



# Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 02:02 am BST

PDB ID : 4A93  
Title : RNA Polymerase II elongation complex containing a CPD Lesion  
Authors : Walmacq, C.; Cheung, A.C.M.; Kireeva, M.L.; Lubkowska, L.; Ye, C.; Gotte, D.; Strathern, J.N.; Carell, T.; Cramer, P.; Kashlev, M.  
Deposited on : 2011-11-23  
Resolution : 3.40 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](mailto: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.

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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 : 2.11  
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) : 2.11

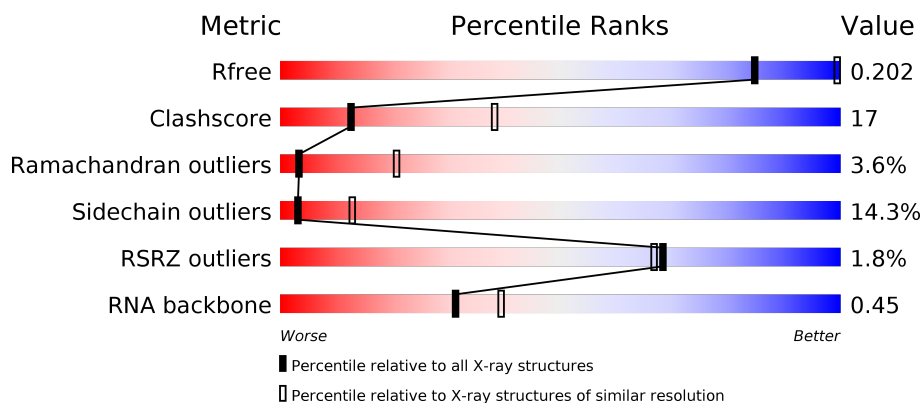
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.40 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	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)
RNA backbone	3102	1006 (3.84-2.96)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	1732	<div> <div>2%</div> <div>45% 30% 6% 18%</div> </div>
2	B	1224	<div> <div>2%</div> <div>54% 30% 7% 9%</div> </div>
3	C	318	<div> <div>52% 27% 5% 16%</div> </div>
4	D	221	<div> <div>42% 27% 10% 19%</div> </div>

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Mol	Chain	Length	Quality of chain
5	E	215	
6	F	155	
7	G	171	
8	H	146	
9	I	122	
10	J	70	
11	K	120	
12	L	70	
13	N	14	
14	P	12	
15	T	25	

## 2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 32105 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1422	Total	C	N	O	S	0	0	0
			11174	7037	1954	2121	62			

- Molecule 2 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1113	Total	C	N	O	S	0	0	0
			8839	5597	1548	1639	55			

- Molecule 3 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB3.

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

- Molecule 4 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	178	Total	C	N	O	S	0	0	0
			1434	887	257	288	2			

- Molecule 5 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 1.

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

- Molecule 6 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 2.

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

- Molecule 7 is a protein called RPB7, DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	171	Total	C	N	O	S	0	0	0
			1340	861	222	249	8			

- Molecule 8 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 3.

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

- Molecule 9 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB9.

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

- Molecule 10 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 5.

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

- Molecule 11 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	115	Total	C	N	O	S	0	0	1
			920	590	157	171	2			

- Molecule 12 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	46	Total	C	N	O	S	0	0	0
			363	224	72	63	4			

- Molecule 13 is a DNA chain called 5'-D(\*TP\*AP\*AP\*GP\*TP\*AP\*CP\*TP\*TP\*GP\*AP\*GP\*CP\*TP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	N	12	Total	C	N	O	P	0	0	0
			247	118	44	73	12			

- Molecule 14 is a RNA chain called 5'-R(\*UP\*UP\*CP\*GP\*AP\*CP\*CP\*AP\*GP\*GP\*AP\*AP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	P	9	Total	C	N	O	P	0	0	0
			197	88	41	59	9			

- Molecule 15 is a DNA chain called 5'-D(\*AP\*GP\*CP\*TP\*CP\*AP\*AP\*GP\*TP\*AP\*CP\*TT\*TP\*TP\*TP\*CP\*C BRUP\*GP\*GP\*TP\*CP\*AP\*TP\*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	T	23	Total	Br	C	N	O	P	0	0
			485	1	234	81	146	23		

- Molecule 16 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	J	1	Total	Zn	0	0
			1	1		
16	B	1	Total	Zn	0	0
			1	1		
16	I	2	Total	Zn	0	0
			2	2		
16	C	1	Total	Zn	0	0
			1	1		
16	A	2	Total	Zn	0	0
			2	2		
16	L	1	Total	Zn	0	0
			1	1		

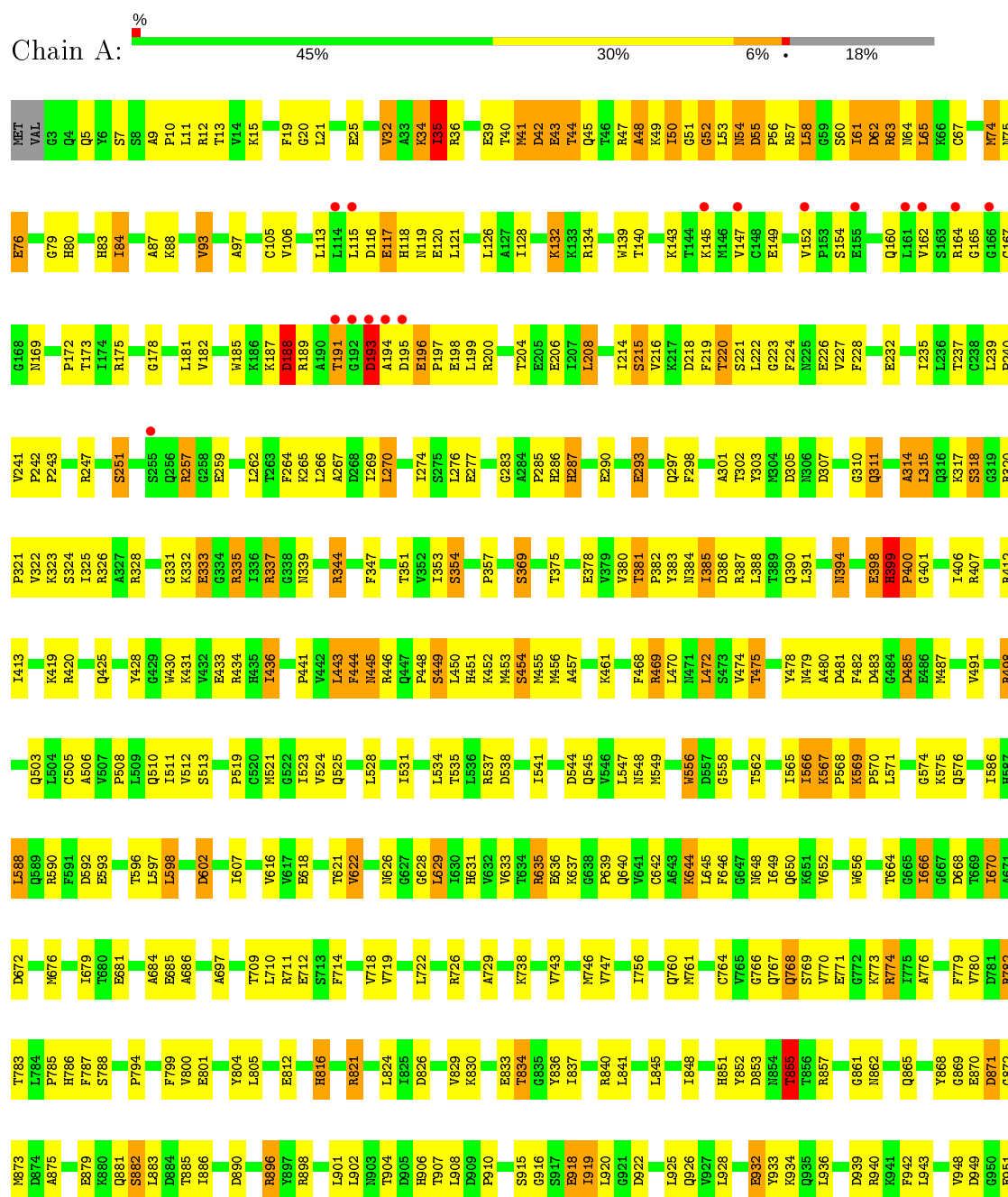
- Molecule 17 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

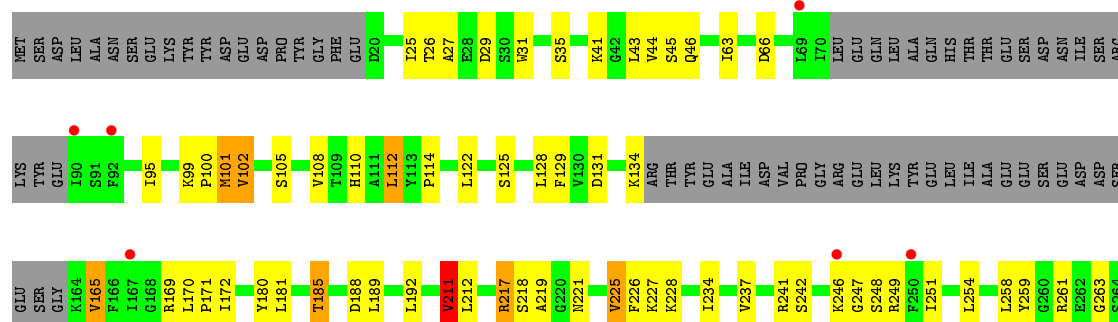
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	1	Total	Mg	0	0
			1	1		

### 3 Residue-property plots

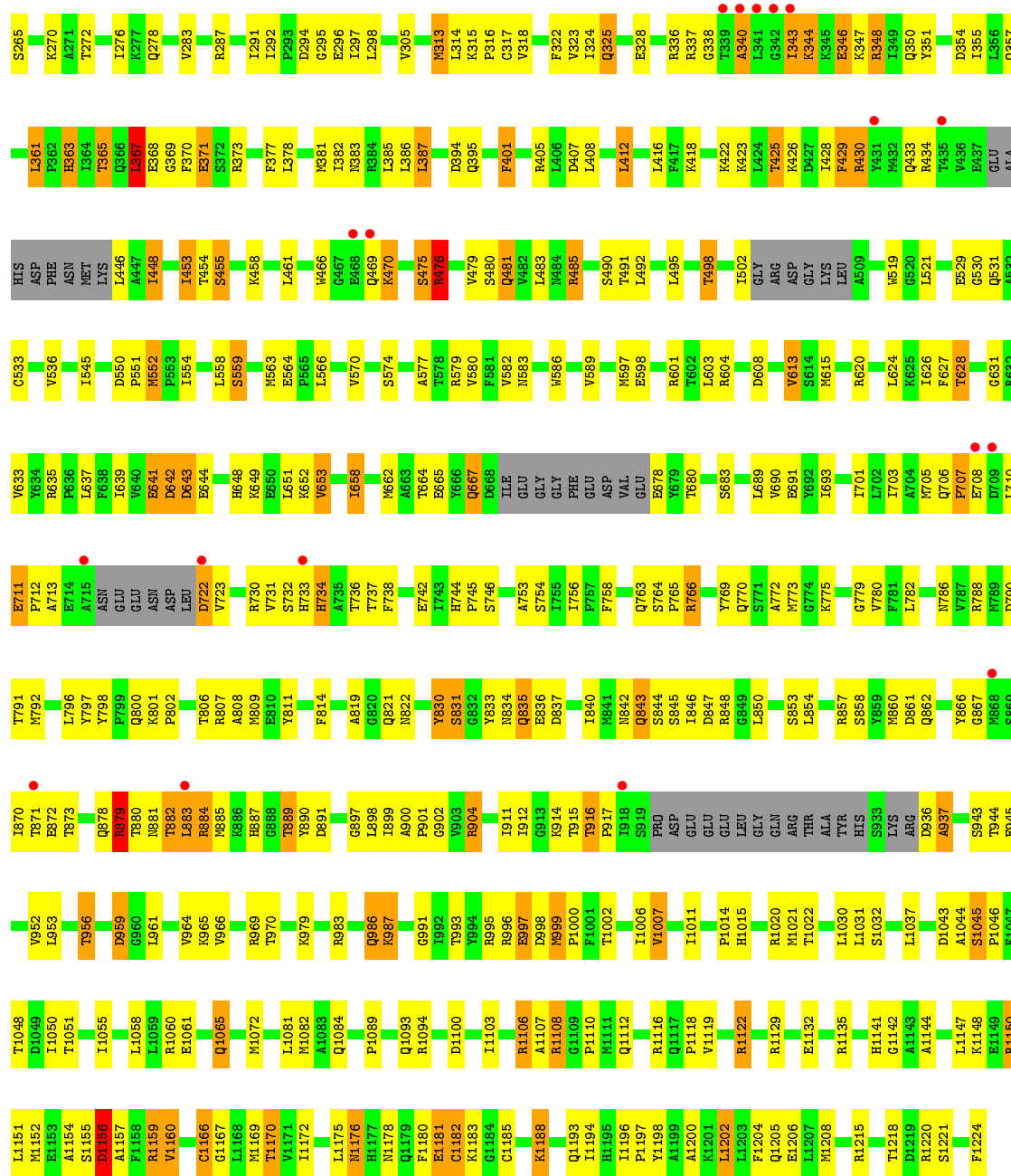
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

