1:B:806:GLU:OE1	1:B:845:PRO:CB	2.58	0.52
4:G:9:DC:H2''	4:G:10:DA:C8	2.45	0.52
1:A:126:GLN:NE2	1:A:130:ILE:HD11	2.24	0.52
1:A:469:TYR:O	1:A:472:SER:N	2.42	0.52
1:A:478:LEU:N	1:A:478:LEU:CD1	2.73	0.52
1:A:1182:THR:HG21	1:A:1187:ILE:HG23	1.92	0.52
1:B:198:PHE:C	1:B:200:SER:H	2.13	0.52
1:A:144:GLU:HG3	1:A:232:ILE:HD13	1.92	0.52
1:A:298:GLY:O	1:A:374:ARG:HD2	2.10	0.52
1:A:1269:ALA:O	1:A:1273:ILE:HG13	2.10	0.52
1:B:269:ILE:CG2	1:B:388:TYR:HE2	2.20	0.52
1:B:565:VAL:HB	1:B:708:ARG:NE	2.13	0.52
1:B:867:GLU:O	1:B:883:SER:CB	2.58	0.52
1:B:993:ILE:N	1:B:993:ILE:CD1	2.72	0.52
1:A:142:GLU:O	1:A:146:ILE:HG13	2.10	0.51
1:A:545:GLN:CG	1:A:755:TYR:CD2	2.93	0.51
1:B:98:SER:OG	1:B:98:SER:O	2.18	0.51
1:B:228:VAL:O	1:B:231:MSE:N	2.43	0.51
1:B:328:LYS:O	1:B:329:SER:C	2.47	0.51
1:B:810:ILE:HG21	1:B:846:LEU:HD12	1.92	0.51
1:B:1071:ARG:O	1:B:1074:SER:HB3	2.10	0.51
1:B:1173:ASN:ND2	1:B:1173:ASN:C	2.63	0.51
2:C:64:G:O5'	2:C:64:G:H8	1.92	0.51
1:A:546:ARG:CG	1:A:546:ARG:NH2	2.73	0.51
1:A:1090:PRO:HD2	3:E:14:DT:OP1	2.09	0.51
1:B:126:GLN:CG	1:B:225:PHE:HE1	2.20	0.51
1:B:257:VAL:HG23	1:B:346:PHE:CG	2.43	0.51
1:B:329:SER:OG	1:B:330:LEU:N	2.43	0.51
1:B:665:VAL:C	1:B:668:GLU:HG3	2.31	0.51
1:B:686:ILE:N	1:B:686:ILE:CD1	2.73	0.51
1:B:1207:ARG:HD2	1:B:1236:PRO:CG	2.33	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:36:U:C3'	2:D:36:U:C6	2.92	0.51
1:A:152:ARG:HD2	4:G:8:DG:H4'	1.92	0.51
1:A:257:VAL:HB	1:A:346:PHE:HB2	1.91	0.51
1:A:341:LEU:HD23	1:A:341:LEU:C	2.30	0.51
1:A:438:GLU:O	1:A:441:VAL:HG13	2.10	0.51
1:A:440:LEU:HD21	1:A:471:PHE:HA	1.92	0.51
1:A:543:HIS:O	1:A:543:HIS:HD2	1.92	0.51
1:A:720:PHE:CD1	1:A:755:TYR:HE1	2.28	0.51
1:A:801:TYR:HA	2:C:23:A:O2'	2.10	0.51
1:A:998:ILE:HG21	1:A:1045:LYS:HD2	1.92	0.51
1:A:1029:SER:O	1:A:1033:ILE:HG13	2.10	0.51
1:A:1164:LYS:O	1:A:1164:LYS:HD2	2.10	0.51
1:B:102:ILE:CG2	1:B:295:THR:HG22	2.30	0.51
1:B:337:PRO:C	1:B:339:ASP:H	2.13	0.51
1:B:1033:ILE:O	1:B:1036:GLU:HB2	2.09	0.51
1:B:1210:LEU:CD1	1:B:1210:LEU:N	2.73	0.51
4:G:6:DG:C2'	4:G:7:DT:C5'	2.59	0.51
1:B:306:LYS:HB2	1:B:371:GLN:OE1	2.10	0.51
1:B:471:PHE:CE1	1:B:475:LEU:HB2	2.45	0.51
1:B:1086:TYR:CD1	1:B:1086:TYR:C	2.84	0.51
1:A:359:LEU:O	1:A:860:PHE:HD1	1.91	0.51
1:A:565:VAL:CB	1:A:566:PRO:HD3	2.37	0.51
1:A:1159:TRP:CE3	1:A:1159:TRP:HA	2.45	0.51
1:B:80:LEU:HD12	1:B:88:LEU:HD22	1.93	0.51
2:D:65:A:C8	2:D:65:A:C3'	2.93	0.51
2:D:107:U:C2'	2:D:108:A:H5''	2.41	0.51
1:A:441:VAL:O	1:A:444:VAL:HB	2.11	0.51
1:A:543:HIS:C	1:A:543:HIS:CD2	2.84	0.51
1:A:584:ASP:O	1:A:588:LYS:CD	2.50	0.51
1:B:60:GLU:OE1	1:B:891:ARG:CZ	2.58	0.51
1:B:546:ARG:O	1:B:549:PHE:N	2.43	0.51
1:B:1193:ASP:HB2	1:B:1211:THR:HG22	1.92	0.51
1:B:1204:ARG:HA	2:D:84:C:H4'	1.93	0.51
2:C:28:G:H8	2:C:28:G:O5'	1.93	0.51
1:A:810:ILE:CD1	1:A:810:ILE:N	2.73	0.51
1:B:548:ASP:OD1	1:B:721:SER:OG	2.28	0.51
1:B:690:GLU:OE1	1:B:690:GLU:N	2.39	0.51
2:D:62:C:O2	2:D:62:C:H2'	2.10	0.51
1:A:555:TRP:CZ2	1:A:714:PRO:CD	2.94	0.51
1:A:819:ASP:HB2	1:A:823:ASN:O	2.11	0.51
1:B:238:ARG:HB3	1:B:238:ARG:HH11	1.73	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:396:ILE:HG22	1:B:448:LEU:CD1	2.35	0.51
1:B:714:PRO:O	1:B:717:ILE:HB	2.10	0.51
1:B:1046:ILE:CG2	1:B:1084:PHE:CE2	2.84	0.51
2:D:62:C:H4'	2:D:62:C:OP1	2.11	0.51
1:A:1250:PHE:HD2	1:A:1262:GLY:CA	2.17	0.51
1:B:145:SER:O	1:B:149:LYS:N	2.43	0.51
1:B:228:VAL:O	1:B:231:MSE:HG3	2.11	0.51
1:B:471:PHE:C	1:B:471:PHE:CD1	2.83	0.51
1:B:1060:GLU:HB2	1:B:1142:ALA:CB	2.38	0.51
1:B:1207:ARG:CZ	1:B:1236:PRO:CG	2.88	0.51
2:C:22:G:N2	2:C:41:C:C2	2.79	0.51
2:D:122:A:H2'	2:D:123:A:C8	2.46	0.51
1:A:193:GLU:HB2	1:A:218:MSE:HE1	1.93	0.51
1:A:266:TYR:CE1	1:A:517:LEU:HD23	2.46	0.51
1:A:558:ASN:N	1:A:558:ASN:OD1	2.42	0.51
1:A:1234:ARG:CG	1:A:1250:PHE:HE1	2.24	0.51
1:A:1234:ARG:HG3	1:A:1250:PHE:HE1	1.76	0.51
1:B:1221:LEU:O	1:B:1221:LEU:HG	2.11	0.51
1:A:19:TYR:O	1:A:23:ILE:HG13	2.11	0.50
1:A:20:ARG:HD2	1:A:1099:LEU:CD1	2.41	0.50
1:A:858:ASN:HB3	1:A:861:VAL:HG12	1.93	0.50
1:B:785:LEU:CD1	1:B:902:LEU:HD22	2.41	0.50
1:B:787:TYR:CD1	1:B:787:TYR:C	2.83	0.50
2:C:110:A:H5''	2:C:110:A:C8	2.46	0.50
1:A:433:SER:O	1:A:436:LEU:N	2.44	0.50
1:A:1266:ASP:O	1:A:1270:ALA:HB2	2.11	0.50
1:B:817:VAL:CG1	1:B:828:PRO:HB2	2.41	0.50
1:A:433:SER:OG	1:A:478:LEU:HD11	2.10	0.50
1:A:766:LEU:HD22	1:A:934:VAL:HG21	1.92	0.50
1:B:216:ASP:CG	1:B:227:SER:HA	2.31	0.50
1:B:744:THR:CA	1:B:747:GLU:OE2	2.46	0.50
1:A:743:ILE:O	1:A:743:ILE:HG13	2.10	0.50
1:A:1210:LEU:N	1:A:1210:LEU:CD1	2.74	0.50
1:B:17:ARG:NH1	2:D:20:A:OP1	2.45	0.50
1:B:59:LEU:CD2	1:B:892:LEU:CD1	2.87	0.50
1:B:976:ALA:CB	1:B:1266:ASP:HB2	2.37	0.50
2:D:37:U:O2	2:D:37:U:H2'	2.10	0.50
1:A:60:GLU:HG2	1:A:60:GLU:O	2.12	0.50
1:A:288:TYR:O	1:A:292:HIS:ND1	2.41	0.50
1:B:135:VAL:CG1	1:B:138:PHE:HB2	2.40	0.50
1:B:1201:TYR:CE1	1:B:1209:PRO:CD	2.90	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1251:CYS:O	1:B:1259:HIS:HA	2.11	0.50
2:D:11:G:O5'	2:D:11:G:H8	1.94	0.50
1:A:130:ILE:HD12	1:A:225:PHE:CZ	2.47	0.50
1:A:597:GLU:HG3	1:A:641:TYR:HB3	1.93	0.50
1:A:1253:TYR:N	1:A:1253:TYR:CD1	2.80	0.50
1:A:82:THR:O	1:A:87:SER:HB2	2.11	0.50
1:A:102:ILE:CG2	1:A:295:THR:CG2	2.90	0.50
1:A:144:GLU:OE1	1:A:232:ILE:HG23	2.11	0.50
1:A:625:ALA:O	1:A:628:ASP:HB2	2.11	0.50
1:B:1163:GLU:HA	1:B:1166:ALA:HB2	1.93	0.50
1:A:267:MSE:HE2	1:A:267:MSE:HA	1.93	0.50
1:B:599:ILE:HG13	1:B:600:GLY:N	2.26	0.50
1:B:674:TYR:CD1	1:B:674:TYR:C	2.85	0.50
1:B:1073:LEU:CG	1:B:1077:TYR:HE2	2.25	0.50
1:A:585:PHE:O	1:A:585:PHE:HD1	1.95	0.50
1:A:785:LEU:HD12	1:A:902:LEU:HD22	1.93	0.50
1:A:1150:SER:H	1:A:1268:ASN:ND2	2.09	0.50
1:B:585:PHE:HA	1:B:588:LYS:CB	2.41	0.50
1:B:810:ILE:CG2	1:B:846:LEU:HD12	2.42	0.50
2:C:37:U:O2	2:C:37:U:H2'	2.12	0.50
1:A:1152:CYS:SG	1:A:1251:CYS:SG	3.10	0.49
1:B:819:ASP:HB2	1:B:823:ASN:O	2.12	0.49
1:B:915:ARG:HB2	1:B:948:PRO:HB2	1.94	0.49
1:B:1006:LEU:CD2	1:B:1076:VAL:HG11	2.42	0.49
1:A:144:GLU:HG3	1:A:232:ILE:CD1	2.42	0.49
1:A:864:VAL:HG23	1:A:885:LEU:HD11	1.93	0.49
1:B:97:LEU:HD11	1:B:267:MSE:CB	2.40	0.49
1:B:972:GLU:HG3	1:B:1007:ILE:HD11	1.94	0.49
2:C:80:G:C8	2:C:80:G:C5'	2.86	0.49
1:A:139:ILE:HB	1:A:140:PRO:HD2	1.94	0.49
1:A:432:HIS:CD2	1:A:432:HIS:C	2.85	0.49
1:A:759:LEU:HD12	1:A:759:LEU:C	2.27	0.49
1:B:336:VAL:HG13	1:B:337:PRO:HD3	0.64	0.49
1:B:400:ASN:N	1:B:400:ASN:ND2	2.59	0.49
2:D:54:C:H2'	2:D:55:C:OP2	2.12	0.49
1:A:364:LYS:O	1:A:364:LYS:HG3	2.13	0.49
1:A:733:ASN:O	1:A:736:PHE:CZ	2.65	0.49
1:A:1084:PHE:N	1:A:1084:PHE:CD1	2.80	0.49
1:B:655:LEU:HD23	1:B:655:LEU:H	1.78	0.49
1:B:707:ARG:NH1	1:B:749:ILE:HD12	2.26	0.49
1:A:76:ILE:O	1:A:79:ALA:HB3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:693:THR:O	1:A:696:HIS:HB2	2.13	0.49
1:A:966:LEU:O	1:A:1057:PRO:HA	2.13	0.49
1:A:975:LEU:HD23	1:A:998:ILE:HG13	1.87	0.49
1:B:288:TYR:CD1	1:B:288:TYR:C	2.85	0.49
1:B:918:MSE:HE1	2:D:116:A:HI'	1.93	0.49
2:D:20:A:H61	2:D:42:C:H42	1.61	0.49
1:A:149:LYS:HG3	1:A:150:GLY:N	2.28	0.49
1:A:1173:ASN:HD21	1:A:1181:THR:HG23	1.78	0.49
1:A:1174:VAL:HG22	1:A:1180:LEU:HD22	1.94	0.49
1:B:139:ILE:O	1:B:143:LEU:HG	2.12	0.49
1:B:836:ARG:CG	1:B:843:PHE:HE2	2.17	0.49
2:D:5:A:C2	2:D:106:U:O2	2.65	0.49
1:A:84:GLU:O	1:A:87:SER:OG	2.22	0.49
1:A:990:THR:HG1	1:A:1275:ARG:NH2	2.11	0.49
1:A:1256:CYS:SG	1:A:1259:HIS:N	2.85	0.49
1:B:568:PHE:CE2	1:B:707:ARG:CG	2.95	0.49
1:B:807:TRP:CZ3	1:B:810:ILE:HG21	2.47	0.49
1:B:967:ALA:CA	1:B:1058:VAL:CG2	2.66	0.49
1:A:537:SER:O	1:A:541:ILE:HG13	2.13	0.49
1:B:257:VAL:C	1:B:258:ASP:OD1	2.50	0.49
1:B:584:ASP:O	1:B:588:LYS:CB	2.61	0.49
1:B:593:ARG:HD3	1:B:641:TYR:HA	1.95	0.49
1:B:807:TRP:HZ3	1:B:810:ILE:HG21	1.77	0.49
1:B:975:LEU:HD22	1:B:1000:ILE:HD11	1.95	0.49
2:C:99:G:H5''	2:C:99:G:C8	2.46	0.49
1:A:37:ARG:NH2	1:A:48:GLU:OE1	2.44	0.49
1:A:215:LEU:CD2	1:A:219:LEU:HD12	2.43	0.49
1:A:829:THR:HG22	1:A:829:THR:O	2.10	0.49
1:A:1107:THR:HG22	1:A:1133:LYS:CG	2.29	0.49
1:B:478:LEU:O	1:B:481:ILE:HB	2.13	0.49
1:B:964:ASN:HD22	1:B:981:SER:HA	1.76	0.49
2:C:38:U:H2'	2:C:39:A:H8	1.70	0.49
1:A:1267:GLU:O	1:A:1270:ALA:HB3	2.12	0.49
1:B:98:SER:OG	1:B:347:ILE:CD1	2.61	0.49
1:B:583:THR:HG23	1:B:587:ALA:CB	2.42	0.49
1:B:952:HIS:H	1:B:952:HIS:CD2	2.31	0.49
1:B:1173:ASN:HD22	1:B:1174:VAL:N	2.11	0.49
2:C:78:C:C6	2:C:78:C:C3'	2.96	0.49
1:A:584:ASP:HB3	1:A:588:LYS:HD2	1.94	0.48
1:B:61:VAL:O	1:B:61:VAL:HG13	2.13	0.48
1:B:329:SER:HB2	1:B:334:PHE:CD1	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:703:LYS:CE	1:B:753:ASN:HD21	2.14	0.48
1:B:1251:CYS:O	1:B:1259:HIS:ND1	2.38	0.48
1:A:59:LEU:HD21	1:A:892:LEU:CD1	2.42	0.48
1:A:249:PHE:CD1	1:A:249:PHE:C	2.86	0.48
1:A:552:VAL:HG22	1:A:717:ILE:CG2	2.42	0.48
1:B:44:ASP:HB2	1:B:47:GLN:CB	2.43	0.48
1:B:149:LYS:HG2	1:B:150:GLY:H	1.77	0.48
1:B:400:ASN:N	1:B:400:ASN:HD22	2.10	0.48
1:B:479:GLY:C	1:B:482:ARG:HG2	2.29	0.48
1:B:805:ASP:N	1:B:805:ASP:OD1	2.46	0.48
1:B:807:TRP:O	1:B:810:ILE:HB	2.13	0.48
1:A:441:VAL:HG21	1:A:445:ARG:NH1	2.26	0.48
1:A:595:LEU:HD21	1:A:667:TRP:HE3	1.77	0.48
1:A:719:PHE:CD1	1:A:719:PHE:N	2.73	0.48
1:A:719:PHE:CE1	1:A:721:SER:HB3	2.49	0.48
1:B:140:PRO:HB3	1:B:231:MSE:HE2	1.81	0.48
2:D:22:G:H22	2:D:40:U:H3	1.61	0.48
2:D:63:C:O2	2:D:63:C:H2'	2.14	0.48
1:A:152:ARG:NH2	4:G:8:DG:O4'	2.46	0.48
1:A:250:THR:OG1	1:A:253:ALA:CB	2.59	0.48
1:A:398:LEU:HD13	1:A:514:LEU:HD22	1.92	0.48
1:A:604:ARG:NH2	1:A:632:TYR:HE1	2.10	0.48
1:A:615:TYR:HB2	1:A:633:PHE:CE2	2.49	0.48
1:A:1174:VAL:HG22	1:A:1180:LEU:CD2	2.43	0.48
1:A:1233:ARG:HA	1:A:1248:GLN:O	2.14	0.48
1:B:536:GLU:OE1	1:B:540:GLN:CG	2.61	0.48
1:B:570:VAL:HG23	1:B:663:ILE:HG12	1.95	0.48
1:B:772:TYR:CD1	1:B:772:TYR:C	2.85	0.48
1:B:786:ILE:HD12	1:B:872:GLU:HG3	1.95	0.48
1:B:789:ALA:HA	1:B:852:HIS:HA	1.95	0.48
1:B:1073:LEU:HG	1:B:1077:TYR:HE2	1.76	0.48
1:A:60:GLU:CD	1:A:891:ARG:HH11	2.16	0.48
1:B:190:PHE:CE1	1:B:214:LEU:HD22	2.48	0.48
1:B:531:LEU:CD2	1:B:927:GLN:NE2	2.73	0.48
1:B:852:HIS:ND1	1:B:852:HIS:O	2.47	0.48
1:A:255:ILE:HG22	1:A:257:VAL:HG13	1.95	0.48
1:A:674:TYR:CD1	1:A:674:TYR:C	2.86	0.48
1:A:1232:LEU:HD22	1:A:1249:TYR:CE2	2.48	0.48
1:A:1249:TYR:CD1	1:A:1249:TYR:C	2.85	0.48
1:B:334:PHE:CD1	1:B:334:PHE:C	2.85	0.48
1:B:871:ILE:O	1:B:871:ILE:HG12	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1046:ILE:O	1:B:1050:MSE:HG3	2.14	0.48
1:B:1160:LEU:O	1:B:1164:LYS:CB	2.61	0.48
1:B:1277:PHE:O	1:B:1280:ALA:HB3	2.13	0.48
2:C:28:G:C5'	2:C:28:G:C8	2.96	0.48
2:C:62:C:C6	2:C:62:C:C4'	2.97	0.48
2:D:7:U:H6	2:D:7:U:O5'	1.95	0.48
1:A:78:ASN:OD1	1:A:523:GLY:CA	2.62	0.48
1:A:294:THR:OG1	1:A:382:ASP:OD1	2.32	0.48
1:A:555:TRP:CZ2	1:A:714:PRO:HD3	2.48	0.48
1:A:1138:ARG:CG	1:A:1138:ARG:NH1	2.71	0.48
1:B:266:TYR:CD1	1:B:266:TYR:N	2.81	0.48
1:B:906:PHE:C	1:B:906:PHE:CD1	2.86	0.48
2:C:101:A:H8	2:C:101:A:C5'	2.12	0.48
2:D:14:U:C2	2:D:53:G:N3	2.82	0.48
1:A:76:ILE:CD1	1:A:359:LEU:HD11	2.29	0.48
1:A:482:ARG:O	1:A:486:GLU:HG3	2.14	0.48
1:A:565:VAL:N	1:A:566:PRO:CD	2.76	0.48
1:B:870:VAL:O	1:B:882:ALA:O	2.32	0.48
1:B:1175:ASN:OD1	1:B:1179:GLU:O	2.32	0.48
1:A:168:ASN:HD22	1:A:173:ARG:HB3	1.79	0.48
1:B:158:TRP:CE3	1:B:163:ILE:HD11	2.48	0.48
1:B:608:ASP:HB2	1:B:690:GLU:HG3	1.96	0.48
1:B:754:LEU:HD13	1:B:758:PHE:CZ	2.49	0.48
2:D:86:U:C6	2:D:86:U:C3'	2.97	0.48
1:B:867:GLU:O	1:B:883:SER:OG	2.30	0.48
1:B:978:ALA:CB	1:B:1271:ILE:HD13	2.44	0.48
1:B:1210:LEU:N	1:B:1210:LEU:HD12	2.29	0.48
2:C:88:C:C6	2:C:88:C:C5'	2.85	0.48
1:A:656:ARG:HE	1:A:658:ASP:HB3	1.79	0.47
1:B:88:LEU:HD12	1:B:88:LEU:HA	1.56	0.47
1:B:708:ARG:CG	1:B:708:ARG:NH1	2.72	0.47
1:B:915:ARG:NH1	3:F:19:DC:OP2	2.47	0.47
1:B:1050:MSE:HE3	1:B:1057:PRO:HD3	1.96	0.47
1:B:1073:LEU:HD11	1:B:1077:TYR:OH	2.14	0.47
1:B:1231:ASN:O	1:B:1234:ARG:NE	2.45	0.47
1:A:329:SER:HB2	1:A:334:PHE:CE1	2.49	0.47
1:A:578:ASN:C	1:A:578:ASN:HD22	2.16	0.47
1:B:126:GLN:HG2	1:B:225:PHE:HE1	1.69	0.47
1:B:514:LEU:HA	1:B:515:PRO:HD3	1.75	0.47
1:B:582:SER:O	1:B:582:SER:OG	2.24	0.47
1:B:844:TYR:HB2	1:B:845:PRO:HD3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:38:U:C2'	2:C:39:A:H8	2.25	0.47
3:F:11:DC:H2''	3:F:12:DG:H8	1.79	0.47
1:A:11:ILE:HD13	1:A:1051:LYS:HD3	1.95	0.47
1:A:61:VAL:HA	1:A:890:PHE:CD1	2.50	0.47
1:A:436:LEU:O	1:A:440:LEU:HB3	2.13	0.47
1:B:632:TYR:HE2	1:B:633:PHE:HE1	1.61	0.47
1:B:681:ILE:HG22	1:B:681:ILE:O	2.13	0.47
1:B:1207:ARG:NE	1:B:1236:PRO:CG	2.76	0.47
1:A:67:LEU:HA	1:A:68:PRO:HD3	1.58	0.47
1:A:171:PHE:HD2	1:A:187:LEU:HD11	1.79	0.47
1:A:469:TYR:O	1:A:472:SER:HB3	2.14	0.47
1:B:24:ALA:O	1:B:27:SER:OG	2.21	0.47
1:B:580:GLU:HG3	1:B:582:SER:H	1.78	0.47
2:C:84:C:H5''	2:C:84:C:C6	2.40	0.47
2:D:86:U:C6	2:D:86:U:C4'	2.97	0.47
1:A:863:SER:C	1:A:885:LEU:HD13	2.35	0.47
1:A:1200:PHE:O	1:A:1203:ARG:N	2.46	0.47
1:B:227:SER:OG	1:B:230:LYS:HB2	2.14	0.47
1:B:733:ASN:HB3	1:B:750:THR:HG21	1.96	0.47
1:B:827:ALA:O	1:B:830:LEU:CB	2.63	0.47
1:B:49:LEU:CD1	1:B:953:LEU:CD1	2.74	0.47
1:B:112:PHE:CE1	1:B:250:THR:HG22	2.50	0.47
1:B:167:LEU:HD23	1:B:167:LEU:HA	1.64	0.47
1:B:296:THR:O	1:B:297:ASN:HB2	2.13	0.47
1:B:312:ILE:HG21	1:B:351:CYS:CB	2.45	0.47
1:B:756:SER:OG	1:B:757:SER:N	2.48	0.47
1:B:858:ASN:HB3	1:B:861:VAL:HG12	1.97	0.47
1:B:1204:ARG:HG2	2:D:84:C:O2'	2.14	0.47
1:A:20:ARG:HD2	1:A:1099:LEU:HD12	1.96	0.47
1:A:359:LEU:C	1:A:359:LEU:HD12	2.35	0.47
1:A:437:PHE:O	1:A:441:VAL:N	2.48	0.47
1:A:766:LEU:CD2	1:A:934:VAL:HG21	2.45	0.47
1:A:915:ARG:NH1	3:E:19:DC:OP1	2.48	0.47
1:A:975:LEU:HD22	1:A:998:ILE:CG1	2.37	0.47
1:A:1119:LYS:HD3	1:A:1119:LYS:O	2.13	0.47
1:A:1150:SER:N	1:A:1268:ASN:HD21	2.11	0.47
1:A:1201:TYR:CD2	1:A:1208:THR:CA	2.85	0.47
1:B:44:ASP:HB2	1:B:47:GLN:HB3	1.97	0.47
1:B:238:ARG:NH1	1:B:238:ARG:CB	2.73	0.47
1:B:843:PHE:N	1:B:843:PHE:CD1	2.82	0.47
2:C:63:C:H6	2:C:63:C:O5'	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:438:GLU:C	1:A:441:VAL:HG12	2.34	0.47
1:A:477:ARG:NH1	1:A:477:ARG:CG	2.73	0.47
1:A:1257:ALA:O	1:A:1261:SER:HB2	2.15	0.47
1:B:314:LYS:H	1:B:314:LYS:HG2	1.40	0.47
1:B:528:GLN:NE2	1:B:936:ALA:H	2.13	0.47
1:B:577:ILE:HD13	1:B:577:ILE:HA	1.56	0.47
1:B:780:VAL:HG23	1:B:780:VAL:O	2.13	0.47
1:A:471:PHE:CD1	1:A:471:PHE:C	2.86	0.47
1:A:540:GLN:O	1:A:544:TYR:HD1	1.98	0.47
1:B:827:ALA:HB3	1:B:828:PRO:HD3	1.96	0.47
1:B:1035:ARG:HE	1:B:1072:GLN:HE22	1.63	0.47
1:A:549:PHE:CE1	1:A:706:LEU:HD21	2.49	0.47
1:A:643:PRO:O	1:A:646:SER:OG	2.21	0.47
1:A:866:ARG:HE	1:A:866:ARG:H	1.63	0.47
1:A:968:ILE:HD12	1:A:1046:ILE:HG12	1.96	0.47
1:A:1073:LEU:O	1:A:1073:LEU:HD22	2.15	0.47
1:B:67:LEU:HA	1:B:68:PRO:HD3	1.53	0.47
1:B:658:ASP:C	1:B:658:ASP:OD1	2.53	0.47
1:B:1189:LEU:N	1:B:1189:LEU:HD23	2.30	0.47
2:C:20:A:H61	2:C:42:C:H42	1.62	0.47
4:G:10:DA:H2''	4:G:11:DA:O5'	2.14	0.47
1:A:734:VAL:O	1:A:734:VAL:HG12	2.15	0.46
1:B:36:ARG:O	1:B:36:ARG:HG2	2.13	0.46
1:B:714:PRO:HB2	1:B:717:ILE:HB	1.96	0.46
2:C:83:C:H42	2:C:103:G:H1	1.63	0.46
2:D:59:A:H8	2:D:59:A:O5'	1.98	0.46
1:A:228:VAL:HA	1:A:231:MSE:HG3	1.98	0.46
1:A:391:ARG:HH12	2:C:120:C:H4'	1.81	0.46
1:A:438:GLU:CA	1:A:441:VAL:CG1	2.81	0.46
1:A:612:LYS:O	1:A:615:TYR:HB3	2.15	0.46
1:B:396:ILE:CG2	1:B:448:LEU:CD2	2.77	0.46
2:C:61:G:H3'	2:C:61:G:C8	2.50	0.46
1:A:78:ASN:OD1	1:A:523:GLY:HA3	2.15	0.46
1:A:97:LEU:HD12	1:A:97:LEU:HA	1.62	0.46
1:A:152:ARG:HG2	3:E:22:DT:H5'	1.98	0.46
1:A:723:PRO:HB2	1:A:726:TYR:CE2	2.50	0.46
1:B:9:HIS:HD2	2:D:109:U:N3	2.13	0.46
1:B:468:PHE:HE2	1:B:517:LEU:HD13	1.80	0.46
1:B:723:PRO:CB	1:B:726:TYR:CD2	2.92	0.46
1:B:1148:THR:HG23	1:B:1154:ARG:O	2.16	0.46
2:C:28:G:O5'	2:C:28:G:C8	2.68	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:88:C:C6	2:C:88:C:C3'	2.98	0.46
2:D:61:G:C8	2:D:61:G:H5''	2.50	0.46
1:A:258:ASP:O	1:A:259:ILE:HD12	2.15	0.46
1:A:450:LYS:HG2	1:A:455:ASP:HB3	1.97	0.46
1:A:665:VAL:HA	1:A:668:GLU:OE2	2.16	0.46
1:A:1119:LYS:HE2	1:A:1119:LYS:HA	1.96	0.46
1:A:1173:ASN:HD21	1:A:1181:THR:CG2	2.28	0.46
1:A:1270:ALA:O	1:A:1273:ILE:HB	2.16	0.46
1:B:338:ASP:HA	1:B:341:LEU:HB2	1.98	0.46
1:B:787:TYR:CZ	1:B:852:HIS:HB3	2.51	0.46
1:B:809:MSE:SE	1:B:810:ILE:HD13	2.64	0.46
1:B:1119:LYS:HE2	1:B:1120:GLU:OE1	2.16	0.46
2:C:78:C:H3'	2:C:78:C:H6	1.79	0.46
1:A:139:ILE:HG13	1:A:142:GLU:HB2	1.98	0.46
1:A:438:GLU:O	1:A:441:VAL:CG1	2.63	0.46
1:A:593:ARG:HD3	1:A:640:ILE:O	2.14	0.46
1:A:730:LEU:HD21	1:A:734:VAL:O	2.14	0.46
1:A:776:LYS:O	1:A:776:LYS:HD2	2.16	0.46
1:A:1201:TYR:HD1	1:A:1201:TYR:HA	1.64	0.46
1:B:158:TRP:HE3	1:B:201:TRP:CD1	2.33	0.46
1:B:219:LEU:HD23	1:B:225:PHE:CD2	2.51	0.46
1:B:871:ILE:CD1	1:B:906:PHE:CZ	2.96	0.46
1:B:1190:PHE:HA	1:B:1213:PRO:HA	1.97	0.46
2:D:64:G:C8	2:D:64:G:H3'	2.51	0.46
4:H:10:DA:H2''	4:H:11:DA:O5'	2.15	0.46
1:A:471:PHE:O	1:A:475:LEU:CG	2.59	0.46
1:B:54:THR:HG21	2:D:115:A:H1'	1.98	0.46
1:B:328:LYS:NZ	1:B:348:LYS:CG	2.78	0.46
1:B:336:VAL:CG1	1:B:337:PRO:CD	2.48	0.46
1:B:844:TYR:N	1:B:845:PRO:CD	2.79	0.46
1:B:952:HIS:CD2	1:B:952:HIS:N	2.82	0.46
1:A:126:GLN:HB3	1:A:225:PHE:CE1	2.51	0.46
1:A:469:TYR:O	1:A:473:ASP:N	2.48	0.46
1:A:482:ARG:HD2	1:A:509:LYS:O	2.15	0.46
1:A:686:ILE:N	1:A:686:ILE:CD1	2.73	0.46