#### • Molecule 1: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB1



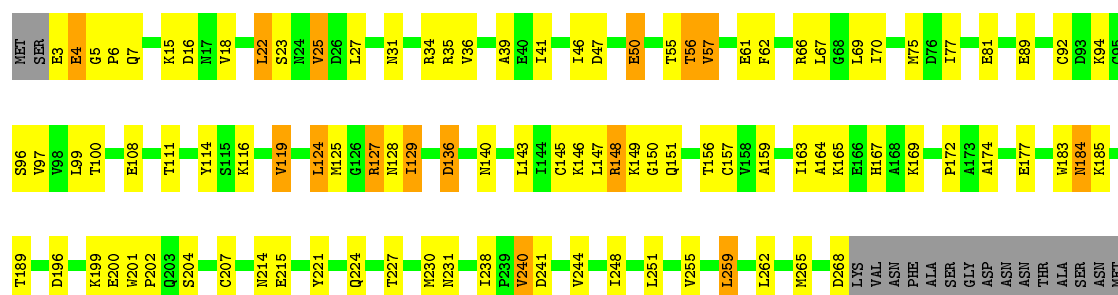






• Molecule 3: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB3

Chain C: 52% 27% 5% 16%



LEU  
GLY  
SER  
ASN  
S4  
GLU  
ASP  
VAL  
MET  
MET  
THR  
GLY  
ALA  
GLU  
GLN  
ASP  
PRO  
TYR  
SER  
ASN  
ALA  
SER  
GLN  
MET  
MET  
GLY  
ASN  
THR

• Molecule 4: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB4

Chain D: 42% 27% 10% 19%

MET  
ASN  
V3  
S4  
T5  
S6  
T7  
F8  
G9  
T10  
T11  
R12  
R13  
R14  
L15  
K16  
K17  
K18  
V18  
E19  
N23  
A24  
A25  
T26  
L27  
E32  
F33  
Q34  
Q37  
T38  
N39  
R40  
Q41  
Q42  
E43  
E46  
L47  
L50  
N51  
L52  
S53  
E54  
A55  
R56  
L57  
V58  
L63  
V64  
E65  
R68  
S73  
R76

HIS  
LYS  
LYS  
LYS  
LEU  
LEU  
LYS  
HIS  
GLU  
ASN  
ALA  
ASN  
ASP  
GLU  
THR  
THR  
ALA  
VAL  
GLU  
ASP  
GLU  
GLU  
ASP  
ASP  
ASP  
ASP  
ASP  
PHE  
MET  
HIS  
SER  
GLU  
T118  
T119  
R119  
E120  
K121  
T126  
L130  
T133  
T134  
G135  
G136  
N137  
M138  
K139  
D140  
L141  
K142

R143  
T144  
M145  
Q146  
Y147  
L148  
S152  
R155  
E158  
T159  
V163  
L167  
K168  
S169  
H173  
E176  
D186  
T187  
A188  
D189  
E190  
A191  
S197  
L198  
K201  
I202  
S203  
E206  
L207  
E208  
R209  
T210  
L211  
R212  
E213  
L217  
E218  
T219  
L220  
Y221

• Molecule 5: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 1

Chain E: 4% 60% 36%

MET  
D2  
Q3  
E4  
N5  
E6  
R7  
S10  
W13  
F16  
R17  
T18  
V19  
E20  
V23  
R26  
F29  
I30  
T31  
Q32  
E33  
E34  
D189  
E190  
A191  
L37  
P38  
L39  
F42  
K43  
A44  
K45  
S49  
R52  
P53  
K56  
P57  
P58  
M63  
P64  
T65  
E67  
S68  
I69  
S70  
K71  
F72  
L78

W79  
V80  
E81  
F82  
G83  
D84  
V90  
M93  
T95  
I98  
H99  
I100  
F105  
I109  
F110  
Q113  
N114  
P118  
M121  
R122  
L123  
S126  
I127  
T131  
I132  
E133  
T134  
F135  
L140  
V141  
V142  
T145  
V150  
P151  
K152  
H153  
I154  
R155  
L156  
E160  
K161  
R162  
E163  
R167

K171  
E172  
S173  
Q174  
L175  
P176  
A181  
L186  
Y187  
K191  
R192  
V195  
I198  
I199  
E203  
T204  
Y208  
Y211  
R212  
I213  
C214  
R215

• Molecule 6: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 2

Chain F: 30% 19% 5% 46%

MET  
SER  
THR  
TRR  
GLU  
GLU  
ALA  
PHE  
ASN  
ASP  
GLY  
ASN  
GLU  
ASN  
PHE  
GLU  
ASP  
PHE  
ASP  
VAL  
GLU  
HIS  
PHE  
PHE  
SER  
ASP  
GLU  
GLU  
THR  
THR  
ASP  
GLY  
THR  
THR  
ALA  
ASP  
ASN  
GLY  
LYS  
ILE  
THR  
VAL  
GLY  
GLY  
ASN  
PRO  
GLU  
ASP  
PHE  
GLN  
GLN

HIS  
GLU  
GLN  
ILE  
ARG  
ARG  
LYS  
THR  
LEU  
LYS  
K72  
A73  
I74  
P75  
K76  
R79  
A80  
T81  
P83  
Y84  
K87  
Y88  
E89  
R90  
A91  
R92  
I93  
L94  
R97  
I101  
A105  
V109  
D110  
L111  
T115  
D116  
P117  
L118  
R119  
I120  
A121  
M122  
K123  
K128  
R135  
R136  
F143  
E144

V148  
E149  
I152  
V153  
D154  
L155

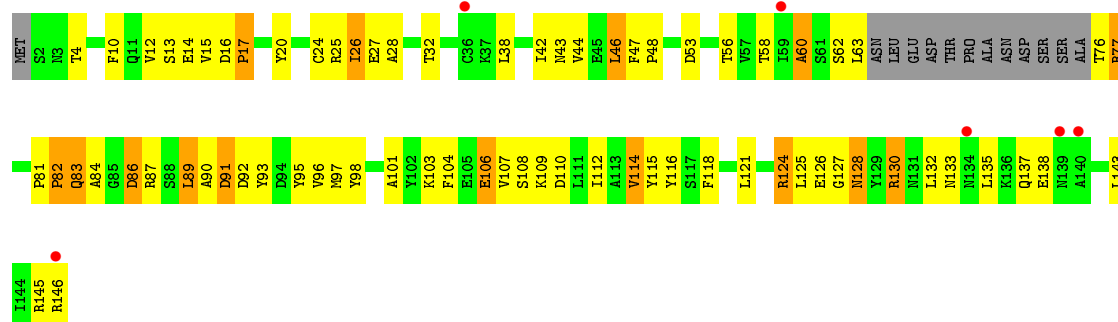
• Molecule 7: RPB7, DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB7

Chain G: 62% 31% 6%

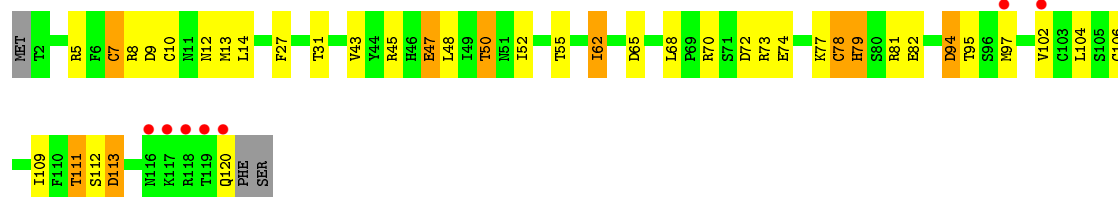
K1  
F2  
F3  
I4  
K5  
L13  
H14  
P15  
S16  
F17  
K22  
K23  
L26  
K27  
L30  
V34  
E35  
G36  
S37  
I45  
L46  
L49  
I54  
P55  
I56  
Q57  
R58  
G59  
B60  
P63  
T64  
S67  
V72  
K73  
R75  
A76  
V77  
V78  
F79  
R80  
K83  
Y92  
S95  
M106



• Molecule 8: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 3



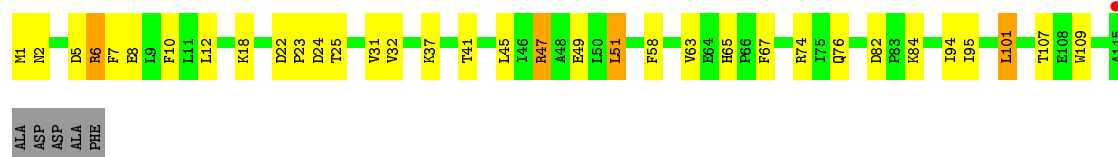
• Molecule 9: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB9



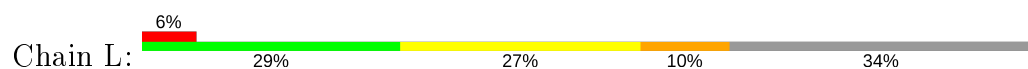
• Molecule 10: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 5

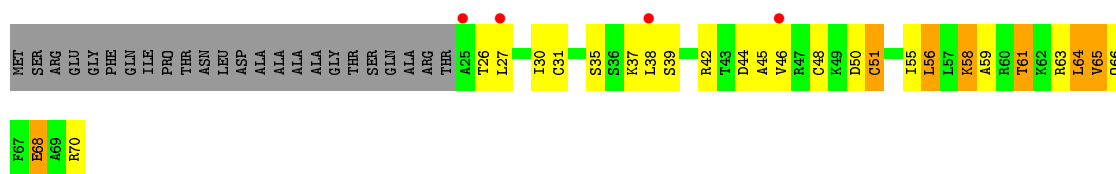


• Molecule 11: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB11



• Molecule 12: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 4





- Molecule 13: 5'-D(\*TP\*AP\*AP\*GP\*TP\*AP\*CP\*TP\*TP\*GP\*AP\*GP\*CP\*TP)-3'

Chain N: 14% 29% 43% 14%

- Molecule 14: 5'-R(\*UP\*UP\*CP\*GP\*AP\*CP\*CP\*AP\*GP\*GP\*AP\*AP)-3'

Chain P: 25% 17% 33% 25%

- Molecule 15: 5'-D(\*AP\*GP\*CP\*TP\*CP\*AP\*AP\*GP\*TP\*AP\*CP\*T\*TTP\*TP\*TP\*CP\*C B RUP\*GP\*GP\*TP\*CP\*AP\*TP\*T)-3'

Chain T: 4% 24% 48% 20% 8%



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	221.64Å 391.52Å 281.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.09 – 3.40 54.09 – 3.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (54.09-3.40) 99.9 (54.09-3.40)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.25 (at 3.40Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.165 , 0.199 0.171 , 0.202	Depositor DCC
$R_{free}$ test set	3298 reflections (1.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	103.5	Xtriage
Anisotropy	0.405	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 100.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.025 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.029 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	32105	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	117.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.85% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: MG, ZN, BRU, TT

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.53	0/11374	0.75	1/15383 (0.0%)
2	B	0.50	0/9010	0.73	3/12149 (0.0%)
3	C	0.49	0/2133	0.67	0/2891
4	D	0.62	2/1444 (0.1%)	0.76	1/1935 (0.1%)
5	E	0.44	0/1788	0.63	0/2406
6	F	0.64	0/691	0.88	1/933 (0.1%)
7	G	0.51	0/1368	0.71	0/1844
8	H	0.39	0/1086	0.63	0/1470
9	I	0.41	0/989	0.63	0/1331
10	J	0.50	0/541	0.79	2/727 (0.3%)
11	K	0.52	0/938	0.68	0/1267
12	L	0.51	0/365	0.83	0/485
13	N	0.94	0/276	1.92	11/424 (2.6%)
14	P	0.69	0/221	1.21	0/343
15	T	0.76	0/475	1.52	12/725 (1.7%)
All	All	0.52	2/32699 (0.0%)	0.77	31/44313 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
4	D	0	1
All	All	0	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	187	THR	CB-CG2	9.38	1.83	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	187	THR	CA-CB	8.33	1.75	1.53

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	N	3	DA	O4'-C1'-N9	11.17	115.82	108.00
15	T	18	DT	O4'-C1'-N1	11.08	115.76	108.00
13	N	3	DA	O4'-C1'-C2'	-11.01	97.09	105.90
13	N	3	DA	C1'-O4'-C4'	-9.53	100.57	110.10
4	D	187	THR	CA-CB-CG2	7.69	123.17	112.40
13	N	8	DT	O4'-C1'-N1	7.52	113.27	108.00
15	T	19	DT	N3-C4-O4	6.98	124.09	119.90
15	T	11	DA	O4'-C1'-N9	6.97	112.88	108.00
13	N	7	DC	O4'-C1'-N1	6.87	112.81	108.00
15	T	19	DT	N3-C2-O2	6.80	126.38	122.30
15	T	19	DT	C5-C4-O4	-6.78	120.16	124.90
15	T	18	DT	N3-C4-O4	6.65	123.89	119.90
13	N	6	DA	O4'-C1'-N9	6.36	112.45	108.00
15	T	16	DT	O4'-C1'-N1	6.35	112.44	108.00
13	N	5	DT	N3-C2-O2	-5.90	118.76	122.30
13	N	8	DT	N3-C4-O4	5.83	123.40	119.90
15	T	13	DT	N3-C4-O4	5.75	123.35	119.90
13	N	3	DA	N9-C1'-C2'	5.74	123.51	112.60
13	N	11	DA	O4'-C1'-N9	5.51	111.86	108.00
15	T	24	DG	O4'-C4'-C3'	-5.49	102.30	104.50
1	A	65	LEU	CA-CB-CG	5.47	127.89	115.30
10	J	3	VAL	CB-CA-C	-5.42	101.10	111.40
15	T	18	DT	C5-C4-O4	-5.42	121.11	124.90
15	T	13	DT	C5-C4-O4	-5.40	121.12	124.90
6	F	135	ARG	NE-CZ-NH1	-5.37	117.61	120.30
2	B	1160	VAL	CB-CA-C	-5.34	101.25	111.40
13	N	5	DT	O4'-C1'-N1	5.22	111.66	108.00
2	B	211	VAL	CB-CA-C	-5.11	101.68	111.40
15	T	12	DG	C4'-C3'-C2'	-5.05	98.56	103.10
2	B	446	LEU	CA-CB-CG	5.03	126.88	115.30
10	J	64	ASN	N-CA-C	5.01	124.54	111.00

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	311	GLN	Peptide

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Mol	Chain	Res	Type	Group
1	A	34	LYS	Peptide
1	A	399	HIS	Peptide
1	A	55	ASP	Peptide
1	A	63	ARG	Peptide
4	D	25	ALA	Peptide

## 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	11174	0	11233	432	0
2	B	8839	0	8876	286	0
3	C	2095	0	2051	72	0
4	D	1434	0	1460	64	0
5	E	1752	0	1776	53	0
6	F	679	0	701	30	0
7	G	1340	0	1357	42	0
8	H	1068	0	1040	50	0
9	I	971	0	927	23	0
10	J	532	0	542	24	0
11	K	920	0	929	28	0
12	L	363	0	386	14	0
13	N	247	0	137	14	0
14	P	197	0	99	28	0
15	T	485	0	273	22	0
16	A	2	0	0	0	0
16	B	1	0	0	0	0
16	C	1	0	0	0	0
16	I	2	0	0	0	0
16	J	1	0	0	0	0
16	L	1	0	0	0	0
17	A	1	0	0	0	0
All	All	32105	0	31787	1066	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 17.