1:A:756:SER:OG	1:A:757:SER:N	2.48	0.46
1:B:16:SER:O	1:B:20:ARG:HG3	2.16	0.46
1:B:329:SER:CB	1:B:334:PHE:CG	2.94	0.46
1:B:662:THR:HG22	1:B:665:VAL:CG2	2.45	0.46
1:B:691:PHE:CE1	1:B:695:LEU:CG	2.98	0.46
1:B:1193:ASP:CG	1:B:1211:THR:CG2	2.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1234:ARG:N	1:B:1248:GLN:O	2.43	0.46
1:B:1278:LEU:HD23	1:B:1281:LEU:HD12	1.97	0.46
2:C:62:C:C6	2:C:62:C:C5'	2.85	0.46
1:A:681:ILE:HD13	1:A:681:ILE:HA	1.75	0.46
1:A:855:CYS:HB3	1:A:890:PHE:O	2.16	0.46
1:A:1219:TYR:CB	1:A:1224:ILE:HD11	2.46	0.46
1:B:112:PHE:CZ	1:B:250:THR:CG2	2.98	0.46
1:B:112:PHE:HE1	1:B:250:THR:CG2	2.29	0.46
1:B:259:ILE:O	1:B:264:MSE:HE3	2.16	0.46
1:B:371:GLN:O	1:B:374:ARG:CG	2.55	0.46
1:B:568:PHE:CD1	1:B:568:PHE:C	2.88	0.46
1:B:625:ALA:O	1:B:629:LEU:HB2	2.16	0.46
1:B:760:ASN:O	1:B:764:ILE:HG13	2.14	0.46
4:G:2:DT:H2'	4:G:3:DC:C6	2.51	0.46
1:A:72:ARG:NE	1:A:75:GLN:OE1	2.48	0.46
1:A:661:ASP:OD2	1:A:669:LYS:HE3	2.16	0.46
1:A:730:LEU:CD1	1:A:730:LEU:N	2.72	0.46
1:A:787:TYR:O	1:A:870:VAL:HB	2.15	0.46
1:B:123:PHE:CD1	1:B:123:PHE:C	2.88	0.46
1:B:157:ASP:HB2	1:B:162:ASN:HD22	1.81	0.46
1:B:1157:PHE:CD1	1:B:1157:PHE:O	2.69	0.46
1:B:1279:THR:OG1	1:B:1280:ALA:N	2.49	0.46
2:C:28:G:N3	2:C:28:G:H2'	2.31	0.46
2:C:87:C:O2	2:C:87:C:H2'	2.16	0.46
2:D:22:G:C5'	2:D:22:G:H8	2.27	0.46
1:A:106:SER:OG	4:G:7:DT:OP1	2.30	0.46
1:A:131:PHE:CE2	1:A:183:PHE:HA	2.51	0.46
1:A:1226:ARG:NH1	1:A:1226:ARG:CB	2.73	0.46
1:B:98:SER:HG	1:B:347:ILE:HD11	1.79	0.46
2:D:65:A:H3'	2:D:65:A:H8	1.79	0.46
1:A:131:PHE:CD2	1:A:183:PHE:HB2	2.50	0.45
1:A:214:LEU:C	1:A:214:LEU:CD2	2.85	0.45
1:A:867:GLU:O	1:A:883:SER:HB2	2.17	0.45
1:A:1056:PHE:CD1	1:A:1056:PHE:O	2.70	0.45
1:B:552:VAL:O	1:B:556:ALA:N	2.49	0.45
1:B:666:VAL:O	1:B:669:LYS:N	2.49	0.45
1:B:786:ILE:CG2	1:B:889:LEU:CD1	2.76	0.45
1:B:801:TYR:CD1	2:D:23:A:H1'	2.51	0.45
1:A:91:LEU:HD21	1:A:309:LEU:CD1	2.46	0.45
1:A:982:LEU:HD12	1:A:982:LEU:HA	1.57	0.45
1:A:1050:MSE:HE2	1:A:1050:MSE:HB3	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1207:ARG:CD	1:A:1236:PRO:CG	2.82	0.45
1:B:97:LEU:HD11	1:B:268:ALA:N	2.31	0.45
1:B:345:LYS:O	1:B:349:GLU:HG3	2.15	0.45
2:C:3:A:C8	2:C:3:A:O5'	2.69	0.45
1:A:112:PHE:HE2	1:A:250:THR:CG2	2.29	0.45
1:A:334:PHE:C	1:A:334:PHE:CD1	2.85	0.45
1:A:334:PHE:HE2	1:A:341:LEU:HD12	1.82	0.45
1:A:899:LYS:O	1:A:902:LEU:HB2	2.17	0.45
1:B:727:TYR:C	1:B:727:TYR:CD1	2.86	0.45
1:B:1196:LYS:CB	1:B:1201:TYR:CZ	3.00	0.45
1:A:49:LEU:HD13	1:A:953:LEU:HD11	1.98	0.45
1:A:1004:ARG:CD	1:A:1008:HIS:ND1	2.78	0.45
1:A:1224:ILE:HD13	1:A:1224:ILE:H	1.80	0.45
1:B:707:ARG:CD	1:B:749:ILE:HD12	2.45	0.45
1:B:1005:ARG:O	1:B:1009:SER:HB3	2.16	0.45
1:B:1206:GLU:O	1:B:1207:ARG:HG2	2.17	0.45
2:C:64:G:O5'	2:C:64:G:C8	2.70	0.45
2:D:36:U:H3'	2:D:36:U:C6	2.46	0.45
1:A:186:PHE:HE1	1:A:218:MSE:CB	2.29	0.45
1:A:471:PHE:O	1:A:471:PHE:CD1	2.70	0.45
1:A:543:HIS:O	1:A:543:HIS:CD2	2.69	0.45
1:B:432:HIS:O	1:B:432:HIS:CD2	2.69	0.45
1:B:447:THR:HG22	1:B:464:ASP:HB2	1.98	0.45
1:B:565:VAL:CA	1:B:708:ARG:HD3	2.30	0.45
1:B:693:THR:O	1:B:696:HIS:HB2	2.16	0.45
2:C:28:G:H22	2:C:34:U:H3	1.64	0.45
1:A:277:ARG:NH1	1:A:454:ILE:HA	2.32	0.45
1:A:528:GLN:HE21	1:A:936:ALA:H	1.63	0.45
1:A:817:VAL:HG13	1:A:832:LYS:HE3	1.98	0.45
1:A:1280:ALA:C	1:A:1282:ARG:N	2.70	0.45
1:B:139:ILE:HB	1:B:140:PRO:CD	2.43	0.45
1:B:328:LYS:HE3	1:B:344:LEU:HD21	1.98	0.45
1:B:399:VAL:HG12	1:B:445:ARG:HE	1.81	0.45
1:B:674:TYR:CD1	1:B:674:TYR:O	2.70	0.45
1:B:720:PHE:HE2	1:B:754:LEU:HB2	1.81	0.45
1:B:1089:GLU:HA	1:B:1090:PRO:HD3	1.82	0.45
1:B:1135:PHE:CD1	1:B:1135:PHE:N	2.84	0.45
2:C:35:C:C5	2:C:35:C:OP2	2.70	0.45
2:C:64:G:C8	2:C:64:G:OP2	2.69	0.45
3:E:11:DC:H2''	3:E:12:DG:H8	1.81	0.45
1:A:594:PHE:CD1	1:A:641:TYR:CE2	2.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:808:LYS:O	1:A:812:ASP:OD1	2.33	0.45
1:A:835:GLU:O	1:A:837:GLU:OE1	2.34	0.45
1:B:830:LEU:HD23	1:B:869:ASN:O	2.17	0.45
1:B:896:ALA:N	1:B:897:PRO:HD2	2.31	0.45
1:A:556:ALA:O	1:A:560:HIS:N	2.50	0.45
1:A:742:GLU:O	1:A:744:THR:HG23	2.17	0.45
1:A:868:LYS:HD2	1:A:868:LYS:HA	1.73	0.45
1:A:1233:ARG:NH1	1:A:1265:ALA:CB	2.79	0.45
3:F:25:DA:H2''	3:F:26:DC:H5'	1.99	0.45
1:A:681:ILE:HG13	1:A:694:PHE:CG	2.52	0.45
1:B:123:PHE:CD1	1:B:123:PHE:O	2.70	0.45
1:B:722:LEU:HA	1:B:723:PRO:HD3	1.57	0.45
1:B:756:SER:O	1:B:760:ASN:HB2	2.17	0.45
1:B:804:SER:HB3	2:D:23:A:H4'	1.99	0.45
2:D:2:G:C8	2:D:2:G:OP1	2.70	0.45
4:G:10:DA:C8	4:G:10:DA:O5'	2.70	0.45
1:A:291:SER:HB2	1:A:292:HIS:HD1	1.81	0.45
1:A:304:PHE:CD1	1:A:304:PHE:O	2.70	0.45
1:A:391:ARG:O	1:A:395:LEU:N	2.46	0.45
1:A:674:TYR:CD1	1:A:674:TYR:O	2.70	0.45
1:A:963:GLU:O	1:A:982:LEU:CB	2.58	0.45
1:B:83:ILE:HD13	1:B:520:LEU:HB2	1.99	0.45
1:B:97:LEU:HD11	1:B:267:MSE:C	2.38	0.45
1:B:173:ARG:HG2	1:B:183:PHE:CE2	2.45	0.45
1:B:470:ALA:O	1:B:473:ASP:HB2	2.16	0.45
1:B:558:ASN:OD1	1:B:558:ASN:N	2.48	0.45
1:B:563:GLU:HB3	1:B:710:GLN:HG2	1.99	0.45
1:B:825:LEU:HB2	1:B:828:PRO:HG2	1.98	0.45
1:B:911:ASP:OD2	1:B:912:LYS:HG3	2.16	0.45
1:B:1138:ARG:CG	1:B:1138:ARG:NH1	2.72	0.45
2:C:64:G:H8	2:C:64:G:P	2.40	0.45
2:D:3:A:C8	2:D:3:A:OP2	2.70	0.45
1:A:441:VAL:HG23	1:A:445:ARG:HH11	1.67	0.44
1:A:461:ASN:O	1:A:464:ASP:HB2	2.18	0.44
1:A:1173:ASN:OD1	1:A:1181:THR:HG23	2.16	0.44
1:A:1177:LYS:H	1:A:1177:LYS:HG3	1.58	0.44
1:A:1232:LEU:HD22	1:A:1249:TYR:HE2	1.82	0.44
1:A:1232:LEU:HD12	1:A:1233:ARG:HG2	1.99	0.44
1:B:259:ILE:HD12	1:B:259:ILE:HA	1.72	0.44
1:B:309:LEU:O	1:B:312:ILE:HG22	2.16	0.44
1:B:691:PHE:CE1	1:B:695:LEU:HG	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:727:TYR:CD1	1:B:727:TYR:O	2.70	0.44
1:B:1133:LYS:O	1:B:1138:ARG:NE	2.46	0.44
2:D:11:G:N1	2:D:12:A:C6	2.85	0.44
1:A:151:ARG:CG	1:A:151:ARG:NH1	2.72	0.44
1:A:681:ILE:HD12	1:A:681:ILE:HG23	1.71	0.44
1:A:840:LEU:HD22	1:A:840:LEU:HA	1.83	0.44
1:A:841:ARG:CG	1:A:841:ARG:NH2	2.75	0.44
1:A:1073:LEU:HD22	1:A:1077:TYR:CE2	2.52	0.44
1:A:1204:ARG:NE	2:C:85:U:OP1	2.50	0.44
1:B:357:ALA:O	1:B:367:LEU:HD13	2.17	0.44
1:B:392:LEU:O	1:B:395:LEU:HB2	2.17	0.44
1:B:817:VAL:HG11	1:B:828:PRO:CB	2.47	0.44
1:B:1259:HIS:CD2	1:B:1260:PHE:HE1	2.29	0.44
2:D:2:G:C8	2:D:2:G:C4'	3.00	0.44
2:D:64:G:O5'	2:D:64:G:C8	2.70	0.44
1:A:90:TYR:OH	1:A:346:PHE:CE1	2.62	0.44
1:A:518:ASN:OD1	1:A:518:ASN:N	2.49	0.44
1:A:547:ILE:O	1:A:551:ARG:HG3	2.17	0.44
1:A:804:SER:CB	2:C:23:A:H4'	2.48	0.44
1:A:966:LEU:HD23	1:A:968:ILE:HD11	1.99	0.44
1:A:1212:LYS:HA	1:A:1213:PRO:HD3	1.60	0.44
1:B:511:LEU:N	1:B:511:LEU:CD1	2.73	0.44
1:B:844:TYR:CB	1:B:845:PRO:HD3	2.47	0.44
1:B:1181:THR:O	1:B:1181:THR:OG1	2.33	0.44
2:C:104:G:C2	2:C:105:U:C2	3.05	0.44
2:D:4:A:H5''	2:D:4:A:C8	2.46	0.44
2:D:14:U:N3	2:D:53:G:C4	2.85	0.44
1:A:10:LEU:HA	1:A:10:LEU:HD23	1.71	0.44
1:A:286:VAL:CG1	1:A:386:ALA:HA	2.44	0.44
1:A:455:ASP:OD1	1:A:457:SER:HB2	2.18	0.44
1:A:615:TYR:CD1	1:A:633:PHE:CD2	3.06	0.44
1:A:691:PHE:CD1	1:A:695:LEU:CD1	3.00	0.44
1:A:719:PHE:H	1:A:719:PHE:HD1	1.62	0.44
1:A:991:LYS:HD2	1:A:991:LYS:HA	1.38	0.44
1:B:328:LYS:HE3	1:B:344:LEU:HD23	2.00	0.44
1:B:543:HIS:O	1:B:543:HIS:CD2	2.70	0.44
1:B:641:TYR:CD1	1:B:641:TYR:O	2.70	0.44
1:B:820:LYS:H	1:B:820:LYS:HG3	1.47	0.44
1:B:1004:ARG:HD2	1:B:1008:HIS:NE2	2.32	0.44
1:B:1106:TRP:O	1:B:1134:VAL:CG2	2.66	0.44
2:D:104:G:N3	2:D:104:G:H2'	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:ASN:N	1:A:400:ASN:ND2	2.61	0.44
1:A:459:SER:HA	1:A:460:PRO:HD3	1.69	0.44
1:A:481:ILE:O	1:A:484:GLN:N	2.45	0.44
1:B:1032:PHE:CD1	1:B:1032:PHE:O	2.70	0.44
1:B:1253:TYR:N	1:B:1253:TYR:CD1	2.85	0.44
1:B:1258:LEU:O	1:B:1262:GLY:N	2.51	0.44
2:D:11:G:C2	2:D:12:A:C4	3.05	0.44
1:A:471:PHE:CD1	1:A:475:LEU:HG	2.53	0.44
1:A:980:PHE:CE1	1:A:1274:GLY:HA3	2.53	0.44
1:B:304:PHE:O	1:B:304:PHE:CD1	2.71	0.44
1:B:571:ASP:C	1:B:571:ASP:OD1	2.56	0.44
1:B:783:SER:HB3	1:B:875:LYS:HD2	2.00	0.44
2:C:35:C:OP2	2:C:35:C:C6	2.70	0.44
2:D:10:C:H3'	2:D:10:C:H6	1.77	0.44
3:F:7:DT:C6	3:F:7:DT:H5'	2.53	0.44
1:A:35:GLU:HA	1:A:38:LYS:HE2	2.00	0.44
1:A:364:LYS:HA	1:A:864:VAL:HA	1.98	0.44
1:A:394:GLU:O	1:A:398:LEU:HG	2.18	0.44
1:A:708:ARG:HG3	1:A:708:ARG:O	2.17	0.44
1:A:1056:PHE:O	1:A:1056:PHE:CG	2.70	0.44
1:A:1226:ARG:HG2	1:A:1227:ARG:N	2.33	0.44
1:B:438:GLU:HA	1:B:441:VAL:CG1	2.48	0.44
1:B:691:PHE:O	1:B:691:PHE:CD1	2.70	0.44
1:A:255:ILE:HG13	1:A:340:LYS:HD2	2.00	0.44
1:A:294:THR:HG21	1:A:378:ALA:CA	2.45	0.44
1:A:354:LEU:CD1	1:A:370:TYR:CZ	3.00	0.44
1:A:593:ARG:O	1:A:596:LEU:HB2	2.18	0.44
1:A:1249:TYR:CD1	1:A:1249:TYR:O	2.71	0.44
1:B:328:LYS:HZ1	1:B:348:LYS:HG3	1.83	0.44