All (1066) 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)
4:D:187:THR:CA	4:D:187:THR:CB	1.75	1.60
4:D:187:THR:CG2	4:D:187:THR:CB	1.83	1.55
14:P:11:A:C8	14:P:11:A:H5'	1.77	1.18
1:A:1100:ARG:HH21	1:A:1351:GLU:HG2	1.11	1.14
14:P:11:A:C8	14:P:11:A:C5'	2.30	1.13
2:B:1182:CYS:SG	2:B:1185:CYS:HB2	2.00	1.02
3:C:148:ARG:H	3:C:151:GLN:HG3	1.26	0.99
1:A:53:LEU:HD23	1:A:54:ASN:H	1.30	0.95
3:C:66:ARG:NH2	10:J:3:VAL:O	2.00	0.95
7:G:26:LEU:HD13	7:G:56:ILE:HD11	1.46	0.94
4:D:40:HIS:HB3	7:G:73:LYS:HE3	1.50	0.93
2:B:338:GLY:HA3	2:B:340:ALA:H	1.35	0.90
7:G:1:MET:SD	7:G:2:PHE:N	2.45	0.90
2:B:766:ARG:HE	2:B:1020:ARG:HG2	1.36	0.88
1:A:902:LEU:HG	1:A:926:GLN:HG3	1.56	0.87
2:B:114:PRO:HG3	2:B:181:LEU:HD11	1.53	0.87
1:A:433:GLU:OE1	2:B:1108:ARG:NH2	2.09	0.85
1:A:855:THR:HG21	1:A:857:ARG:HE	1.42	0.84
15:T:17:TT:H3R	15:T:17:TT:H3'	1.60	0.84
1:A:868:TYR:CE1	1:A:1064:VAL:HG11	2.13	0.83
1:A:115:LEU:HD21	1:A:145:LYS:HG3	1.59	0.83
2:B:806:THR:HG22	2:B:808:ALA:H	1.41	0.83
10:J:44:TYR:HA	10:J:47:ARG:HG3	1.60	0.83
14:P:11:A:H8	14:P:11:A:C5'	1.89	0.82
10:J:48:ARG:HE	10:J:49:MET:HE2	1.43	0.82
7:G:27:LYS:HE2	7:G:54:ILE:HB	1.61	0.82
1:A:53:LEU:CD2	1:A:54:ASN:H	1.93	0.82
1:A:1444:MET:HE1	6:F:135:ARG:HB2	1.60	0.81
2:B:637:LEU:HD13	2:B:693:ILE:HD12	1.61	0.81
2:B:323:VAL:HG23	2:B:324:ILE:HD12	1.64	0.80
2:B:295:GLY:HA2	2:B:298:LEU:HB2	1.63	0.79
14:P:11:A:C8	14:P:11:A:C3'	2.66	0.79
2:B:705:MET:H	2:B:710:LEU:HD12	1.47	0.79
13:N:9:DT:H2'	13:N:10:DG:H8	1.47	0.78
4:D:130:LEU:HD13	4:D:142:LYS:HG2	1.66	0.77
14:P:11:A:H3'	14:P:11:A:H8	1.49	0.77
2:B:1037:LEU:O	10:J:47:ARG:NH1	2.17	0.77
6:F:111:LEU:H	6:F:111:LEU:HD12	1.50	0.77
1:A:709:THR:HG22	1:A:711:ARG:H	1.49	0.77
1:A:53:LEU:HD23	1:A:54:ASN:N	2.00	0.76
1:A:1438:THR:HG22	2:B:1144:ALA:HB3	1.65	0.76
10:J:10:CYS:SG	10:J:43:ARG:NH2	2.57	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:N:13:DC:N4	15:T:6:DG:O6	2.18	0.76
1:A:834:THR:HG21	1:A:1077:THR:HG23	1.68	0.76
1:A:976:THR:OG1	1:A:977:LYS:N	2.18	0.76
1:A:1100:ARG:NH2	1:A:1351:GLU:HG2	1.96	0.75
1:A:61:ILE:HG22	1:A:62:ASP:H	1.52	0.75
1:A:32:VAL:HG11	1:A:80:HIS:HB3	1.69	0.75
2:B:287:ARG:HG2	2:B:292:ILE:HA	1.68	0.75
14:P:10:A:N6	15:T:19:DT:O4	2.14	0.74
2:B:642:ASP:HA	2:B:649:LYS:HA	1.68	0.74
2:B:843:GLN:HG2	2:B:993:THR:HB	1.69	0.74
4:D:187:THR:HA	4:D:187:THR:CB	2.09	0.74
1:A:332:LYS:H	1:A:337:ARG:HB3	1.52	0.74
2:B:639:ILE:HD11	2:B:691:GLU:HB2	1.70	0.74
5:E:100:ILE:HG23	5:E:105:PHE:HB2	1.70	0.74
1:A:200:ARG:NH2	1:A:206:GLU:OE2	2.20	0.74
1:A:52:GLY:H	1:A:56:PRO:HG3	1.53	0.74
1:A:1348:LEU:HG	1:A:1372:VAL:HG22	1.68	0.73
4:D:24:ALA:HB3	4:D:26:THR:HG23	1.69	0.73
14:P:11:A:H3'	14:P:11:A:C8	2.24	0.73
1:A:55:ASP:HA	1:A:58:LEU:H	1.54	0.73
2:B:642:ASP:O	2:B:644:GLU:N	2.22	0.73
12:L:68:GLU:HB2	12:L:70:ARG:HD2	1.70	0.72
4:D:4:SER:OG	4:D:5:THR:N	2.20	0.72
1:A:54:ASN:HB3	1:A:247:ARG:HH22	1.54	0.72
4:D:187:THR:HB	4:D:187:THR:CA	2.11	0.72
7:G:138:THR:HG22	7:G:139:ILE:H	1.54	0.72
4:D:53:SER:HB3	4:D:152:SER:HB3	1.72	0.72
1:A:1111:MET:HG3	1:A:1114:PRO:HG3	1.71	0.72
1:A:709:THR:HB	1:A:712:GLU:H	1.54	0.72
2:B:1180:PHE:H	2:B:1188:LYS:NZ	1.88	0.72
2:B:322:PHE:O	2:B:325:GLN:NE2	2.23	0.71
10:J:48:ARG:O	10:J:52:THR:HG22	1.90	0.71
1:A:1116:LEU:HD12	1:A:1329:THR:HB	1.71	0.71
2:B:429:PHE:O	2:B:433:GLN:NE2	2.23	0.71
14:P:11:A:C8	14:P:11:A:C4'	2.72	0.71
1:A:768:GLN:HG2	1:A:816:HIS:HA	1.73	0.71
1:A:855:THR:HG23	1:A:857:ARG:HG3	1.70	0.71
1:A:868:TYR:HE1	1:A:1064:VAL:HG11	1.56	0.71
2:B:641:GLU:HB2	2:B:643:ASP:HB2	1.71	0.71
9:I:7:CYS:SG	9:I:10:CYS:HB2	2.30	0.71
12:L:46:VAL:HG13	12:L:56:LEU:HD12	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:469:ARG:NH2	2:B:991:GLY:O	2.24	0.70
2:B:291:ILE:HG22	2:B:297:ILE:HG13	1.74	0.70
2:B:996:ARG:NH2	3:C:174:ALA:O	2.24	0.70
1:A:446:ARG:HD2	1:A:480:ALA:HB2	1.74	0.70
2:B:344:LYS:HB3	2:B:347:LYS:HB2	1.74	0.69
13:N:3:DA:H2"	13:N:4:DG:N7	2.07	0.69
1:A:12:ARG:HD2	2:B:1218:THR:HB	1.74	0.69
1:A:88:LYS:HG3	1:A:276:LEU:HD21	1.74	0.69
1:A:871:ASP:OD1	1:A:1366:ARG:NH2	2.26	0.69
5:E:135:PHE:HB3	5:E:140:LEU:HD11	1.74	0.69
13:N:9:DT:H2'	13:N:10:DG:C8	2.26	0.69
14:P:11:A:C8	14:P:11:A:H5'	2.28	0.69
2:B:315:LYS:HG2	9:I:13:MET:HE1	1.74	0.68
14:P:3:G:O2'	14:P:4:A:OP1	2.11	0.68
7:G:34:VAL:O	7:G:37:SER:HB3	1.93	0.68
13:N:8:DT:O2	15:T:12:DG:N2	2.22	0.68
6:F:73:ALA:HB2	6:F:143:PHE:CZ	2.29	0.68
11:K:24:ASP:OD2	11:K:74:ARG:NH1	2.26	0.68
1:A:1148:ILE:HD12	1:A:1196:GLU:HG2	1.76	0.68
1:A:331:GLY:HA3	1:A:337:ARG:HB2	1.76	0.68
1:A:548:ASN:HD21	11:K:47:ARG:HE	1.43	0.67
1:A:879:GLU:OE2	1:A:962:ARG:NH2	2.27	0.67
1:A:42:ASP:O	1:A:44:THR:N	2.28	0.67
3:C:184:ASN:ND2	3:C:189:THR:O	2.28	0.67
6:F:76:LYS:HA	6:F:79:ARG:HD3	1.75	0.67
2:B:531:GLN:NE2	15:T:18:DT:O4	2.28	0.67
1:A:187:LYS:HE3	1:A:198:GLU:HB2	1.77	0.66
1:A:1323:ASP:OD1	1:A:1325:THR:HG22	1.96	0.66
2:B:890:TYR:OH	2:B:936:ASP:OD2	2.11	0.66
1:A:544:ASP:OD1	1:A:545:GLN:N	2.27	0.66
2:B:831:SER:HB2	2:B:833:TYR:HD2	1.60	0.66
8:H:44:VAL:HG13	8:H:48:PRO:HA	1.78	0.66
1:A:1118:VAL:HB	1:A:1306:LEU:HB2	1.75	0.66
1:A:265:LYS:HG3	1:A:303:TYR:HB2	1.78	0.66
8:H:62:SER:OG	8:H:63:LEU:N	2.28	0.66
14:P:10:A:C2'	14:P:11:A:OP1	2.44	0.66
1:A:5:GLN:O	2:B:1159:ARG:NH2	2.28	0.66
1:A:890:ASP:OD1	1:A:940:ARG:NH1	2.29	0.66
2:B:641:GLU:HG3	2:B:652:LYS:HE2	1.78	0.66
1:A:193:ASP:HA	1:A:195:ASP:HB2	1.78	0.65
1:A:34:LYS:HA	1:A:35:ILE:HB	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:969:ARG:NH1	3:C:61:GLU:OE1	2.30	0.65
7:G:30:LEU:HD22	7:G:72:VAL:HG11	1.78	0.65
4:D:18:VAL:HG22	4:D:19:GLU:HA	1.77	0.65
11:K:49:GLU:HG3	11:K:94:ILE:HG12	1.77	0.65
2:B:889:THR:HG22	2:B:891:ASP:H	1.61	0.65
15:T:23:DG:H2"	15:T:24:DG:H8	1.60	0.65
1:A:347:PHE:H	2:B:1107:ALA:HA	1.61	0.65
1:A:1279:ILE:HG23	1:A:1308:THR:HG23	1.78	0.65
6:F:128:LYS:HG3	6:F:149:GLU:HA	1.79	0.65
9:I:78:CYS:SG	9:I:106:CYS:HB3	2.36	0.65
2:B:801:LYS:O	10:J:52:THR:OG1	2.15	0.65
12:L:61:THR:HB	12:L:63:ARG:HG2	1.79	0.65
8:H:124:ARG:HE	8:H:126:GLU:HG3	1.61	0.64
2:B:328:GLU:N	2:B:328:GLU:OE1	2.26	0.64
4:D:155:ARG:HB3	4:D:219:THR:HG21	1.78	0.64
3:C:6:PRO:HB3	3:C:25:VAL:HG13	1.80	0.64
1:A:369:SER:HB3	11:K:2:ASN:OD1	1.97	0.64
4:D:40:HIS:HB3	7:G:73:LYS:CE	2.25	0.64
3:C:183:TRP:O	3:C:185:LYS:N	2.30	0.64
1:A:445:ASN:HB2	1:A:455:MET:HG2	1.80	0.64
4:D:187:THR:HB	4:D:187:THR:CG2	2.19	0.64
14:P:11:A:H8	14:P:11:A:C3'	2.07	0.64
1:A:1376:THR:HG23	5:E:212:ARG:HH22	1.63	0.63
1:A:1387:HIS:CE1	13:N:7:DC:H5'	2.33	0.63
2:B:102:VAL:HG13	2:B:112:LEU:HD22	1.81	0.63
1:A:41:MET:CB	1:A:49:LYS:HA	2.29	0.63
1:A:79:GLY:H	2:B:1205:GLN:HE22	1.47	0.63
1:A:353:ILE:HG21	1:A:487:MET:HE3	1.79	0.63
1:A:302:THR:HA	1:A:305:ASP:O	1.99	0.63
2:B:298:LEU:HD23	2:B:314:LEU:HD13	1.82	0.62
8:H:17:PRO:HB3	8:H:24:CYS:SG	2.39	0.62
1:A:1224:LEU:HD11	1:A:1240:CYS:HB3	1.80	0.62
1:A:93:VAL:HG22	1:A:301:ALA:HA	1.82	0.62
2:B:1082:MET:HA	3:C:189:THR:HA	1.81	0.62
2:B:822:ASN:O	10:J:48:ARG:NH1	2.32	0.62
5:E:145:THR:HG21	5:E:187:TYR:CD2	2.34	0.62
5:E:4:GLU:HB3	5:E:7:ARG:NE	2.15	0.62
1:A:481:ASP:OD1	1:A:481:ASP:N	2.30	0.62
3:C:148:ARG:HD3	3:C:149:LYS:HG2	1.82	0.62
7:G:23:LYS:HE3	7:G:27:LYS:HE3	1.80	0.62
2:B:904:ARG:NH1	12:L:66:GLN:O	2.31	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:30:LEU:HD22	10:J:34:THR:HB	1.80	0.62
6:F:109:VAL:HG11	6:F:123:LYS:HG2	1.81	0.62
3:C:148:ARG:HG3	3:C:149:LYS:H	1.65	0.61
4:D:23:ASN:N	4:D:23:ASN:OD1	2.33	0.61
2:B:408:LEU:HD21	2:B:545:ILE:HD13	1.82	0.61
7:G:45:ILE:HA	7:G:78:VAL:HG12	1.82	0.61