1:B:571:ASP:OD1	1:B:572:ALA:N	2.50	0.44
1:B:583:THR:HG23	1:B:587:ALA:HB2	2.00	0.44
1:B:787:TYR:O	1:B:787:TYR:CD1	2.70	0.44
1:B:1108:ILE:HD13	1:B:1108:ILE:N	2.32	0.44
1:A:126:GLN:HB3	1:A:225:PHE:HE1	1.83	0.44
1:A:162:ASN:O	1:A:166:VAL:HG13	2.18	0.44
1:A:471:PHE:O	1:A:471:PHE:HD1	2.01	0.44
1:A:510:LYS:HE3	1:A:510:LYS:HB2	1.67	0.44
1:A:596:LEU:HD21	1:A:623:PHE:CE2	2.53	0.44
1:A:804:SER:HB3	2:C:23:A:H4'	1.99	0.44
1:B:78:ASN:OD1	1:B:523:GLY:CA	2.65	0.44
1:B:97:LEU:HD21	1:B:267:MSE:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1175:ASN:O	1:B:1215:ALA:HB1	2.17	0.44
1:B:1180:LEU:HD22	1:B:1180:LEU:HA	1.52	0.44
2:C:111:A:O2'	2:C:112:G:H5'	2.18	0.44
2:D:24:U:O2	2:D:24:U:H2'	2.18	0.44
3:E:7:DT:H2''	3:E:8:DG:O5'	2.18	0.44
1:A:49:LEU:CD1	1:A:953:LEU:HD11	2.48	0.43
1:A:962:PHE:N	1:A:962:PHE:CD1	2.85	0.43
1:A:1081:ASN:ND2	1:A:1085:LEU:CD1	2.80	0.43
1:A:1140:VAL:O	1:A:1140:VAL:HG23	2.18	0.43
1:A:1156:VAL:HG22	1:A:1156:VAL:O	2.18	0.43
1:B:198:PHE:O	1:B:200:SER:N	2.51	0.43
1:B:399:VAL:CG1	1:B:445:ARG:HE	2.31	0.43
1:B:673:PHE:CD1	1:B:673:PHE:C	2.90	0.43
1:B:811:LEU:HA	1:B:811:LEU:HD23	1.69	0.43
1:B:892:LEU:O	1:B:899:LYS:NZ	2.32	0.43
1:B:899:LYS:O	1:B:902:LEU:N	2.50	0.43
1:A:391:ARG:NH1	2:C:120:C:H4'	2.34	0.43
1:A:668:GLU:O	1:A:672:THR:HG22	2.18	0.43
1:A:706:LEU:HD11	1:A:748:TYR:CE2	2.53	0.43
1:A:866:ARG:HH21	1:A:869:ASN:HD21	1.65	0.43
1:A:903:ASP:O	1:A:906:PHE:HB3	2.19	0.43
1:A:1159:TRP:HE1	1:A:1182:THR:HA	1.83	0.43
1:B:154:ASN:HD22	1:B:154:ASN:H	1.66	0.43
1:B:311:LEU:HD12	1:B:311:LEU:HA	1.55	0.43
1:B:536:GLU:OE1	1:B:540:GLN:HG2	2.18	0.43
1:B:1115:THR:CG2	1:B:1130:VAL:HG22	2.40	0.43
1:B:1173:ASN:C	1:B:1174:VAL:HG13	2.36	0.43
2:C:49:U:C2	2:C:111:A:C2	3.06	0.43
1:A:392:LEU:O	1:A:395:LEU:N	2.51	0.43
1:A:470:ALA:HA	1:A:473:ASP:HB2	2.00	0.43
1:A:864:VAL:HG23	1:A:865:GLY:H	1.83	0.43
1:B:362:GLY:O	1:B:365:GLY:CA	2.66	0.43
1:B:371:GLN:O	1:B:374:ARG:HD3	2.18	0.43
1:B:1267:GLU:O	1:B:1271:ILE:HG12	2.18	0.43
2:C:35:C:O5'	2:C:35:C:H6	2.01	0.43
2:C:103:G:O5'	2:C:103:G:C8	2.70	0.43
1:A:655:LEU:C	1:A:655:LEU:HD12	2.38	0.43
1:A:864:VAL:N	1:A:885:LEU:CD1	2.81	0.43
1:B:363:GLU:O	1:B:364:LYS:CB	2.58	0.43
1:B:396:ILE:HG23	1:B:448:LEU:CD1	2.21	0.43
1:B:1203:ARG:HE	1:B:1203:ARG:HB3	1.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1273:ILE:HG12	1:B:1273:ILE:H	1.54	0.43
2:C:62:C:H42	2:C:80:G:H1	1.65	0.43
1:A:336:VAL:HG13	1:A:337:PRO:N	2.34	0.43
1:A:1086:TYR:CD1	1:A:1086:TYR:O	2.71	0.43
1:A:1252:VAL:H	1:A:1252:VAL:HG23	1.55	0.43
1:B:396:ILE:CB	1:B:448:LEU:HD21	2.49	0.43
1:B:555:TRP:CZ3	1:B:561:CYS:SG	3.11	0.43
1:B:566:PRO:HG3	1:B:667:TRP:CD1	2.52	0.43
1:B:641:TYR:CD1	1:B:641:TYR:C	2.91	0.43
1:B:1009:SER:OG	1:B:1034:MSE:HE1	2.19	0.43
1:A:53:LYS:CB	1:A:951:TYR:CE1	2.94	0.43
1:A:120:ASN:ND2	1:A:141:SER:OG	2.48	0.43
1:A:818:PHE:N	1:A:818:PHE:CD1	2.84	0.43
1:A:871:ILE:CD1	1:A:906:PHE:HZ	2.30	0.43
1:B:816:LEU:HB3	1:B:829:THR:HG23	2.00	0.43
1:B:1159:TRP:NE1	1:B:1182:THR:HA	2.34	0.43
2:C:78:C:C6	2:C:78:C:O5'	2.71	0.43
2:D:21:G:C2	2:D:42:C:N3	2.86	0.43
2:D:61:G:C8	2:D:61:G:O5'	2.70	0.43
1:A:8:LEU:HD23	1:A:8:LEU:HA	1.78	0.43
1:A:462:GLU:HA	1:A:465:ILE:CD1	2.48	0.43
1:A:891:ARG:HH22	2:C:45:A:P	2.41	0.43
1:A:915:ARG:HB2	1:A:948:PRO:HB2	1.99	0.43
1:B:61:VAL:HG23	1:B:890:PHE:CZ	2.53	0.43
1:B:329:SER:HB2	1:B:334:PHE:CE1	2.53	0.43
1:B:564:THR:C	1:B:566:PRO:HD2	2.39	0.43
1:B:595:LEU:HD22	1:B:595:LEU:HA	1.56	0.43
1:B:730:LEU:HA	1:B:731:PRO:HD3	1.65	0.43
1:B:746:SER:O	1:B:746:SER:OG	2.34	0.43
1:B:806:GLU:OE1	1:B:845:PRO:HG2	2.19	0.43
1:B:994:ALA:C	1:B:995:VAL:HG23	2.39	0.43
2:C:78:C:C6	2:C:78:C:H3'	2.53	0.43
2:D:62:C:C6	2:D:62:C:C5'	3.02	0.43
1:A:529:GLU:O	1:A:533:LYS:HG3	2.18	0.43
1:A:1088:LYS:C	1:A:1088:LYS:HD3	2.39	0.43
1:B:147:LEU:HD22	1:B:211:ALA:HB1	2.00	0.43
1:B:354:LEU:HD12	1:B:355:PRO:HD2	2.00	0.43
1:B:562:LEU:HD12	1:B:562:LEU:C	2.37	0.43
1:B:786:ILE:HD11	1:B:872:GLU:HG3	2.00	0.43
1:B:1046:ILE:CD1	1:B:1084:PHE:HE2	2.32	0.43
1:B:1123:LYS:HA	1:B:1123:LYS:NZ	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1200:PHE:HZ	1:B:1204:ARG:CD	2.19	0.43
2:C:21:G:N2	2:C:42:C:C2	2.87	0.43
1:A:8:LEU:HD22	1:A:8:LEU:C	2.39	0.43
1:A:263:VAL:HA	1:A:266:TYR:CD2	2.52	0.43
1:A:319:SER:H	1:A:327:SER:HB2	1.84	0.43
1:A:768:ARG:O	1:A:927:GLN:HG2	2.17	0.43
1:A:1060:GLU:HG2	1:A:1273:ILE:HD11	2.01	0.43
1:B:54:THR:HG21	2:D:115:A:C1'	2.49	0.43
1:B:234:ASP:OD1	1:B:238:ARG:CD	2.67	0.43
1:B:477:ARG:NH1	1:B:477:ARG:CG	2.73	0.43
1:B:728:ASP:OD1	1:B:728:ASP:N	2.52	0.43
1:B:831:LYS:NZ	1:B:867:GLU:HB3	2.34	0.43
1:B:964:ASN:C	1:B:1055:ALA:CB	2.88	0.43
2:C:54:C:H2'	2:C:55:C:C6	2.54	0.43
1:A:101:ARG:HD3	1:A:101:ARG:HA	1.36	0.43
1:A:144:GLU:O	1:A:148:LYS:HB2	2.19	0.43
1:A:993:ILE:N	1:A:993:ILE:HD13	2.33	0.43
1:A:993:ILE:HA	1:A:993:ILE:HD12	1.81	0.43
1:B:328:LYS:HZ3	1:B:348:LYS:CG	2.31	0.43
1:B:730:LEU:HD12	1:B:730:LEU:O	2.19	0.43
2:D:36:U:H6	2:D:36:U:C3'	2.26	0.43
1:A:77:TYR:CE1	1:A:81:GLU:HG3	2.54	0.42
1:A:90:TYR:O	1:A:94:ALA:N	2.46	0.42
1:B:701:ARG:NH1	1:B:701:ARG:CG	2.73	0.42
1:B:1002:SER:HB2	1:B:1038:VAL:HG22	2.00	0.42
2:C:38:U:H2'	2:C:39:A:N7	2.32	0.42
3:F:7:DT:H2''	3:F:8:DG:O5'	2.19	0.42
1:A:358:SER:O	1:A:359:LEU:HG	2.18	0.42
1:A:436:LEU:O	1:A:440:LEU:CB	2.67	0.42
1:A:641:TYR:C	1:A:641:TYR:HD1	2.21	0.42
1:A:1032:PHE:O	1:A:1032:PHE:CD1	2.72	0.42
1:B:47:GLN:O	1:B:47:GLN:HG3	2.19	0.42
1:B:186:PHE:O	1:B:189:LYS:N	2.52	0.42
1:B:328:LYS:NZ	1:B:348:LYS:HG3	2.34	0.42
1:B:526:LYS:O	1:B:530:LEU:HG	2.20	0.42
1:B:665:VAL:O	1:B:669:LYS:HB2	2.19	0.42
1:B:1157:PHE:O	1:B:1157:PHE:CG	2.72	0.42
2:C:9:C:C2	2:C:58:G:N2	2.87	0.42
4:H:2:DT:H2'	4:H:3:DC:C6	2.54	0.42
1:A:143:LEU:HA	1:A:143:LEU:HD13	1.63	0.42
1:A:578:ASN:ND2	1:A:578:ASN:C	2.73	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:595:LEU:O	1:A:595:LEU:HD12	2.19	0.42
1:A:740:ASN:N	1:A:740:ASN:ND2	2.64	0.42
1:A:865:GLY:N	1:A:885:LEU:HD12	2.34	0.42
1:B:335:SER:HB2	1:B:340:LYS:HB2	2.02	0.42
1:B:395:LEU:HD11	1:B:517:LEU:CD1	2.49	0.42
1:B:629:LEU:C	1:B:629:LEU:CD2	2.88	0.42
1:B:713:ILE:HA	1:B:714:PRO:HD3	1.76	0.42
1:B:979:VAL:HG21	1:B:1053:PHE:CD2	2.54	0.42
2:C:12:A:H8	2:C:12:A:O5'	2.01	0.42
2:C:123:A:C8	2:C:123:A:O5'	2.72	0.42
2:D:11:G:N1	2:D:12:A:C5	2.87	0.42
1:A:138:PHE:CD2	1:A:183:PHE:CE1	3.08	0.42
1:A:186:PHE:HE1	1:A:218:MSE:HB3	1.83	0.42
1:A:267:MSE:HE2	1:A:267:MSE:CA	2.50	0.42
1:B:190:PHE:CE1	1:B:214:LEU:CD2	3.03	0.42
1:B:310:ASP:OD1	1:B:311:LEU:N	2.52	0.42
1:B:471:PHE:HA	1:B:474:VAL:HG21	2.01	0.42
1:B:617:TRP:CD1	1:B:673:PHE:HB2	2.55	0.42
1:B:857:ARG:NH1	1:B:872:GLU:OE2	2.53	0.42
1:B:1278:LEU:HD23	1:B:1278:LEU:HA	1.67	0.42
2:D:3:A:O5'	2:D:3:A:H8	2.02	0.42
1:A:313:ARG:NE	1:A:351:CYS:O	2.52	0.42
1:A:392:LEU:O	1:A:395:LEU:HB2	2.20	0.42
1:A:564:THR:CB	1:A:567:LYS:CB	2.52	0.42
1:A:722:LEU:HD23	1:A:723:PRO:CD	2.48	0.42
1:A:772:TYR:HD2	1:A:922:ASP:HB3	1.84	0.42
1:A:1146:SER:HB2	1:A:1233:ARG:NH2	2.00	0.42
1:B:585:PHE:O	1:B:586:ALA:C	2.58	0.42
2:C:61:G:C8	2:C:61:G:C3'	3.03	0.42
1:A:662:THR:HG22	1:A:665:VAL:CB	2.48	0.42
1:A:967:ALA:HA	1:A:1058:VAL:HG22	2.00	0.42
1:B:519:GLY:O	2:D:119:U:H4'	2.18	0.42
1:B:563:GLU:HG2	1:B:710:GLN:HE21	1.84	0.42
1:B:680:GLU:O	1:B:683:LYS:HG2	2.19	0.42
2:C:86:U:H3	2:C:100:A:H61	1.68	0.42
1:A:1163:GLU:N	1:A:1163:GLU:CD	2.72	0.42
1:A:1250:PHE:CD1	1:A:1250:PHE:N	2.86	0.42
1:B:218:MSE:HE3	1:B:218:MSE:HB2	1.73	0.42
1:B:754:LEU:HD23	1:B:754:LEU:HA	1.73	0.42
1:B:783:SER:CB	1:B:875:LYS:HD2	2.49	0.42
1:B:815:VAL:HA	1:B:832:LYS:CB	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:842:LEU:HD13	1:B:842:LEU:H	1.81	0.42
1:B:1190:PHE:CD1	1:B:1190:PHE:N	2.88	0.42
2:C:25:G:C8	2:C:25:G:C5'	3.02	0.42
1:A:664:GLU:H	1:A:664:GLU:HG2	1.37	0.42
1:B:329:SER:CA	1:B:334:PHE:CG	3.03	0.42
1:B:662:THR:CG2	1:B:665:VAL:HG23	2.46	0.42
2:C:25:G:H4'	2:C:25:G:OP1	2.19	0.42
1:A:455:ASP:C	1:A:456:ILE:HD13	2.40	0.42
1:A:844:TYR:N	1:A:845:PRO:CD	2.83	0.42
1:B:333:LEU:HA	1:B:333:LEU:HD23	1.57	0.42
1:B:448:LEU:HD12	1:B:448:LEU:C	2.40	0.42
1:B:667:TRP:O	1:B:671:GLU:HB2	2.19	0.42
1:B:815:VAL:CG1	1:B:836:ARG:HG2	2.50	0.42
1:B:1152:CYS:SG	1:B:1152:CYS:O	2.77	0.42
1:B:1152:CYS:SG	1:B:1253:TYR:CD2	3.13	0.42
2:D:86:U:H6	2:D:86:U:C4'	2.32	0.42
1:A:120:ASN:OD1	1:A:140:PRO:HG2	2.19	0.42
1:A:276:TYR:HB2	1:A:288:TYR:CD2	2.55	0.42
1:A:478:LEU:N	1:A:478:LEU:HD13	2.35	0.42
1:A:593:ARG:O	1:A:596:LEU:N	2.53	0.42
1:A:874:ASN:HD22	1:A:875:LYS:H	1.68	0.42