1:A:407:ARG:HG2	1:A:430:TRP:CZ2	2.35	0.61
6:F:87:LYS:HA	6:F:155:LEU:HD11	1.82	0.61
7:G:83:LYS:HG3	7:G:149:GLY:HA2	1.82	0.61
2:B:914:LYS:HB3	2:B:937:ALA:HB3	1.80	0.61
1:A:635:ARG:HH11	1:A:635:ARG:HA	1.65	0.61
2:B:806:THR:HB	2:B:809:MET:HG3	1.82	0.61
3:C:147:LEU:HB3	3:C:151:GLN:HB2	1.80	0.61
14:P:6:C:H2'	14:P:7:A:H8	1.65	0.61
2:B:583:ASN:HD21	2:B:628:THR:HG22	1.65	0.61
3:C:148:ARG:N	3:C:151:GLN:HG3	2.07	0.61
9:I:102:VAL:HG22	9:I:109:ILE:HG13	1.82	0.61
11:K:45:LEU:HG	11:K:94:ILE:HD13	1.83	0.61
1:A:1141:THR:HG23	1:A:1205:LYS:HD3	1.82	0.61
1:A:1116:LEU:HD13	1:A:1311:VAL:HG22	1.83	0.61
1:A:1211:GLN:HE22	1:A:1274:ARG:HH12	1.49	0.61
1:A:1350:LYS:O	1:A:1354:ASN:ND2	2.34	0.60
2:B:1084:GLN:HG2	3:C:201:TRP:CZ2	2.35	0.60
1:A:485:ASP:N	1:A:485:ASP:OD1	2.30	0.60
2:B:169:ARG:N	2:B:454:THR:OG1	2.34	0.60
1:A:845:LEU:HD12	1:A:1069:ALA:HB2	1.84	0.60
4:D:26:THR:OG1	4:D:26:THR:O	2.18	0.60
14:P:11:A:H8	14:P:11:A:H5'	1.61	0.60
1:A:567:LYS:HA	1:A:568:PRO:C	2.22	0.60
1:A:588:LEU:HD22	1:A:607:ILE:HD12	1.83	0.60
1:A:1170:ILE:O	1:A:1174:PHE:HB2	2.02	0.60
1:A:335:ARG:NH1	2:B:1206:GLU:OE2	2.33	0.60
3:C:3:GLU:N	3:C:7:GLN:HE22	2.00	0.60
2:B:1103:ILE:O	2:B:1122:ARG:NH1	2.35	0.60
2:B:651:LEU:HD12	2:B:651:LEU:H	1.65	0.60
2:B:475:SER:O	2:B:476:ARG:HB2	2.01	0.60
1:A:315:LEU:HA	1:A:321:PRO:HA	1.85	0.59
1:A:49:LYS:HE2	1:A:61:ILE:H	1.66	0.59
1:A:646:PHE:O	1:A:650:GLN:HG2	2.01	0.59
1:A:875:ALA:HB2	1:A:1366:ARG:HD3	1.84	0.59
8:H:4:THR:HA	8:H:60:ALA:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:709:THR:HG23	9:I:94:ASP:HA	1.85	0.59
1:A:1437:GLY:O	1:A:1440:ALA:N	2.35	0.59
1:A:383:TYR:HB3	6:F:115:THR:HG22	1.83	0.59
4:D:158:GLU:CD	4:D:158:GLU:H	2.06	0.59
3:C:149:LYS:HG3	3:C:150:GLY:H	1.68	0.59
8:H:82:PRO:O	8:H:84:ALA:N	2.36	0.59
2:B:1116:ARG:HG3	2:B:1198:TYR:CD2	2.38	0.59
2:B:705:MET:HE2	2:B:745:PRO:HB3	1.85	0.59
10:J:14:VAL:HG13	10:J:50:ILE:HD11	1.85	0.59
2:B:580:VAL:HG22	2:B:624:LEU:HB3	1.85	0.59
1:A:407:ARG:HD3	1:A:413:ILE:HD11	1.83	0.58
2:B:102:VAL:HG11	2:B:122:LEU:HD13	1.86	0.58
2:B:363:HIS:O	2:B:365:THR:N	2.36	0.58
2:B:378:LEU:O	2:B:382:ILE:HG13	2.03	0.58
1:A:448:PRO:HB2	1:A:450:LEU:HD11	1.86	0.58
5:E:23:VAL:HG13	5:E:78:LEU:HD23	1.84	0.58
1:A:567:LYS:HG2	1:A:569:LYS:H	1.67	0.58
1:A:836:TYR:CZ	1:A:840:ARG:HD2	2.39	0.58
2:B:428:ILE:HG12	2:B:448:ILE:HG23	1.85	0.58
2:B:936:ASP:OD1	2:B:937:ALA:N	2.36	0.58
4:D:15:LEU:O	4:D:17:LYS:N	2.37	0.58
8:H:127:GLY:HA3	8:H:130:ARG:HH21	1.67	0.58
1:A:118:HIS:HB3	1:A:152:VAL:HG11	1.86	0.58
8:H:63:LEU:HB3	8:H:90:ALA:HB2	1.85	0.58
2:B:860:MET:HB2	2:B:965:LYS:HG2	1.86	0.58
1:A:779:PHE:CE2	1:A:785:PRO:HD3	2.39	0.58
8:H:43:ASN:HD21	8:H:46:LEU:HD23	1.69	0.58
11:K:8:GLU:O	11:K:37:LYS:HD2	2.03	0.57
1:A:483:ASP:C	1:A:483:ASP:OD1	2.42	0.57
2:B:758:PHE:CE1	2:B:1044:ALA:HA	2.39	0.57
3:C:148:ARG:HD3	3:C:149:LYS:HE2	1.86	0.57
4:D:188:ALA:HB2	4:D:208:GLU:HG3	1.85	0.57
2:B:102:VAL:HG23	2:B:110:HIS:HB3	1.87	0.57
2:B:365:THR:HG23	2:B:367:LEU:HG	1.87	0.57
3:C:100:THR:HG22	3:C:119:VAL:HG13	1.87	0.57
4:D:118:THR:HB	4:D:121:LYS:HG3	1.86	0.57
5:E:78:LEU:HD11	5:E:109:ILE:HG13	1.87	0.57
2:B:29:ASP:HB3	2:B:658:ILE:HG12	1.87	0.57
2:B:351:TYR:CZ	2:B:355:ILE:HD11	2.39	0.57
10:J:57:ILE:HA	10:J:60:PHE:CD2	2.40	0.57
1:A:1349:TYR:HA	1:A:1372:VAL:HG21	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1437:GLY:O	1:A:1439:GLY:N	2.38	0.56
2:B:1181:GLU:HB2	2:B:1188:LYS:HE3	1.87	0.56
1:A:590:ARG:NH2	1:A:621:THR:OG1	2.37	0.56
1:A:35:ILE:HG21	1:A:241:VAL:HG21	1.86	0.56
2:B:732:SER:HB2	2:B:734:HIS:NE2	2.19	0.56
2:B:766:ARG:HH11	2:B:766:ARG:HA	1.70	0.56
2:B:847:ASP:OD2	11:K:6:ARG:NH2	2.38	0.56
1:A:836:TYR:CE2	1:A:840:ARG:HD2	2.40	0.56
14:P:10:A:H2'	14:P:11:A:OP1	2.05	0.56
1:A:629:LEU:O	1:A:633:VAL:HG23	2.05	0.56
1:A:882:SER:O	1:A:1025:ARG:NH2	2.36	0.56
2:B:1043:ASP:OD1	2:B:1045:SER:HB2	2.05	0.56
1:A:41:MET:HG3	1:A:257:ARG:HH21	1.70	0.56
1:A:52:GLY:N	1:A:56:PRO:HG3	2.19	0.56
1:A:79:GLY:HA3	1:A:243:PRO:HG2	1.86	0.56
1:A:399:HIS:HB3	1:A:400:PRO:HD3	1.87	0.56
1:A:982:THR:H	1:A:985:ASP:HB2	1.70	0.56
2:B:830:TYR:CZ	2:B:1000:PRO:HD3	2.40	0.56
1:A:226:GLU:HG3	1:A:227:VAL:HG23	1.88	0.56
2:B:579:ARG:HB2	2:B:586:TRP:NE1	2.21	0.56
2:B:872:GLU:HG2	2:B:916:THR:HG23	1.88	0.56
3:C:177:GLU:HB2	3:C:231:ASN:HB3	1.88	0.56
1:A:870:GLU:HG2	5:E:208:TYR:CG	2.40	0.56
1:A:848:ILE:HG21	1:A:1370:LEU:HD21	1.88	0.55
1:A:639:PRO:HG2	1:A:640:GLN:HG2	1.88	0.55
1:A:852:TYR:O	6:F:81:THR:HG22	2.06	0.55
1:A:1172:LEU:C	1:A:1174:PHE:H	2.09	0.55
1:A:35:ILE:HG21	1:A:84:ILE:HG22	1.88	0.55
2:B:577:ALA:HB1	2:B:589:VAL:HB	1.89	0.55
2:B:834:ASN:HB3	2:B:840:ILE:HG13	1.87	0.55
3:C:114:TYR:HB3	3:C:140:ASN:O	2.07	0.55
3:C:56:THR:HG21	3:C:145:CYS:SG	2.46	0.55
4:D:118:THR:O	4:D:120:GLU:N	2.39	0.55
1:A:332:LYS:H	1:A:337:ARG:CB	2.20	0.55
2:B:882:THR:HG22	2:B:884:ARG:H	1.71	0.55
8:H:56:THR:OG1	8:H:146:ARG:NH1	2.38	0.55
1:A:172:PRO:HB3	1:A:185:TRP:CE2	2.41	0.55
4:D:118:THR:N	4:D:155:ARG:HH12	2.05	0.55
1:A:335:ARG:HD2	2:B:1206:GLU:OE1	2.07	0.55
1:A:508:PRO:O	1:A:511:ILE:HG13	2.06	0.55
2:B:226:PHE:HA	2:B:395:GLN:HG3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:7:THR:CG2	7:G:5:LYS:HZ1	2.19	0.55
2:B:1180:PHE:H	2:B:1188:LYS:HZ1	1.52	0.55
1:A:898:ARG:O	1:A:1029:ARG:NH1	2.40	0.54
1:A:1130:GLN:O	1:A:1134:ILE:HG13	2.06	0.54
6:F:76:LYS:HA	6:F:79:ARG:CD	2.37	0.54
6:F:79:ARG:HG2	6:F:144:GLU:HB3	1.89	0.54
8:H:43:ASN:ND2	8:H:46:LEU:HD23	2.21	0.54
15:T:18:DT:H1'	15:T:19:DT:C5	2.42	0.54
1:A:290:GLU:HA	1:A:293:GLU:HB2	1.88	0.54
1:A:568:PRO:HG2	8:H:46:LEU:HD12	1.88	0.54
1:A:939:ASP:OD2	1:A:1023:ARG:NH1	2.40	0.54
5:E:16:PHE:CE2	5:E:20:LYS:HE2	2.42	0.54
1:A:1267:MET:HA	1:A:1271:ILE:HD12	1.89	0.54
1:A:87:ALA:HB3	1:A:276:LEU:HD23	1.89	0.54
4:D:8:PHE:HZ	4:D:37:GLN:NE2	2.03	0.54
8:H:106:GLU:HA	8:H:112:ILE:HD12	1.89	0.54
1:A:1155:ASP:HB3	1:A:1241:ARG:HH21	1.73	0.54
1:A:1402:PHE:CE2	1:A:1403:GLU:HG3	2.42	0.54
1:A:586:ILE:HD11	1:A:637:LYS:HG2	1.90	0.54
1:A:981:LEU:HD21	1:A:1039:LYS:HA	1.90	0.54
1:A:855:THR:CG2	1:A:857:ARG:HE	2.16	0.54
1:A:1101:LEU:HB2	1:A:1355:VAL:HG11	1.90	0.54
1:A:636:GLU:OE1	1:A:962:ARG:NH1	2.40	0.54
10:J:9:SER:OG	10:J:48:ARG:NH2	2.41	0.54
1:A:132:LYS:HD2	1:A:1411:GLU:OE1	2.08	0.54
1:A:149:GLU:HB3	1:A:164:ARG:HH21	1.73	0.54
1:A:41:MET:HB2	1:A:49:LYS:HA	1.90	0.54
1:A:34:LYS:HB3	1:A:83:HIS:CE1	2.42	0.54
2:B:361:LEU:HD11	2:B:381:MET:HE1	1.90	0.54
2:B:707:PRO:O	2:B:710:LEU:N	2.41	0.54
1:A:472:LEU:O	1:A:475:THR:HB	2.08	0.54
5:E:176:PRO:O	5:E:212:ARG:HA	2.07	0.54
1:A:785:PRO:HB2	2:B:703:ILE:HD12	1.88	0.54
1:A:974:ASP:C	1:A:976:THR:H	2.11	0.54
1:A:12:ARG:O	2:B:1194:ILE:HG22	2.08	0.54
3:C:22:LEU:HD23	3:C:230:MET:HE3	1.89	0.54
2:B:998:ASP:OD1	3:C:35:ARG:NH2	2.40	0.54
9:I:77:LYS:O	9:I:79:HIS:N	2.40	0.54
1:A:337:ARG:HD3	2:B:1132:GLU:OE2	2.08	0.53
1:A:761:MET:HA	1:A:804:TYR:HB2	1.90	0.53
1:A:836:TYR:CZ	15:T:16:DT:H2''	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:604:ARG:NH1	2:B:691:GLU:OE2	2.41	0.53
2:B:711:GLU:HB2	2:B:712:PRO:HD3	1.90	0.53
11:K:47:ARG:HB3	11:K:47:ARG:NH1	2.24	0.53
1:A:668:ASP:HB3	1:A:743:VAL:HG23	1.90	0.53
3:C:244:VAL:O	3:C:248:ILE:HG13	2.08	0.53
2:B:800:GLN:HB3	10:J:52:THR:HG23	1.88	0.53
1:A:590:ARG:NH1	1:A:592:ASP:OD2	2.41	0.53
15:T:16:DT:H5'	15:T:17:TT:O2P	2.08	0.53
1:A:1116:LEU:H	1:A:1308:THR:HB	1.73	0.53
2:B:766:ARG:NE	2:B:1020:ARG:HG2	2.16	0.53
4:D:13:ARG:HH12	4:D:18:VAL:H	1.57	0.53
10:J:36:LEU:HD11	10:J:51:LEU:HB2	1.91	0.53