1:A:1016:LYS:CB	1:A:1030:THR:HG21	2.50	0.42
1:B:565:VAL:N	1:B:566:PRO:HD2	2.30	0.42
1:B:1150:SER:N	1:B:1268:ASN:HD21	2.18	0.42
2:C:61:G:H8	2:C:61:G:O5'	2.03	0.42
1:A:93:PHE:O	1:A:97:LEU:HB2	2.20	0.41
1:A:596:LEU:O	1:A:600:GLY:N	2.53	0.41
1:A:713:ILE:HA	1:A:714:PRO:HD3	1.77	0.41
1:A:1062:ASP:OD1	1:A:1063:VAL:N	2.53	0.41
1:B:84:GLU:H	1:B:84:GLU:HG3	1.45	0.41
1:B:717:ILE:HA	1:B:717:ILE:HD12	1.81	0.41
1:B:879:PRO:HB3	1:B:906:PHE:HE1	1.85	0.41
1:B:1163:GLU:O	1:B:1164:LYS:C	2.58	0.41
1:B:1187:ILE:HG22	1:B:1253:TYR:CD1	2.55	0.41
1:B:1200:PHE:CE2	1:B:1204:ARG:CD	2.98	0.41
2:D:12:A:N1	2:D:54:C:O2	2.53	0.41
3:F:5:DT:H1'	3:F:6:DA:H5'	2.02	0.41
1:A:397:GLU:O	1:A:401:GLN:N	2.51	0.41
1:A:551:ARG:NH2	1:A:719:PHE:CE1	2.88	0.41
1:A:563:GLU:HG2	1:A:567:LYS:HE2	1.99	0.41
1:A:1034:MSE:O	1:A:1034:MSE:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1189:LEU:CD2	1:A:1231:ASN:ND2	2.83	0.41
1:A:1226:ARG:HH11	1:A:1226:ARG:N	2.12	0.41
1:B:540:GLN:O	1:B:543:HIS:HB3	2.21	0.41
1:B:836:ARG:CB	1:B:843:PHE:CE2	2.96	0.41
1:B:966:LEU:HD22	1:B:968:ILE:HD11	2.02	0.41
1:B:1041:ASP:OD1	1:B:1041:ASP:N	2.50	0.41
1:B:1108:ILE:HD12	1:B:1108:ILE:HG23	1.87	0.41
2:D:2:G:C8	2:D:2:G:C3'	3.03	0.41
1:A:70:PHE:CD1	1:A:923:GLN:HB2	2.54	0.41
1:A:434:LEU:HD23	1:A:434:LEU:C	2.41	0.41
1:A:549:PHE:HZ	1:A:705:LEU:HD23	1.84	0.41
1:A:612:LYS:HB3	1:A:612:LYS:HE2	1.49	0.41
1:A:730:LEU:HD13	1:A:730:LEU:N	2.26	0.41
1:B:76:ILE:CD1	1:B:359:LEU:CD1	2.89	0.41
1:B:825:LEU:C	1:B:828:PRO:HD2	2.40	0.41
1:B:1003:ILE:CD1	1:B:1077:TYR:OH	2.67	0.41
1:A:37:ARG:HH21	1:A:48:GLU:CD	2.24	0.41
1:A:471:PHE:CD1	1:A:475:LEU:CD2	3.03	0.41
1:A:479:GLY:O	1:A:482:ARG:N	2.53	0.41
1:A:1189:LEU:HD22	1:A:1231:ASN:ND2	2.35	0.41
1:B:1235:ALA:HB1	1:B:1236:PRO:HD2	0.49	0.41
1:A:214:LEU:O	1:A:214:LEU:HD22	2.20	0.41
1:A:393:PHE:HA	1:A:396:ILE:HG12	2.02	0.41
1:A:673:PHE:CD1	1:A:673:PHE:C	2.91	0.41
1:A:1200:PHE:O	1:A:1200:PHE:CD1	2.74	0.41
1:B:228:VAL:HG22	1:B:231:MSE:HE2	2.02	0.41
1:B:257:VAL:O	1:B:258:ASP:C	2.56	0.41
1:B:632:TYR:CD2	1:B:633:PHE:CD1	3.08	0.41
1:B:760:ASN:HD22	1:B:760:ASN:HA	1.55	0.41
1:B:858:ASN:HA	1:B:859:PRO:HD2	1.74	0.41
1:B:1186:VAL:O	1:B:1253:TYR:HA	2.21	0.41
1:A:396:ILE:HG13	1:A:397:GLU:H	1.85	0.41
1:A:629:LEU:O	1:A:630:ASN:C	2.57	0.41
1:A:693:THR:O	1:A:693:THR:HG22	2.21	0.41
1:A:722:LEU:CD2	1:A:723:PRO:HD2	2.49	0.41
1:A:794:LEU:HB3	1:A:823:ASN:HB3	2.02	0.41
1:A:1031:ALA:HB3	3:E:11:DC:OP2	2.21	0.41
1:A:1207:ARG:C	1:A:1208:THR:OG1	2.58	0.41
1:A:1246:GLN:OE1	1:A:1246:GLN:CA	2.69	0.41
1:B:110:LYS:HG3	1:B:239:ASN:OD1	2.20	0.41
1:B:537:SER:O	1:B:541:ILE:CG1	2.66	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:655:LEU:H	1:B:655:LEU:CD2	2.33	0.41
1:B:723:PRO:HB2	1:B:726:TYR:CE2	2.55	0.41
1:B:797:ILE:CG2	1:B:801:TYR:HD2	2.34	0.41
1:B:799:ASN:HA	1:B:802:TRP:HZ3	1.85	0.41
1:B:806:GLU:OE1	1:B:845:PRO:HB2	2.21	0.41
1:B:866:ARG:HD3	1:B:885:LEU:HD11	2.01	0.41
2:D:21:G:N2	2:D:42:C:C2	2.89	0.41
1:A:76:ILE:HG21	1:A:76:ILE:HD13	1.71	0.41
1:A:102:ILE:HG23	1:A:295:THR:HG21	1.98	0.41
1:A:666:VAL:O	1:A:670:PHE:N	2.30	0.41
1:A:720:PHE:CD2	1:A:720:PHE:O	2.74	0.41
1:A:827:ALA:N	1:A:828:PRO:HD2	2.35	0.41
1:A:863:SER:HA	1:A:885:LEU:HD13	2.03	0.41
1:B:100:PHE:O	1:B:101:ARG:CD	2.65	0.41
1:B:130:ILE:HD11	1:B:224:PRO:HD2	2.01	0.41
1:B:1184:ASP:OD1	1:B:1184:ASP:N	2.54	0.41
1:B:1198:PRO:HG2	1:B:1199:LYS:H	1.85	0.41
2:D:37:U:O2	2:D:37:U:C2'	2.69	0.41
2:D:84:C:H6	2:D:84:C:O5'	2.04	0.41
1:A:34:LEU:HD11	1:A:956:PRO:HB3	2.03	0.41
1:A:568:PHE:CZ	1:A:707:ARG:HG2	2.56	0.41
1:A:661:ASP:CG	1:A:669:LYS:HE3	2.40	0.41
1:A:819:ASP:HB3	1:A:823:ASN:H	1.86	0.41
1:A:1150:SER:HB2	1:A:1271:ILE:HG21	2.03	0.41
1:A:1162:THR:CG2	1:A:1163:GLU:OE1	2.66	0.41
1:B:247:ILE:HD13	1:B:247:ILE:HG21	1.85	0.41
1:B:471:PHE:O	1:B:472:SER:C	2.56	0.41
1:B:938:LEU:N	1:B:938:LEU:CD1	2.83	0.41
1:B:1249:TYR:O	1:B:1249:TYR:CD1	2.74	0.41
2:C:36:U:H2'	2:C:37:U:C6	2.47	0.41
1:A:59:LEU:HD21	1:A:892:LEU:HD11	2.01	0.41
1:A:154:ASN:ND2	1:A:154:ASN:H	2.19	0.41
1:A:193:GLU:HG2	1:A:218:MSE:CE	2.51	0.41
1:A:255:ILE:CD1	1:A:340:LYS:HB3	2.51	0.41
1:A:327:SER:C	1:A:329:SER:N	2.74	0.41
1:A:363:GLU:O	1:A:364:LYS:CG	2.65	0.41
1:A:391:ARG:HD3	1:A:391:ARG:HA	1.33	0.41
1:A:396:ILE:N	1:A:448:LEU:CD1	2.84	0.41
1:A:511:LEU:HD12	1:A:511:LEU:HA	1.78	0.41
1:A:662:THR:CG2	1:A:665:VAL:H	2.32	0.41
1:A:768:ARG:O	1:A:927:GLN:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:772:TYR:CD2	1:A:922:ASP:HB3	2.56	0.41
1:A:793:ARG:NH1	2:C:42:C:OP1	2.54	0.41
1:A:891:ARG:HH21	1:A:891:ARG:HD2	1.70	0.41
1:A:953:LEU:HB2	1:A:954:GLU:H	1.65	0.41
1:A:1073:LEU:HD23	1:A:1073:LEU:HA	1.74	0.41
1:A:1159:TRP:CE3	1:A:1159:TRP:CA	3.04	0.41
1:A:1279:THR:O	1:A:1282:ARG:NH2	2.54	0.41
1:B:152:ARG:HB2	4:H:9:DC:H5'	2.02	0.41
1:B:473:ASP:O	1:B:476:ASN:HB3	2.21	0.41
1:B:785:LEU:HD12	1:B:914:LEU:HD11	2.02	0.41
1:B:818:PHE:C	1:B:825:LEU:HD11	2.41	0.41
1:B:939:GLU:HB3	1:B:940:SER:H	1.69	0.41
1:B:977:TYR:CE2	1:B:1053:PHE:CE2	3.08	0.41
1:B:1083:HIS:O	1:B:1096:ARG:HG3	2.20	0.41
1:B:1085:LEU:N	1:B:1085:LEU:HD23	2.36	0.41
2:C:27:A:H4'	2:C:27:A:OP1	2.20	0.41
1:A:149:LYS:CG	1:A:150:GLY:N	2.84	0.41
1:A:259:ILE:HD12	1:A:259:ILE:HA	1.84	0.41
1:A:565:VAL:H	1:A:565:VAL:HG23	1.40	0.41
1:A:1211:THR:O	1:A:1211:THR:CG2	2.69	0.41
1:B:162:ASN:O	1:B:162:ASN:OD1	2.38	0.41
1:B:839:ASP:OD2	1:B:842:LEU:HD11	2.21	0.41
1:B:1193:ASP:OD2	1:B:1201:TYR:OH	2.38	0.41
2:D:63:C:C6	2:D:63:C:C5'	3.03	0.41
1:A:112:PHE:CE2	1:A:250:THR:CG2	3.00	0.40
1:A:131:PHE:HD2	1:A:183:PHE:N	2.18	0.40
1:A:333:LEU:HD23	1:A:333:LEU:HA	1.86	0.40
1:A:800:ALA:O	2:C:23:A:O2'	2.23	0.40
1:A:844:TYR:HD1	1:A:844:TYR:HA	1.71	0.40
1:A:1251:CYS:H	1:A:1258:LEU:HB2	1.86	0.40
1:B:549:PHE:CE2	1:B:706:LEU:HD21	2.56	0.40
1:B:806:GLU:O	1:B:806:GLU:HG3	2.21	0.40
1:B:817:VAL:HG23	1:B:825:LEU:HD12	1.81	0.40
1:B:947:VAL:O	1:B:947:VAL:CG2	2.68	0.40
1:B:975:LEU:HD23	1:B:975:LEU:C	2.41	0.40
1:B:975:LEU:CD2	1:B:998:ILE:HD13	2.50	0.40
2:D:6:C:O5'	2:D:6:C:C6	2.69	0.40
2:D:26:A:H2'	2:D:27:A:C4'	2.51	0.40
4:H:6:DG:C2'	4:H:7:DT:H5'	2.45	0.40
1:A:98:SER:OG	1:A:343:GLY:O	2.26	0.40
1:A:215:LEU:HD21	1:A:219:LEU:HD11	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:397:GLU:HG3	1:A:401:GLN:HB3	2.03	0.40
1:A:793:ARG:HD2	1:A:851:PRO:CG	2.51	0.40
1:A:1174:VAL:HA	1:A:1179:GLU:O	2.22	0.40
1:B:312:ILE:HG12	1:B:348:LYS:HG2	2.03	0.40
1:B:595:LEU:C	1:B:595:LEU:CD1	2.85	0.40
1:B:748:TYR:O	1:B:752:PHE:HB2	2.22	0.40
1:B:797:ILE:CG2	1:B:801:TYR:CD2	3.04	0.40
1:B:1111:ILE:C	1:B:1112:GLU:HG2	2.41	0.40
1:B:1174:VAL:CG1	1:B:1180:LEU:HD23	2.47	0.40
2:C:84:C:H6	2:C:84:C:C5'	2.27	0.40
1:A:100:PHE:O	1:A:101:ARG:HD3	2.21	0.40
1:A:107:SER:O	1:A:111:THR:HG23	2.22	0.40
1:A:994:ALA:C	1:A:995:VAL:CG2	2.90	0.40
1:A:1114:VAL:CG2	1:A:1129:ILE:HG22	2.48	0.40
1:B:154:ASN:N	1:B:154:ASN:ND2	2.69	0.40
1:B:306:LYS:O	1:B:306:LYS:HG2	2.20	0.40
1:B:471:PHE:HA	1:B:474:VAL:CG2	2.50	0.40
1:B:565:VAL:CB	1:B:708:ARG:CD	2.28	0.40
2:C:21:G:C2	2:C:42:C:N3	2.89	0.40
2:D:9:C:C2	2:D:58:G:N2	2.90	0.40
2:D:25:G:OP1	2:D:25:G:C4'	2.70	0.40
2:D:64:G:C8	2:D:64:G:C3'	3.04	0.40
1:A:134:MSE:HE3	1:A:134:MSE:HB2	1.61	0.40
1:A:241:LEU:HA	1:A:242:PRO:HD3	1.85	0.40
1:A:267:MSE:HE2	1:A:267:MSE:N	2.36	0.40
1:A:595:LEU:O	1:A:595:LEU:CD1	2.69	0.40
1:A:1226:ARG:NH1	1:A:1226:ARG:N	2.69	0.40
1:B:14:LYS:HA	1:B:14:LYS:HD3	1.84	0.40
1:B:23:ILE:O	1:B:23:ILE:HG22	2.22	0.40
1:B:25:CYS:SG	1:B:955:GLU:O	2.80	0.40
1:B:659:ASN:OD1	1:B:659:ASN:C	2.57	0.40
1:B:681:ILE:O	1:B:681:ILE:CG2	2.70	0.40
1:B:793:ARG:HE	1:B:793:ARG:HB2	1.36	0.40
1:B:797:ILE:HG22	1:B:801:TYR:CD2	2.56	0.40
1:B:819:ASP:N	1:B:825:LEU:HD11	2.36	0.40
1:B:838:GLY:O	1:B:840:LEU:HD12	2.22	0.40
1:B:1130:VAL:HG12	1:B:1131:PRO:HD2	2.04	0.40
2:C:5:A:H5'	2:C:6:C:OP2	2.22	0.40
1:A:23:ILE:O	1:A:23:ILE:HG22	2.20	0.40
1:B:53:LYS:NZ	1:B:1098:GLN:O	2.49	0.40
1:B:77:TYR:HE2	1:B:776:LYS:H	1.70	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:126:GLN:O	1:B:126:GLN:HG3	2.18	0.40
1:B:629:LEU:HA	1:B:629:LEU:HD23	1.88	0.40
1:B:817:VAL:HG21	1:B:825:LEU:HD13	1.79	0.40
1:B:972:GLU:HG3	1:B:1007:ILE:HD13	2.00	0.40
1:B:1149:CYS:CA	1:B:1249:TYR:OH	2.67	0.40
2:C:78:C:C3'	2:C:78:C:H6	2.35	0.40
2:C:80:G:C8	2:C:80:G:C4'	3.04	0.40
2:D:62:C:O2	2:D:62:C:C2'	2.70	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	1197/1310 (91%)	1130 (94%)	59 (5%)	8 (1%)	22	61
1	B	1177/1310 (90%)	1092 (93%)	68 (6%)	17 (1%)	11	46
All	All	2374/2620 (91%)	2222 (94%)	127 (5%)	25 (1%)	14	51