1:A:932:GLU:O	1:A:936:LEU:HG	2.09	0.53
14:P:10:A:C2	14:P:11:A:C2	2.97	0.53
1:A:441:PRO:HD2	1:A:498:ARG:NH2	2.23	0.53
2:B:338:GLY:HA3	2:B:340:ALA:N	2.16	0.53
1:A:1333:ILE:HD12	1:A:1333:ILE:H	1.73	0.53
6:F:72:LYS:HG2	6:F:72:LYS:O	2.09	0.53
7:G:122:ASN:ND2	7:G:125:SER:HB3	2.23	0.53
1:A:119:ASN:OD1	1:A:120:GLU:N	2.42	0.52
2:B:43:LEU:HD13	2:B:492:LEU:HD13	1.91	0.52
2:B:662:MET:HA	2:B:665:GLU:HG3	1.90	0.52
3:C:31:ASN:O	3:C:35:ARG:HG3	2.09	0.52
9:I:82:GLU:HG2	9:I:104:LEU:HD12	1.91	0.52
2:B:979:LYS:NZ	14:P:11:A:OP2	2.41	0.52
2:B:315:LYS:N	2:B:316:PRO:HD2	2.25	0.52
1:A:761:MET:HG3	2:B:1021:MET:HG2	1.91	0.52
4:D:134:THR:HG22	4:D:136:GLY:H	1.75	0.52
1:A:285:PRO:O	1:A:287:HIS:N	2.39	0.52
2:B:842:ASN:HB3	2:B:845:SER:HB2	1.91	0.52
2:B:986:GLN:HE22	2:B:1022:THR:HG21	1.75	0.52
12:L:48:CYS:HB3	12:L:51:CYS:SG	2.50	0.52
1:A:216:VAL:O	1:A:220:THR:HB	2.09	0.52
1:A:567:LYS:HA	1:A:569:LYS:N	2.25	0.52
1:A:767:GLN:HA	1:A:799:PHE:HA	1.91	0.52
4:D:65:GLU:HA	4:D:68:ARG:HG3	1.92	0.52
1:A:1404:GLU:O	1:A:1408:ILE:HG13	2.10	0.52
1:A:821:ARG:HB2	1:A:821:ARG:NH1	2.24	0.52
2:B:564:GLU:HB2	2:B:589:VAL:HG23	1.91	0.52
5:E:152:LYS:HD2	5:E:199:ILE:HB	1.92	0.52
9:I:50:THR:HG22	9:I:52:ILE:HG12	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1149:ALA:HB2	9:I:47:GLU:HA	1.91	0.52
3:C:196:ASP:HB3	3:C:199:LYS:HB2	1.92	0.52
3:C:92:CYS:SG	3:C:94:LYS:HB2	2.49	0.52
11:K:23:PRO:HA	11:K:31:VAL:HG23	1.92	0.52
1:A:1293:SER:OG	1:A:1295:THR:HG23	2.10	0.51
2:B:25:ILE:HD12	2:B:653:VAL:HB	1.93	0.51
2:B:899:ILE:HD11	2:B:911:ILE:HA	1.91	0.51
4:D:50:LEU:HD21	7:G:4:ILE:HD12	1.92	0.51
7:G:127:PRO:HB2	7:G:139:ILE:HD12	1.93	0.51
1:A:172:PRO:HD3	1:A:185:TRP:NE1	2.24	0.51
2:B:259:TYR:CE1	2:B:270:LYS:HD2	2.44	0.51
4:D:173:HIS:CE1	4:D:201:LYS:HE3	2.46	0.51
5:E:20:LYS:HE3	5:E:34:GLU:HG2	1.92	0.51
4:D:37:GLN:HE22	7:G:5:LYS:NZ	2.09	0.51
4:D:32:GLU:O	7:G:5:LYS:HE2	2.10	0.51
1:A:1276:VAL:HG11	1:A:1315:GLU:HB3	1.90	0.51
2:B:873:THR:O	2:B:914:LYS:HA	2.10	0.51
1:A:1268:LEU:HD13	9:I:48:LEU:HD21	1.93	0.51
1:A:1444:MET:HG2	7:G:58:ARG:HB3	1.92	0.51
1:A:907:THR:HG22	1:A:908:LEU:O	2.10	0.51
4:D:159:THR:O	4:D:163:VAL:HG23	2.11	0.51
1:A:40:THR:HG21	1:A:259:GLU:OE2	2.10	0.51
1:A:436:ILE:HD11	1:A:491:VAL:HG11	1.92	0.51
2:B:466:TRP:HB2	2:B:479:VAL:HG21	1.91	0.51
5:E:26:ARG:NH2	5:E:133:GLU:OE1	2.44	0.51
1:A:1259:MET:HA	1:A:1262:LYS:HD2	1.92	0.51
4:D:41:GLN:HB2	4:D:43:GLU:HG2	1.91	0.51
1:A:378:GLU:OE2	1:A:387:ARG:NH2	2.43	0.51
2:B:41:LYS:HB3	2:B:45:SER:HB3	1.93	0.51
2:B:597:MET:HG3	2:B:601:ARG:HH12	1.76	0.51
1:A:357:PRO:HD2	2:B:833:TYR:CZ	2.46	0.51
8:H:84:ALA:HA	8:H:87:ARG:HD2	1.93	0.51
10:J:22:LEU:O	10:J:26:GLN:HG3	2.11	0.51
1:A:998:LEU:HA	1:A:1011:GLN:HE22	1.75	0.50
1:A:283:GLY:O	1:A:285:PRO:HD3	2.11	0.50
3:C:165:LYS:O	11:K:6:ARG:NH1	2.39	0.50
2:B:900:ALA:HB3	12:L:61:THR:HG23	1.92	0.50
1:A:855:THR:HG21	1:A:857:ARG:NE	2.19	0.50
7:G:13:LEU:HD22	7:G:17:PHE:HB2	1.94	0.50
1:A:483:ASP:OD2	14:P:11:A:O3'	2.30	0.50
1:A:483:ASP:OD1	1:A:485:ASP:OD1	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:997:GLU:HG2	3:C:39:ALA:HB2	1.92	0.50
9:I:65:ASP:HB3	9:I:68:LEU:HD12	1.93	0.50
11:K:58:PHE:HB3	11:K:76:GLN:HB3	1.92	0.50
15:T:6:DG:H2"	15:T:7:DC:OP2	2.11	0.50
1:A:1286:LYS:HD2	1:A:1304:TRP:CZ2	2.45	0.50
1:A:188:ASP:O	1:A:193:ASP:HB2	2.11	0.50
1:A:390:GLN:O	1:A:394:ASN:HB2	2.11	0.50
1:A:457:ALA:HB3	1:A:506:ALA:HA	1.92	0.50
2:B:842:ASN:O	2:B:846:ILE:HG13	2.12	0.50
1:A:354:SER:O	1:A:469:ARG:HA	2.11	0.50
1:A:523:ILE:HB	1:A:622:VAL:HG13	1.93	0.50
2:B:999:MET:HG3	2:B:1000:PRO:HD2	1.92	0.50
7:G:128:PRO:O	7:G:138:THR:HG23	2.11	0.50
1:A:780:VAL:O	1:A:782:ARG:HD3	2.12	0.50
2:B:1106:ARG:HG3	2:B:1107:ALA:N	2.24	0.50
2:B:779:GLY:HA2	2:B:796:LEU:HB2	1.92	0.50
5:E:16:PHE:CZ	5:E:20:LYS:HE2	2.47	0.50
8:H:103:LYS:HB3	8:H:115:TYR:CD1	2.47	0.50
1:A:833:GLU:HG2	13:N:3:DA:H2	1.76	0.50
14:P:6:C:H2'	14:P:7:A:C8	2.45	0.50
1:A:239:LEU:HD12	1:A:240:PRO:HD2	1.94	0.50
1:A:481:ASP:OD2	1:A:483:ASP:OD2	2.30	0.50
1:A:565:ILE:O	1:A:570:PRO:HA	2.12	0.50
1:A:531:ILE:HG21	1:A:622:VAL:HG11	1.94	0.50
2:B:258:LEU:HB2	2:B:385:LEU:HD21	1.94	0.50
2:B:287:ARG:NH1	2:B:324:ILE:O	2.41	0.50
2:B:791:THR:O	2:B:792:MET:HB2	2.11	0.50
2:B:882:THR:CG2	2:B:884:ARG:H	2.24	0.50
2:B:897:GLY:O	2:B:898:LEU:HD23	2.12	0.50
1:A:537:ARG:HB2	8:H:20:TYR:CE1	2.46	0.50
1:A:164:ARG:HG3	1:A:165:GLY:H	1.76	0.49
1:A:317:LYS:O	1:A:318:SER:HB3	2.12	0.49
2:B:1152:MET:HB3	2:B:1157:ALA:HB2	1.94	0.49
1:A:62:ASP:O	1:A:64:ASN:N	2.43	0.49
1:A:756:ILE:O	1:A:760:GLN:HG3	2.12	0.49
1:A:1294:PRO:HG2	1:A:1295:THR:HG22	1.95	0.49
1:A:746:MET:SD	2:B:1015:HIS:HD2	2.35	0.49
2:B:840:ILE:HB	2:B:1011:ILE:HB	1.94	0.49
1:A:1383:SER:HB2	1:A:1385:THR:HG23	1.95	0.49
1:A:399:HIS:CG	1:A:400:PRO:N	2.78	0.49
1:A:862:ASN:HA	5:E:174:GLN:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:198:ILE:HD13	5:E:212:ARG:HG3	1.95	0.49
15:T:23:DG:H2"	15:T:24:DG:C8	2.43	0.49
1:A:481:ASP:O	1:A:485:ASP:OD2	2.30	0.49
2:B:861:ASP:OD1	2:B:862:GLN:N	2.42	0.49
4:D:119:ARG:HB3	4:D:119:ARG:CZ	2.42	0.49
8:H:82:PRO:C	8:H:84:ALA:H	2.16	0.49
1:A:1208:THR:OG1	1:A:1211:GLN:HG2	2.12	0.49
1:A:1211:GLN:NE2	1:A:1274:ARG:HH12	2.10	0.49
1:A:535:THR:O	1:A:575:LYS:HE3	2.13	0.49
2:B:653:VAL:HG22	2:B:689:LEU:HB3	1.95	0.49
2:B:732:SER:HB2	2:B:734:HIS:CD2	2.48	0.49
2:B:911:ILE:HG22	2:B:912:ILE:HG13	1.95	0.49
3:C:143:LEU:HD21	3:C:146:LYS:HE3	1.93	0.49
5:E:135:PHE:HD2	5:E:140:LEU:HD21	1.78	0.49
8:H:84:ALA:HA	8:H:87:ARG:HB2	1.93	0.49
1:A:1193:LEU:HB2	1:A:1260:LEU:HD21	1.94	0.49
1:A:1189:SER:HB2	1:A:1242:VAL:HG23	1.95	0.49
2:B:664:THR:HA	2:B:667:GLN:HG3	1.94	0.49
2:B:314:LEU:O	2:B:318:VAL:HG23	2.12	0.49
2:B:371:GLU:N	2:B:371:GLU:OE1	2.46	0.49
7:G:106:MET:HG3	7:G:157:ILE:O	2.13	0.49
14:P:10:A:O2'	14:P:11:A:P	2.70	0.49
1:A:105:CYS:SG	1:A:139:TRP:HA	2.53	0.49
1:A:326:ARG:HG3	1:A:1406:VAL:HG21	1.95	0.49
1:A:670:ILE:HG13	1:A:805:LEU:HD21	1.95	0.49
1:A:853:ASP:OD1	1:A:855:THR:HB	2.12	0.49
3:C:39:ALA:HA	3:C:164:ALA:HB3	1.94	0.49
4:D:119:ARG:NH1	4:D:119:ARG:HB3	2.28	0.49
5:E:90:VAL:HA	5:E:93:MET:HB3	1.95	0.49
12:L:61:THR:HB	12:L:63:ARG:H	1.77	0.49
1:A:1197:LEU:HD11	1:A:1238:ILE:HD11	1.93	0.49
1:A:782:ARG:NH1	1:A:787:PHE:O	2.46	0.49
2:B:843:GLN:HG2	2:B:993:THR:CB	2.40	0.49
8:H:15:VAL:HG22	8:H:26:ILE:HD11	1.95	0.49
2:B:344:LYS:O	2:B:348:ARG:HD2	2.12	0.48
14:P:10:A:O2'	14:P:11:A:OP1	2.30	0.48
1:A:297:GLN:O	1:A:297:GLN:NE2	2.45	0.48
2:B:521:LEU:HD22	2:B:633:VAL:HG12	1.95	0.48
2:B:552:MET:SD	2:B:552:MET:N	2.87	0.48
6:F:105:ALA:HA	7:G:16:SER:HA	1.94	0.48
1:A:974:ASP:O	1:A:976:THR:N	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:697:ALA:HB1	9:I:97:MET:HE3	1.95	0.48
1:A:910:PRO:HA	1:A:916:GLY:HA3	1.95	0.48
2:B:1116:ARG:HG3	2:B:1198:TYR:CE2	2.49	0.48
2:B:234:ILE:HG21	2:B:237:VAL:HG23	1.95	0.48
2:B:885:MET:HB3	2:B:936:ASP:HB2	1.94	0.48
3:C:148:ARG:HG3	3:C:149:LYS:N	2.28	0.48
3:C:183:TRP:CZ2	3:C:207:CYS:HB3	2.48	0.48
2:B:952:VAL:HB	12:L:58:LYS:HB2	1.94	0.48
1:A:1388:GLY:O	1:A:1391:ARG:HG3	2.12	0.48
1:A:41:MET:HB3	1:A:49:LYS:HA	1.96	0.48
1:A:335:ARG:HD3	2:B:1202:LEU:HD13	1.95	0.48
5:E:153:HIS:C	5:E:154:ILE:HD12	2.34	0.48
1:A:836:TYR:OH	1:A:1403:GLU:OE1	2.32	0.48
1:A:990:VAL:O	1:A:994:GLN:HG3	2.12	0.48
2:B:705:MET:N	2:B:710:LEU:HD12	2.24	0.48
6:F:94:LEU:HD13	6:F:122:MET:HG2	1.96	0.48
15:T:17:TT:H6T	15:T:17:TT:H2R2	1.64	0.48
1:A:388:LEU:HA	1:A:388:LEU:HD23	1.64	0.48
1:A:512:VAL:HA	1:A:519:PRO:HA	1.96	0.48