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	656	ARG
1	B	841	ARG
1	A	175	ASN
1	A	328	LYS
1	A	881	VAL
1	A	956	PRO
1	B	199	ASP
1	B	956	PRO
1	B	1009	SER
1	B	1017	LYS

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Mol	Chain	Res	Type
1	A	1235	ALA
1	A	1282	ARG
1	B	180	SER
1	B	296	THR
1	B	879	PRO
1	A	1135	PHE
1	B	337	PRO
1	B	657	SER
1	B	1156	VAL
1	B	1198	PRO
1	B	643	PRO
1	A	337	PRO
1	B	1174	VAL
1	B	515	PRO
1	B	1135	PHE

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	1018/1144 (89%)	750 (74%)	268 (26%)	0	2
1	B	993/1144 (87%)	730 (74%)	263 (26%)	0	2
All	All	2011/2288 (88%)	1480 (74%)	531 (26%)	0	2

All (531) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	LEU
1	A	21	ARG
1	A	23	ILE
1	A	36	ARG
1	A	38	LYS
1	A	44	ASP
1	A	49	LEU
1	A	52	LEU

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Mol	Chain	Res	Type
1	A	56	LYS
1	A	61	VAL
1	A	63	GLU
1	A	71	ASP
1	A	72	ARG
1	A	73	ILE
1	A	80	LEU
1	A	88	LEU
1	A	89	SER
1	A	92	LEU
1	A	97	LEU
1	A	101	ARG
1	A	102	ILE
1	A	111	THR
1	A	114	SER
1	A	125	SER
1	A	126	GLN
1	A	127	ILE
1	A	134	MSE
1	A	143	LEU
1	A	148	LYS
1	A	149	LYS
1	A	151	ARG
1	A	152	ARG
1	A	154	ASN
1	A	168	ASN
1	A	169	SER
1	A	173	ARG
1	A	179	SER
1	A	180	SER
1	A	187	LEU
1	A	189	LYS
1	A	199	ASP
1	A	205	ASN
1	A	214	LEU
1	A	226	ASP
1	A	229	CYS
1	A	235	SER
1	A	241	LEU
1	A	244	LYS
1	A	247	ILE
1	A	259	ILE

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Mol	Chain	Res	Type
1	A	262	SER
1	A	281	SER
1	A	289	VAL
1	A	294	THR
1	A	295	THR
1	A	314	LYS
1	A	317	VAL
1	A	319	SER
1	A	328	LYS
1	A	330	LEU
1	A	333	LEU
1	A	334	PHE
1	A	335	SER
1	A	345	LYS
1	A	367	LEU
1	A	391	ARG
1	A	397	GLU
1	A	398	LEU
1	A	400	ASN
1	A	432	HIS
1	A	441	VAL
1	A	445	ARG
1	A	448	LEU
1	A	455	ASP
1	A	456	ILE
1	A	463	GLN
1	A	464	ASP
1	A	471	PHE
1	A	475	LEU
1	A	478	LEU
1	A	487	ASN
1	A	509	LYS
1	A	510	LYS
1	A	511	LEU
1	A	520	LEU
1	A	524	VAL
1	A	535	LEU
1	A	545	GLN
1	A	546	ARG
1	A	561	CYS
1	A	562	LEU
1	A	565	VAL

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Mol	Chain	Res	Type
1	A	569	LEU
1	A	571	ASP
1	A	575	LYS
1	A	578	ASN
1	A	580	GLU
1	A	582	SER
1	A	583	THR
1	A	585	PHE
1	A	589	GLU
1	A	595	LEU
1	A	604	ARG
1	A	612	LYS
1	A	623	PHE
1	A	624	LEU
1	A	629	LEU
1	A	631	ARG
1	A	633	PHE
1	A	636	CYS
1	A	641	TYR
1	A	645	TYR
1	A	646	SER
1	A	647	LYS
1	A	648	ARG
1	A	650	SER
1	A	658	ASP
1	A	659	ASN
1	A	660	LYS
1	A	663	ILE
1	A	664	GLU
1	A	668	GLU
1	A	673	PHE
1	A	680	GLU
1	A	682	GLU
1	A	687	PHE
1	A	692	GLN
1	A	700	LEU
1	A	706	LEU
1	A	707	ARG
1	A	709	ILE
1	A	710	GLN
1	A	713	ILE
1	A	717	ILE

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Mol	Chain	Res	Type
1	A	719	PHE
1	A	722	LEU
1	A	725	GLU
1	A	727	TYR
1	A	728	ASP
1	A	730	LEU
1	A	736	PHE
1	A	740	ASN
1	A	746	SER
1	A	751	GLN
1	A	760	ASN
1	A	766	LEU
1	A	768	ARG
1	A	776	LYS
1	A	785	LEU
1	A	793	ARG
1	A	794	LEU
1	A	796	LYS
1	A	797	ILE
1	A	801	TYR
1	A	805	ASP
1	A	809	MSE
1	A	810	ILE
1	A	812	ASP
1	A	814	ASN
1	A	815	VAL
1	A	835	GLU
1	A	839	ASP
1	A	840	LEU
1	A	841	ARG
1	A	842	LEU
1	A	844	TYR
1	A	848	ARG
1	A	850	LEU
1	A	857	ARG
1	A	861	VAL
1	A	864	VAL
1	A	866	ARG
1	A	868	LYS
1	A	871	ILE
1	A	874	ASN
1	A	876	GLU

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Mol	Chain	Res	Type
1	A	885	LEU
1	A	891	ARG
1	A	915	ARG
1	A	918	MSE
1	A	919	LEU
1	A	927	GLN
1	A	929	VAL
1	A	934	VAL
1	A	937	SER
1	A	940	SER
1	A	941	CYS
1	A	942	THR
1	A	944	SER
1	A	953	LEU
1	A	955	GLU
1	A	957	LYS
1	A	958	VAL
1	A	959	SER
1	A	961	GLN
1	A	963	GLU
1	A	964	ASN
1	A	966	LEU
1	A	968	ILE
1	A	975	LEU
1	A	981	SER
1	A	985	ILE
1	A	989	GLU
1	A	991	LYS
1	A	993	ILE
1	A	998	ILE
1	A	999	ARG
1	A	1002	SER
1	A	1005	ARG
1	A	1008	HIS
1	A	1021	GLN
1	A	1022	ASN
1	A	1029	SER
1	A	1030	THR
1	A	1037	ASN
1	A	1041	ASP
1	A	1049	LEU
1	A	1058	VAL

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Mol	Chain	Res	Type
1	A	1060	GLU
1	A	1061	TYR
1	A	1062	ASP
1	A	1071	ARG
1	A	1073	LEU
1	A	1078	LYS
1	A	1099	LEU
1	A	1120	GLU
1	A	1126	VAL
1	A	1130	VAL
1	A	1138	ARG
1	A	1143	ARG
1	A	1146	SER
1	A	1148	THR
1	A	1151	CYS
1	A	1155	ASN
1	A	1158	ASP
1	A	1159	TRP
1	A	1161	PHE
1	A	1163	GLU
1	A	1164	LYS
1	A	1173	ASN
1	A	1175	ASN
1	A	1177	LYS
1	A	1180	LEU
1	A	1181	THR
1	A	1191	GLU
1	A	1193	ASP
1	A	1196	LYS
1	A	1201	TYR
1	A	1203	ARG
1	A	1204	ARG
1	A	1210	LEU
1	A	1221	LEU
1	A	1224	ILE
1	A	1226	ARG
1	A	1229	ARG
1	A	1241	SER
1	A	1242	ARG
1	A	1246	GLN
1	A	1249	TYR
1	A	1250	PHE

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Mol	Chain	Res	Type
1	A	1255	ASP
1	A	1256	CYS
1	A	1261	SER
1	A	1263	MSE
1	A	1266	ASP
1	A	1281	LEU
1	A	1282	ARG
1	A	1284	ASN
1	B	10	LEU
1	B	14	LYS
1	B	23	ILE
1	B	31	LYS
1	B	34	LEU
1	B	36	ARG
1	B	38	LYS
1	B	44	ASP
1	B	49	LEU
1	B	52	LEU
1	B	63	GLU
1	B	67	LEU
1	B	72	ARG
1	B	80	LEU
1	B	84	GLU
1	B	88	LEU
1	B	89	SER
1	B	92	LEU
1	B	97	LEU
1	B	101	ARG
1	B	107	SER
1	B	114	SER
1	B	121	ASP
1	B	125	SER
1	B	126	GLN
1	B	127	ILE
1	B	134	MSE
1	B	139	ILE
1	B	148	LYS
1	B	156	LYS
1	B	159	THR
1	B	160	GLU
1	B	161	GLU
1	B	163	ILE

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Mol	Chain	Res	Type
1	B	166	VAL
1	B	173	ARG
1	B	174	LYS
1	B	180	SER
1	B	189	LYS
1	B	196	ARG
1	B	197	LYS
1	B	199	ASP
1	B	215	LEU
1	B	218	MSE
1	B	219	LEU
1	B	226	ASP
1	B	229	CYS
1	B	230	LYS
1	B	231	MSE
1	B	241	LEU
1	B	247	ILE
1	B	254	GLU
1	B	257	VAL
1	B	258	ASP
1	B	259	ILE
1	B	263	VAL
1	B	266	TYR
1	B	279	SER
1	B	281	SER
1	B	286	VAL
1	B	289	VAL
1	B	310	ASP
1	B	311	LEU
1	B	314	LYS
1	B	330	LEU
1	B	331	GLN
1	B	333	LEU
1	B	334	PHE
1	B	336	VAL
1	B	341	LEU
1	B	342	ASP
1	B	344	LEU
1	B	348	LYS
1	B	352	GLU
1	B	366	GLU
1	B	374	ARG

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Mol	Chain	Res	Type
1	B	394	GLU
1	B	397	GLU
1	B	400	ASN
1	B	432	HIS
1	B	433	SER
1	B	436	LEU
1	B	440	LEU
1	B	441	VAL
1	B	448	LEU
1	B	451	LEU
1	B	465	ILE
1	B	471	PHE
1	B	477	ARG
1	B	480	SER
1	B	482	ARG
1	B	514	LEU
1	B	516	LYS
1	B	518	ASN
1	B	527	GLN
1	B	535	LEU
1	B	536	GLU
1	B	542	ARG
1	B	550	GLU
1	B	551	ARG
1	B	558	ASN
1	B	561	CYS
1	B	563	GLU
1	B	567	LYS
1	B	568	PHE
1	B	575	LYS
1	B	576	LYS
1	B	577	ILE
1	B	578	ASN
1	B	579	LYS
1	B	580	GLU
1	B	581	SER
1	B	583	THR
1	B	584	ASP
1	B	623	PHE
1	B	626	LYS
1	B	629	LEU
1	B	631	ARG