3:C:125:MET:HB2	3:C:127:ARG:HE	1.78	0.48
3:C:77:ILE:HA	3:C:129:ILE:HD11	1.95	0.48
4:D:191:ALA:HB2	4:D:211:LEU:HD11	1.95	0.48
1:A:381:THR:HG22	1:A:384:ASN:OD1	2.14	0.48
2:B:351:TYR:CE1	2:B:355:ILE:HD11	2.49	0.48
2:B:701:ILE:HD11	2:B:703:ILE:HD11	1.94	0.48
6:F:82:THR:HG22	6:F:83:PRO:HD2	1.95	0.48
1:A:472:LEU:HD13	2:B:835:GLN:NE2	2.29	0.48
1:A:824:LEU:HD21	2:B:765:PRO:HB3	1.95	0.48
2:B:802:PRO:HG3	2:B:814:PHE:HE2	1.79	0.48
2:B:1224:PHE:CD1	5:E:171:LYS:HG3	2.49	0.48
5:E:56:LYS:HG3	5:E:84:ASP:OD2	2.14	0.48
7:G:137:ILE:HD13	7:G:143:ILE:HD11	1.96	0.48
8:H:110:ASP:HB3	8:H:128:ASN:OD1	2.13	0.48
1:A:1025:ARG:O	1:A:1035:TYR:HE2	1.97	0.48
2:B:361:LEU:HD21	2:B:377:PHE:HD2	1.79	0.48
6:F:90:ARG:HD3	6:F:155:LEU:HD13	1.96	0.48
7:G:83:LYS:H	7:G:83:LYS:HD2	1.78	0.48
1:A:852:TYR:CZ	6:F:136:ARG:HG2	2.49	0.47
1:A:566:ILE:HD12	8:H:96:VAL:HG12	1.96	0.47
15:T:9:DC:H2'	15:T:10:DA:C8	2.49	0.47
1:A:332:LYS:HB2	1:A:337:ARG:CZ	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:67:LEU:HA	3:C:70:ILE:CD1	2.44	0.47
7:G:92:VAL:O	7:G:139:ILE:HG12	2.14	0.47
8:H:38:LEU:HD13	8:H:125:LEU:HD13	1.95	0.47
8:H:89:LEU:HD12	8:H:91:ASP:O	2.13	0.47
1:A:154:SER:HB3	1:A:162:VAL:HG23	1.96	0.47
1:A:353:ILE:HD13	1:A:487:MET:CE	2.45	0.47
1:A:919:ILE:HG13	1:A:925:LEU:HD13	1.96	0.47
2:B:558:LEU:HB3	2:B:563:MET:HE2	1.94	0.47
2:B:559:SER:HA	2:B:563:MET:HB3	1.96	0.47
6:F:83:PRO:O	6:F:152:ILE:HG13	2.13	0.47
7:G:15:PRO:HD3	7:G:67:SER:HA	1.95	0.47
1:A:855:THR:CG2	1:A:857:ARG:HG3	2.43	0.47
1:A:925:LEU:HD22	1:A:983:ILE:HB	1.96	0.47
7:G:49:LEU:HG	7:G:76:ALA:HA	1.96	0.47
8:H:127:GLY:CA	8:H:130:ARG:HH21	2.28	0.47
1:A:882:SER:HB2	1:A:953:ASN:OD1	2.13	0.47
2:B:1150:ARG:HA	2:B:1154:ALA:HB3	1.96	0.47
1:A:1444:MET:HG3	7:G:59:GLY:O	2.15	0.47
1:A:549:MET:CE	1:A:656:TRP:HD1	2.28	0.47
2:B:1204:PHE:O	2:B:1208:MET:HG3	2.15	0.47
8:H:104:PHE:CE1	8:H:114:VAL:HG12	2.50	0.47
11:K:5:ASP:HB2	11:K:8:GLU:HG3	1.96	0.47
1:A:117:GLU:H	1:A:117:GLU:CD	2.17	0.47
1:A:298:PHE:CZ	1:A:314:ALA:HB2	2.50	0.47
13:N:3:DA:H2"	13:N:4:DG:C8	2.49	0.47
1:A:1027:ALA:O	1:A:1031:VAL:HG23	2.15	0.47
1:A:353:ILE:HD13	1:A:487:MET:HE2	1.96	0.47
1:A:598:LEU:HD22	8:H:25:ARG:NH1	2.29	0.47
2:B:780:VAL:HG21	10:J:56:LEU:CD1	2.45	0.47
5:E:161:LYS:HD2	5:E:195:VAL:HG23	1.97	0.47
1:A:1378:GLN:OE1	1:A:1378:GLN:HA	2.14	0.47
1:A:1445:ILE:O	1:A:1445:ILE:HD12	2.14	0.47
1:A:1450:LEU:HD23	1:A:1450:LEU:O	2.14	0.47
2:B:217:ARG:NH1	2:B:407:ASP:OD1	2.47	0.47
2:B:579:ARG:HB2	2:B:586:TRP:HE1	1.78	0.47
1:A:216:VAL:HA	1:A:219:PHE:CE2	2.49	0.47
1:A:399:HIS:O	1:A:400:PRO:C	2.53	0.47
3:C:145:CYS:SG	3:C:146:LYS:N	2.88	0.47
1:A:1343:ALA:HB2	5:E:150:VAL:HG22	1.96	0.47
1:A:870:GLU:HG2	5:E:208:TYR:CD2	2.49	0.47
2:B:100:PRO:HG3	2:B:172:ILE:HG13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1188:LYS:HE2	2:B:1188:LYS:O	2.15	0.47
2:B:635:ARG:NH1	2:B:742:GLU:OE1	2.45	0.47
1:A:187:LYS:HB3	1:A:188:ASP:H	1.65	0.46
2:B:101:MET:HA	2:B:112:LEU:H	1.80	0.46
12:L:31:CYS:O	12:L:35:SER:HA	2.15	0.46
1:A:242:PRO:HA	1:A:243:PRO:HD3	1.58	0.46
1:A:399:HIS:O	1:A:401:GLY:N	2.48	0.46
2:B:1006:ILE:HG22	2:B:1007:VAL:N	2.30	0.46
2:B:1100:ASP:OD2	11:K:1:MET:HB3	2.15	0.46
2:B:373:ARG:HA	2:B:566:LEU:HD23	1.97	0.46
2:B:483:LEU:HD11	2:B:491:THR:HG23	1.97	0.46
1:A:485:ASP:OD1	14:P:11:A:O2'	2.30	0.46
1:A:227:VAL:HG12	1:A:228:PHE:CD1	2.51	0.46
1:A:597:LEU:HD13	1:A:597:LEU:HA	1.69	0.46
2:B:901:PRO:HD3	12:L:58:LYS:HB3	1.96	0.46
9:I:72:ASP:O	9:I:81:ARG:HG2	2.16	0.46
1:A:916:GLY:O	1:A:919:ILE:HG22	2.16	0.46
3:C:97:VAL:HG21	3:C:129:ILE:HG23	1.96	0.46
1:A:270:LEU:HA	1:A:270:LEU:HD22	1.74	0.46
1:A:666:ILE:HD11	2:B:1030:LEU:HD13	1.98	0.46
3:C:262:LEU:HA	3:C:262:LEU:HD23	1.75	0.46
1:A:997:LEU:O	1:A:1011:GLN:NE2	2.48	0.46
1:A:896:ARG:HD3	1:A:1030:ARG:HD2	1.98	0.46
2:B:952:VAL:HG22	2:B:966:VAL:HG13	1.97	0.46
3:C:99:LEU:HB2	3:C:157:CYS:HB2	1.97	0.46
7:G:1:MET:HB2	7:G:1:MET:HE2	1.85	0.46
7:G:34:VAL:HG13	7:G:45:ILE:HG21	1.98	0.46
1:A:1161:THR:HB	1:A:1170:ILE:HD11	1.97	0.46
1:A:121:LEU:HD12	1:A:121:LEU:H	1.79	0.46
1:A:1327:ILE:HD13	1:A:1328:TYR:N	2.30	0.46
1:A:239:LEU:HA	1:A:240:PRO:HD2	1.82	0.46
1:A:524:VAL:HG22	1:A:525:GLN:N	2.30	0.46
1:A:714:PHE:O	1:A:718:VAL:HG23	2.16	0.46
2:B:35:SER:HA	2:B:811:TYR:CE1	2.51	0.46
2:B:583:ASN:HD21	2:B:628:THR:CG2	2.28	0.46
2:B:658:ILE:O	2:B:662:MET:HE2	2.16	0.46
5:E:33:GLU:H	5:E:33:GLU:HG3	1.47	0.46
1:A:483:ASP:OD1	14:P:11:A:O3'	2.30	0.46
1:A:645:LEU:HD11	1:A:649:ILE:HD11	1.98	0.46
2:B:128:LEU:HD21	2:B:170:LEU:HB2	1.98	0.46
2:B:313:MET:HE3	2:B:386:LEU:HD22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:T:17:TT:H3'	15:T:17:TT:C3R	2.40	0.46
1:A:41:MET:HG3	1:A:257:ARG:NH2	2.31	0.46
3:C:69:LEU:HD23	10:J:6:ARG:HB2	1.97	0.46
1:A:1438:THR:N	6:F:88:TYR:HB3	2.31	0.46
1:A:871:ASP:CG	1:A:1366:ARG:HH22	2.19	0.46
1:A:35:ILE:HD12	1:A:53:LEU:HA	1.98	0.46
1:A:446:ARG:HB2	1:A:487:MET:SD	2.56	0.46
1:A:830:LYS:O	1:A:834:THR:HB	2.16	0.46
2:B:212:LEU:HA	2:B:212:LEU:HD23	1.66	0.46
2:B:649:LYS:HD3	2:B:736:THR:O	2.16	0.46
7:G:106:MET:HG2	7:G:107:LYS:N	2.30	0.46
9:I:45:ARG:NH2	9:I:47:GLU:OE1	2.48	0.46
1:A:726:ARG:HD3	1:A:766:GLY:HA3	1.97	0.45
1:A:826:ASP:HA	1:A:829:VAL:HB	1.98	0.45
2:B:979:LYS:HE2	2:B:987:LYS:HB2	1.99	0.45
3:C:149:LYS:C	3:C:151:GLN:H	2.18	0.45
1:A:200:ARG:HH22	1:A:206:GLU:CD	2.16	0.45
1:A:106:VAL:HG21	1:A:214:ILE:HG12	1.99	0.45
3:C:128:ASN:O	3:C:129:ILE:HD12	2.15	0.45
4:D:14:ARG:HD3	4:D:14:ARG:HA	1.65	0.45
9:I:111:THR:OG1	9:I:113:ASP:HB2	2.17	0.45
1:A:776:ALA:O	1:A:783:THR:HG22	2.17	0.45
2:B:221:ASN:N	2:B:241:ARG:O	2.34	0.45
5:E:192:ARG:HA	5:E:214:CYS:HB3	1.98	0.45
3:C:66:ARG:NH2	10:J:2:ILE:HG23	2.32	0.45
1:A:1095:THR:HG21	1:A:1112:LYS:HD2	1.99	0.45
1:A:1195:LEU:HA	1:A:1195:LEU:HD23	1.64	0.45
1:A:1224:LEU:HD12	1:A:1241:ARG:O	2.17	0.45
1:A:19:PHE:O	1:A:1416:ALA:HA	2.15	0.45
1:A:287:HIS:HA	1:A:290:GLU:HG2	1.98	0.45
2:B:796:LEU:HD12	2:B:796:LEU:HA	1.70	0.45
3:C:18:VAL:HG23	3:C:240:VAL:HB	1.98	0.45
3:C:46:ILE:HA	3:C:159:ALA:HA	1.99	0.45
1:A:483:ASP:CG	14:P:11:A:HO3'	2.19	0.45
1:A:1120:LEU:HD12	1:A:1120:LEU:HA	1.71	0.45
1:A:140:THR:HA	1:A:143:LYS:HE2	1.99	0.45
1:A:541:ILE:HD13	1:A:549:MET:HE1	1.98	0.45
2:B:1156:ASP:OD1	2:B:1198:TYR:N	2.49	0.45
2:B:642:ASP:HB3	2:B:649:LYS:HD2	1.99	0.45
1:A:642:CYS:O	1:A:645:LEU:HB3	2.16	0.45
1:A:685:GLU:HG3	1:A:686:ALA:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:185:THR:HG23	2:B:188:ASP:OD2	2.17	0.45
3:C:15:LYS:O	3:C:240:VAL:HG22	2.16	0.45
5:E:79:TRP:HE1	5:E:81:GLU:HB2	1.82	0.45
1:A:128:ILE:HB	1:A:134:ARG:HB2	1.98	0.45
1:A:1444:MET:HE1	6:F:135:ARG:CB	2.41	0.45
1:A:218:ASP:O	1:A:222:LEU:HD12	2.17	0.45
2:B:170:LEU:HD12	2:B:171:PRO:HD2	1.98	0.45
2:B:866:TYR:HB2	2:B:870:ILE:HB	1.99	0.45
3:C:36:VAL:HG21	3:C:251:LEU:HB2	1.99	0.45
4:D:56:ARG:HB2	4:D:148:LEU:HD22	1.98	0.45
14:P:10:A:HO2'	14:P:11:A:P	2.39	0.45
1:A:1446:ASP:HB3	1:A:1449:SER:OG	2.17	0.45
1:A:547:LEU:HD22	11:K:58:PHE:CD2	2.51	0.45
1:A:901:LEU:HD22	1:A:919:ILE:HG23	1.99	0.45
2:B:63:ILE:HA	2:B:63:ILE:HD12	1.80	0.45
2:B:871:THR:HG22	2:B:872:GLU:N	2.31	0.45
5:E:26:ARG:HH22	5:E:133:GLU:CD	2.20	0.45
8:H:46:LEU:HD13	8:H:46:LEU:HA	1.65	0.45
10:J:6:ARG:HG3	10:J:13:VAL:HA	1.97	0.45
1:A:1120:LEU:O	1:A:1323:ASP:HB2	2.17	0.45
1:A:262:LEU:HG	1:A:328:ARG:HH21	1.82	0.45
1:A:262:LEU:HG	1:A:328:ARG:NH2	2.32	0.45
2:B:383:ASN:OD1	2:B:387:LEU:HD22	2.16	0.45
2:B:405:ARG:HB3	2:B:631:GLY:HA3	1.98	0.45
2:B:848:ARG:HD2	10:J:8:PHE:O	2.17	0.45