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Mol	Chain	Res	Type
1	B	635	ASN
1	B	636	CYS
1	B	637	GLN
1	B	640	ILE
1	B	641	TYR
1	B	646	SER
1	B	651	LEU
1	B	655	LEU
1	B	668	GLU
1	B	669	LYS
1	B	673	PHE
1	B	675	LYS
1	B	683	LYS
1	B	687	PHE
1	B	692	GLN
1	B	698	GLU
1	B	700	LEU
1	B	701	ARG
1	B	706	LEU
1	B	707	ARG
1	B	709	ILE
1	B	717	ILE
1	B	719	PHE
1	B	725	GLU
1	B	727	TYR
1	B	730	LEU
1	B	734	VAL
1	B	744	THR
1	B	746	SER
1	B	754	LEU
1	B	760	ASN
1	B	768	ARG
1	B	770	ARG
1	B	772	TYR
1	B	776	LYS
1	B	786	ILE
1	B	787	TYR
1	B	791	GLU
1	B	793	ARG
1	B	801	TYR
1	B	805	ASP
1	B	806	GLU

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Mol	Chain	Res	Type
1	B	809	MSE
1	B	811	LEU
1	B	816	LEU
1	B	817	VAL
1	B	825	LEU
1	B	835	GLU
1	B	836	ARG
1	B	837	GLU
1	B	842	LEU
1	B	844	TYR
1	B	850	LEU
1	B	855	CYS
1	B	860	PHE
1	B	861	VAL
1	B	862	LYS
1	B	866	ARG
1	B	871	ILE
1	B	874	ASN
1	B	875	LYS
1	B	876	GLU
1	B	880	LYS
1	B	881	VAL
1	B	885	LEU
1	B	901	LEU
1	B	915	ARG
1	B	919	LEU
1	B	923	GLN
1	B	927	GLN
1	B	929	VAL
1	B	932	GLN
1	B	934	VAL
1	B	935	GLU
1	B	938	LEU
1	B	942	THR
1	B	944	SER
1	B	953	LEU
1	B	958	VAL
1	B	963	GLU
1	B	966	LEU
1	B	972	GLU
1	B	975	LEU
1	B	981	SER

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Mol	Chain	Res	Type
1	B	983	LYS
1	B	989	GLU
1	B	993	ILE
1	B	1000	ILE
1	B	1003	ILE
1	B	1009	SER
1	B	1018	GLN
1	B	1022	ASN
1	B	1029	SER
1	B	1030	THR
1	B	1034	MSE
1	B	1037	ASN
1	B	1041	ASP
1	B	1049	LEU
1	B	1052	GLU
1	B	1061	TYR
1	B	1082	SER
1	B	1097	LYS
1	B	1099	LEU
1	B	1114	VAL
1	B	1115	THR
1	B	1118	ARG
1	B	1119	LYS
1	B	1123	LYS
1	B	1126	VAL
1	B	1130	VAL
1	B	1138	ARG
1	B	1143	ARG
1	B	1155	ASN
1	B	1156	VAL
1	B	1158	ASP
1	B	1159	TRP
1	B	1160	LEU
1	B	1172	PHE
1	B	1175	ASN
1	B	1176	SER
1	B	1179	GLU
1	B	1180	LEU
1	B	1184	ASP
1	B	1195	SER
1	B	1203	ARG
1	B	1208	THR

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Mol	Chain	Res	Type
1	B	1212	LYS
1	B	1221	LEU
1	B	1224	ILE
1	B	1226	ARG
1	B	1237	LYS
1	B	1239	LYS
1	B	1241	SER
1	B	1243	ASP
1	B	1244	THR
1	B	1247	SER
1	B	1249	TYR
1	B	1250	PHE
1	B	1251	CYS
1	B	1252	VAL
1	B	1261	SER
1	B	1266	ASP
1	B	1273	ILE
1	B	1282	ARG
1	B	1284	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (55) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	GLN
1	A	154	ASN
1	A	168	ASN
1	A	400	ASN
1	A	432	HIS
1	A	446	GLN
1	A	483	ASN
1	A	528	GLN
1	A	543	HIS
1	A	560	HIS
1	A	578	ASN
1	A	635	ASN
1	A	637	GLN
1	A	659	ASN
1	A	710	GLN
1	A	760	ASN
1	A	869	ASN
1	A	874	ASN
1	A	927	GLN

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Mol	Chain	Res	Type
1	A	1022	ASN
1	A	1081	ASN
1	A	1231	ASN
1	A	1240	GLN
1	A	1268	ASN
1	A	1272	ASN
1	B	9	HIS
1	B	47	GLN
1	B	75	GLN
1	B	126	GLN
1	B	154	ASN
1	B	162	ASN
1	B	168	ASN
1	B	278	GLN
1	B	400	ASN
1	B	432	HIS
1	B	528	GLN
1	B	543	HIS
1	B	545	GLN
1	B	621	ASN
1	B	635	ASN
1	B	696	HIS
1	B	710	GLN
1	B	724	GLN
1	B	760	ASN
1	B	849	GLN
1	B	869	ASN
1	B	927	GLN
1	B	961	GLN
1	B	964	ASN
1	B	1072	GLN
1	B	1173	ASN
1	B	1240	GLN
1	B	1259	HIS
1	B	1268	ASN
1	B	1284	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	99/136 (72%)	51 (51%)	9 (9%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	D	87/136 (63%)	49 (56%)	5 (5%)
All	All	186/272 (68%)	100 (53%)	14 (7%)

All (100) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	C	2	G
2	C	5	A
2	C	7	U
2	C	13	C
2	C	15	U
2	C	20	A
2	C	21	G
2	C	23	A
2	C	24	U
2	C	25	G
2	C	27	A
2	C	28	G
2	C	29	U
2	C	34	U
2	C	35	C
2	C	37	U
2	C	38	U
2	C	39	A
2	C	40	U
2	C	44	U
2	C	55	C
2	C	58	G
2	C	62	C
2	C	63	C
2	C	64	G
2	C	80	G
2	C	81	C
2	C	82	G
2	C	83	C
2	C	84	C
2	C	85	U
2	C	87	C
2	C	88	C
2	C	99	G
2	C	100	A
2	C	101	A

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Mol	Chain	Res	Type
2	C	102	G
2	C	103	G
2	C	104	G
2	C	108	A
2	C	109	U
2	C	110	A
2	C	111	A
2	C	114	C
2	C	115	A
2	C	121	G
2	C	122	A
2	C	124	C
2	C	125	A
2	C	126	U
2	C	127	A
2	D	3	A
2	D	4	A
2	D	5	A
2	D	6	C
2	D	7	U
2	D	10	C
2	D	13	C
2	D	15	U
2	D	20	A
2	D	21	G
2	D	22	G
2	D	23	A
2	D	24	U
2	D	25	G
2	D	27	A
2	D	28	G
2	D	37	U
2	D	38	U
2	D	39	A
2	D	40	U
2	D	44	U
2	D	45	A
2	D	53	G
2	D	55	C
2	D	56	G
2	D	58	G
2	D	61	G

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Mol	Chain	Res	Type
2	D	62	C
2	D	63	C
2	D	64	G
2	D	65	A
2	D	82	G
2	D	83	C
2	D	86	U
2	D	102	G
2	D	104	G
2	D	105	U
2	D	107	U
2	D	108	A
2	D	109	U
2	D	110	A
2	D	111	A
2	D	114	C
2	D	115	A
2	D	119	U
2	D	122	A
2	D	123	A
2	D	124	C
2	D	125	A

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	C	27	A
2	C	37	U
2	C	63	C
2	C	80	G
2	C	82	G
2	C	101	A
2	C	102	G
2	C	110	A
2	C	114	C
2	D	4	A
2	D	61	G
2	D	82	G
2	D	110	A
2	D	114	C

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 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	1200/1310 (91%)	0.14	60 (5%) 28 16	12, 61, 132, 179	0
1	B	1182/1310 (90%)	0.23	66 (5%) 24 13	16, 72, 129, 161	0
2	C	103/136 (75%)	0.50	10 (9%) 7 4	10, 81, 167, 198	0
2	D	91/136 (66%)	0.66	7 (7%) 13 7	13, 97, 168, 199	0
3	E	22/31 (70%)	0.58	3 (13%) 3 2	9, 44, 145, 166	0
3	F	26/31 (83%)	-0.07	0 100 100	14, 63, 139, 152	0
4	G	11/23 (47%)	0.09	0 100 100	23, 41, 91, 122	0
4	H	11/23 (47%)	0.02	0 100 100	26, 38, 78, 132	0
All	All	2646/3000 (88%)	0.21	146 (5%) 25 14	9, 67, 139, 199	0

All (146) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	733	ASN	8.7
1	A	578	ASN	6.3
3	E	6	DA	5.8
1	A	1178	GLY	5.5
1	B	455	ASP	5.5
1	A	1187	ILE	5.2
1	A	1189	LEU	5.0
3	E	5	DT	4.9
1	A	1181	THR	4.8
1	B	454	ILE	4.6
1	A	1220	SER	4.5
1	A	457	SER	4.4
1	A	1222	GLU	4.4
2	C	79	G	4.3
1	B	1240	GLN	4.0
1	A	807	TRP	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	437	PHE	3.8
1	B	801	TYR	3.8
1	B	1121	ASP	3.7
1	A	932	GLN	3.6
2	D	62	C	3.6
1	B	211	ALA	3.6
1	B	1224	ILE	3.6
1	A	221	SER	3.6
1	B	1117	GLU	3.5
2	C	63	C	3.5
1	B	1223	GLU	3.5
2	D	63	C	3.4
1	B	1282	ARG	3.4
1	A	1221	LEU	3.4
1	B	732	PRO	3.3
1	B	480	SER	3.3
1	A	444	VAL	3.2
1	A	812	ASP	3.2
1	B	1215	ALA	3.2
1	B	1284	ASN	3.1
1	A	1223	GLU	3.1
2	D	100	A	3.1
1	A	816	LEU	3.1
1	A	459	SER	3.1
1	B	864	VAL	3.1
1	B	1122	GLY	3.0
1	B	483	ASN	3.0
2	D	65	A	3.0
1	A	959	SER	3.0
2	C	78	C	3.0
1	A	336	VAL	2.9
1	B	1219	TYR	2.9
1	A	801	TYR	2.9
1	A	41	GLY	2.8
2	C	61	G	2.8
3	E	7	DT	2.8
1	A	653	PHE	2.8
2	C	82	G	2.7
1	A	661	ASP	2.7
1	A	814	ASN	2.7
1	A	931	ALA	2.6
1	B	807	TRP	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	815	VAL	2.6
1	B	434	LEU	2.6
1	A	222	TYR	2.6
1	A	584	ASP	2.6
2	C	80	G	2.6
1	B	343	GLY	2.6
1	A	804	SER	2.6
1	A	736	PHE	2.6
1	A	811	LEU	2.6
1	A	810	ILE	2.6
1	B	441	VAL	2.5
1	A	1180	LEU	2.5
1	B	215	LEU	2.5
1	B	657	SER	2.5
1	B	823	ASN	2.5
1	A	582	SER	2.5
1	B	479	GLY	2.5
1	B	212	ALA	2.4
1	A	1225	GLU	2.4
1	B	1271	ILE	2.4
1	A	1166	ALA	2.4
1	B	1195	SER	2.4
1	B	730	LEU	2.4
1	A	40	SER	2.4
1	B	1231	ASN	2.4
1	B	1146	SER	2.3
1	B	1283	LYS	2.3
1	B	640	ILE	2.3
1	A	1261	SER	2.3
1	A	1284	ASN	2.3
1	A	1121	ASP	2.3
1	A	487	ASN	2.3
2	C	59	A	2.3
2	C	89	A	2.3
1	A	1157	PHE	2.3
1	B	179	SER	2.3
1	B	433	SER	2.3
1	A	1258	LEU	2.3
1	B	632	TYR	2.3
1	A	583	THR	2.3
1	A	437	PHE	2.3
1	B	575	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	818	PHE	2.3
1	B	639	CYS	2.2
1	B	258	ASP	2.2
1	B	468	PHE	2.2
1	A	745	PRO	2.2
1	A	178	GLY	2.2
1	B	1211	THR	2.2
1	A	1146	SER	2.2
1	B	469	TYR	2.2
1	B	1186	VAL	2.2
2	C	101	A	2.2
1	A	338	ASP	2.2
1	B	1268	ASN	2.2
1	B	795	TRP	2.2
1	A	628	ASP	2.2
1	B	234	ASP	2.2
1	B	1116	ARG	2.2
1	B	1203	ARG	2.1
1	B	449	LYS	2.1
1	A	1260	PHE	2.1
1	B	643	PRO	2.1
1	A	806	GLU	2.1
1	A	1224	ILE	2.1
1	B	644	PRO	2.1
1	B	1176	SER	2.1
1	B	1120	GLU	2.1
1	A	1115	THR	2.1
1	A	1145	THR	2.1
1	A	180	SER	2.1
1	A	1158	ASP	2.1
1	B	810	ILE	2.1
1	B	815	VAL	2.1
1	B	590	ASN	2.1
1	B	1156	VAL	2.1
2	D	7	U	2.1
2	D	86	U	2.1
1	B	866	ARG	2.0
1	B	1108	ILE	2.0
1	B	653	PHE	2.0
1	B	843	PHE	2.0
1	A	802	TRP	2.0
2	C	81	C	2.0

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Mol	Chain	Res	Type	RSRZ
2	D	84	C	2.0
1	A	1231	ASN	2.0
1	B	1145	THR	2.0
1	B	1210	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides 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(\AA^2)	Q<0.9
5	ZN	B	1401	1/1	0.80	0.13	79,79,79,79	0
5	ZN	A	1401	1/1	0.96	0.10	61,61,61,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.