4:D:52:LEU:O	4:D:53:SER:OG	2.24	0.45
12:L:61:THR:CB	12:L:63:ARG:HG2	2.46	0.45
2:B:902:GLY:O	12:L:65:VAL:HG11	2.17	0.45
1:A:419:LYS:HG3	1:A:420:ARG:N	2.31	0.45
1:A:566:ILE:HD11	8:H:98:TYR:HB2	1.99	0.45
1:A:898:ARG:HB2	1:A:933:TYR:CE2	2.52	0.45
1:A:942:PHE:HD2	1:A:943:LEU:HD23	1.80	0.45
4:D:155:ARG:H	4:D:219:THR:HG21	1.81	0.45
4:D:203:SER:OG	4:D:206:GLU:HB2	2.17	0.45
5:E:67:GLU:O	5:E:70:SER:HB3	2.17	0.45
5:E:94:LYS:O	5:E:98:ILE:HG13	2.17	0.45
8:H:133:ASN:O	8:H:135:LEU:HD12	2.16	0.45
1:A:549:MET:HE1	1:A:656:TRP:HD1	1.82	0.44
2:B:1166:CYS:HB3	2:B:1185:CYS:SG	2.56	0.44
2:B:219:ALA:HB2	2:B:405:ARG:HG2	1.99	0.44
1:A:264:PHE:O	1:A:267:ALA:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:LYS:HD2	1:A:55:ASP:HB3	1.99	0.44
1:A:869:GLY:O	5:E:204:THR:HG21	2.17	0.44
1:A:9:ALA:HA	1:A:10:PRO:HD2	1.65	0.44
1:A:1438:THR:HB	2:B:1142:GLY:O	2.17	0.44
2:B:189:LEU:O	2:B:192:LEU:N	2.51	0.44
2:B:550:ASP:HA	2:B:551:PRO:HD3	1.84	0.44
2:B:882:THR:C	2:B:884:ARG:H	2.21	0.44
12:L:30:ILE:O	12:L:56:LEU:HA	2.17	0.44
1:A:483:ASP:CG	14:P:11:A:O3'	2.55	0.44
1:A:1396:ALA:HA	1:A:1399:ARG:NH2	2.32	0.44
1:A:193:ASP:HA	1:A:194:ALA:HA	1.53	0.44
1:A:215:SER:HB3	1:A:218:ASP:OD2	2.17	0.44
1:A:562:THR:O	1:A:576:GLN:NE2	2.51	0.44
1:A:841:LEU:HA	1:A:841:LEU:HD23	1.79	0.44
4:D:186:ASP:O	4:D:187:THR:C	2.55	0.44
1:A:1172:LEU:O	1:A:1174:PHE:N	2.43	0.44
1:A:1402:PHE:O	1:A:1404:GLU:N	2.50	0.44
2:B:291:ILE:HG23	2:B:296:GLU:HG2	1.99	0.44
2:B:753:ALA:HA	2:B:756:ILE:HD12	1.98	0.44
2:B:914:LYS:HE2	2:B:937:ALA:HB1	1.99	0.44
8:H:16:ASP:HA	8:H:17:PRO:HD3	1.83	0.44
11:K:37:LYS:HA	11:K:37:LYS:HD3	1.87	0.44
1:A:337:ARG:HH22	15:T:17:TT:P	2.41	0.44
1:A:922:ASP:CG	1:A:925:LEU:HD12	2.38	0.44
1:A:898:ARG:HD3	1:A:933:TYR:CD2	2.52	0.44
4:D:25:ALA:C	4:D:27:LEU:H	2.21	0.44
4:D:7:THR:HB	4:D:8:PHE:H	1.19	0.44
8:H:95:TYR:CE1	8:H:97:MET:HG3	2.52	0.44
15:T:26:DC:N3	15:T:27:DA:N6	2.66	0.44
1:A:1219:THR:HG21	1:A:1271:ILE:HD11	2.00	0.44
1:A:251:SER:HA	1:A:257:ARG:O	2.17	0.44
2:B:361:LEU:HD21	2:B:377:PHE:CD2	2.53	0.44
2:B:613:VAL:HG22	2:B:627:PHE:O	2.18	0.44
3:C:148:ARG:H	3:C:151:GLN:CG	2.13	0.44
4:D:206:GLU:O	4:D:209:ARG:HB2	2.17	0.44
6:F:72:LYS:N	6:F:72:LYS:HE2	2.33	0.44
11:K:65:HIS:CE1	11:K:67:PHE:CG	3.05	0.44
1:A:270:LEU:O	1:A:274:ILE:HG13	2.17	0.44
1:A:779:PHE:CZ	1:A:785:PRO:HD3	2.53	0.44
2:B:879:ARG:NE	2:B:883:LEU:HG	2.33	0.44
4:D:167:LEU:O	4:D:169:SER:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:176:GLU:OE2	4:D:197:SER:HB2	2.18	0.44
5:E:4:GLU:HB3	5:E:7:ARG:HE	1.83	0.44
6:F:83:PRO:HG2	6:F:84:TYR:CD1	2.53	0.44
8:H:12:VAL:HG23	8:H:53:ASP:O	2.18	0.44
1:A:1015:VAL:HG12	1:A:1019:CYS:SG	2.58	0.44
1:A:1032:LEU:O	1:A:1036:ARG:HD3	2.18	0.44
1:A:993:LEU:HD22	1:A:1046:LEU:HD22	2.00	0.44
1:A:1170:ILE:HG13	1:A:1170:ILE:H	1.64	0.44
1:A:222:LEU:O	1:A:224:PHE:N	2.51	0.44
1:A:644:LYS:HD2	1:A:644:LYS:HA	1.73	0.44
2:B:1032:SER:HB3	2:B:1089:PRO:HB2	2.00	0.44
2:B:351:TYR:O	2:B:354:ASP:HB2	2.18	0.44
8:H:4:THR:HA	8:H:60:ALA:CB	2.48	0.44
11:K:32:VAL:HG22	11:K:74:ARG:HG3	2.00	0.44
15:T:18:DT:C6	15:T:19:DT:H73	2.53	0.44
1:A:1009:ASN:OD1	1:A:1012:ARG:NH1	2.50	0.44
1:A:265:LYS:HA	1:A:265:LYS:HD3	1.84	0.44
1:A:380:VAL:HG12	1:A:428:TYR:HA	2.00	0.44
2:B:871:THR:HG22	2:B:872:GLU:O	2.18	0.44
8:H:101:ALA:HB2	8:H:116:TYR:CE1	2.52	0.44
1:A:1199:ARG:NH2	1:A:1231:ASP:O	2.46	0.43
1:A:1441:PHE:CZ	6:F:89:GLU:HA	2.53	0.43
1:A:394:ASN:OD1	1:A:398:GLU:HG2	2.18	0.43
2:B:1197:PRO:O	2:B:1200:ALA:N	2.47	0.43
2:B:225:VAL:HG11	2:B:385:LEU:HA	2.00	0.43
11:K:51:LEU:HD12	11:K:51:LEU:HA	1.68	0.43
2:B:294:ASP:HB2	9:I:12:ASN:HA	2.00	0.43
2:B:819:ALA:HB1	2:B:1093:GLN:HE21	1.83	0.43
3:C:201:TRP:HA	3:C:202:PRO:HD3	1.71	0.43
7:G:131:GLN:HG2	7:G:136:VAL:HG23	2.00	0.43
1:A:1202:MET:O	1:A:1207:LEU:N	2.47	0.43
1:A:857:ARG:HD3	1:A:861:GLY:O	2.18	0.43
4:D:158:GLU:N	4:D:158:GLU:OE1	2.51	0.43
9:I:62:ILE:HD12	9:I:62:ILE:HA	1.78	0.43
1:A:1430:LEU:HB3	1:A:1432:GLN:HG3	1.99	0.43
1:A:709:THR:HG22	1:A:710:LEU:N	2.34	0.43
1:A:872:GLY:O	1:A:1058:VAL:HG22	2.18	0.43
3:C:124:LEU:O	3:C:127:ARG:HG2	2.18	0.43
3:C:75:MET:HB3	3:C:128:ASN:HB3	1.99	0.43
4:D:217:LEU:O	4:D:219:THR:N	2.52	0.43
4:D:51:ASN:OD1	4:D:54:GLU:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:10:PHE:HB3	8:H:28:ALA:HB1	1.99	0.43
9:I:74:GLU:HB3	9:I:81:ARG:HG3	1.99	0.43
15:T:18:DT:C2	15:T:19:DT:O4	2.71	0.43
1:A:1095:THR:HG21	1:A:1112:LYS:HB3	2.00	0.43
1:A:868:TYR:CD2	1:A:1058:VAL:HG11	2.53	0.43
1:A:949:ASP:OD2	1:A:951:GLU:HB2	2.18	0.43
2:B:1132:GLU:O	2:B:1135:ARG:HB3	2.18	0.43
5:E:44:ALA:O	5:E:45:LYS:HB2	2.19	0.43
2:B:1031:LEU:HB2	2:B:1055:ILE:HD13	2.00	0.43
1:A:7:SER:HB3	2:B:1193:GLN:OE1	2.18	0.43
6:F:97:ARG:HA	6:F:97:ARG:HD2	1.66	0.43
4:D:144:THR:HG21	7:G:46:LEU:HD13	2.00	0.43
8:H:26:ILE:HD12	8:H:26:ILE:HA	1.74	0.43
14:P:11:A:N9	14:P:11:A:H5"	2.23	0.43
1:A:963:ILE:HD13	1:A:1048:ASN:HB3	2.00	0.43
4:D:46:GLU:HG2	4:D:47:LEU:H	1.84	0.43
5:E:13:TRP:CZ3	5:E:39:LEU:HB2	2.54	0.43
6:F:101:ILE:HD13	6:F:120:ILE:CG2	2.49	0.43
1:A:208:LEU:HD23	1:A:235:ILE:HD12	2.01	0.43
2:B:185:THR:O	2:B:188:ASP:HB2	2.19	0.43
2:B:455:SER:HA	2:B:458:LYS:HB2	1.99	0.43
2:B:649:LYS:HE2	2:B:738:PHE:O	2.19	0.43
3:C:177:GLU:O	3:C:230:MET:HA	2.19	0.43
7:G:154:VAL:HG23	7:G:155:SER:H	1.83	0.43
1:A:407:ARG:CD	1:A:413:ILE:HD11	2.48	0.43
1:A:456:MET:HE2	1:A:478:TYR:CZ	2.54	0.43
3:C:241:ASP:HB3	11:K:109:TRP:CE2	2.54	0.43
4:D:121:LYS:HB3	4:D:121:LYS:HE2	1.83	0.43
7:G:126:ASN:HA	7:G:127:PRO:HA	1.81	0.43
8:H:63:LEU:CB	8:H:90:ALA:HB2	2.48	0.43
11:K:7:PHE:HA	11:K:10:PHE:CE1	2.54	0.43
2:B:1058:LEU:O	2:B:1061:GLU:HB2	2.19	0.43
1:A:344:ARG:HB3	2:B:1118:PRO:HB2	2.00	0.43
2:B:1110:PRO:O	2:B:1119:VAL:HG13	2.19	0.43
7:G:1:MET:CG	7:G:2:PHE:N	2.82	0.43
1:A:1364:ASN:OD1	1:A:1366:ARG:HG2	2.18	0.42
1:A:915:SER:HA	1:A:918:GLU:OE2	2.18	0.42
2:B:1176:ASN:H	2:B:1178:ASN:H	1.67	0.42
2:B:401:PHE:HD2	2:B:521:LEU:HD12	1.84	0.42
2:B:498:THR:O	2:B:536:VAL:HA	2.18	0.42
2:B:882:THR:HG22	2:B:884:ARG:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:111:THR:HG22	7:G:113:HIS:H	1.84	0.42
10:J:21:TYR:O	10:J:25:LEU:HG	2.19	0.42
1:A:1173:HIS:HB3	1:A:1227:ILE:HG23	2.00	0.42
1:A:1215:ARG:HD3	1:A:1218:GLN:NE2	2.35	0.42
1:A:436:ILE:HA	1:A:436:ILE:HD12	1.67	0.42
1:A:800:VAL:HG13	1:A:812:GLU:OE1	2.19	0.42
2:B:112:LEU:O	2:B:180:TYR:HE2	2.02	0.42
2:B:408:LEU:HA	2:B:408:LEU:HD13	1.79	0.42
2:B:551:PRO:HG3	2:B:628:THR:HG21	2.01	0.42
5:E:163:GLU:OE2	5:E:167:ARG:NE	2.51	0.42
8:H:92:ASP:H	8:H:93:TYR:HD1	1.67	0.42
1:A:1155:ASP:OD2	1:A:1161:THR:HG23	2.18	0.42
1:A:1189:SER:O	1:A:1241:ARG:HD3	2.19	0.42
1:A:20:GLY:O	1:A:21:LEU:HD23	2.19	0.42
1:A:335:ARG:O	1:A:339:ASN:HB2	2.19	0.42
1:A:49:LYS:CE	1:A:61:ILE:H	2.32	0.42
2:B:125:SER:O	2:B:169:ARG:NH1	2.52	0.42
2:B:344:LYS:HZ3	2:B:346:GLU:H	1.67	0.42
2:B:635:ARG:HH12	2:B:742:GLU:CD	2.22	0.42
3:C:163:ILE:HD12	3:C:165:LYS:HB2	2.00	0.42
3:C:57:VAL:H	3:C:57:VAL:HG13	1.55	0.42
4:D:135:GLY:O	4:D:137:ASN:N	2.45	0.42
7:G:132:SER:HB3	7:G:135:ASP:H	1.83	0.42
1:A:331:GLY:O	1:A:332:LYS:HB3	2.19	0.42
1:A:382:PRO:N	1:A:428:TYR:HE1	2.17	0.42
1:A:743:VAL:O	1:A:747:VAL:HG23	2.20	0.42
1:A:786:HIS:HE1	2:B:519:TRP:CE2	2.37	0.42
1:A:883:LEU:O	1:A:886:ILE:HG22	2.19	0.42
2:B:854:LEU:HD23	2:B:854:LEU:HA	1.73	0.42
3:C:164:ALA:HA	3:C:167:HIS:O	2.19	0.42
4:D:187:THR:O	4:D:190:GLU:HB3	2.18	0.42
4:D:46:GLU:HG2	4:D:47:LEU:N	2.34	0.42
7:G:1:MET:HE1	7:G:80:LYS:O	2.19	0.42
1:A:1147:THR:HG22	9:I:48:LEU:HD13	2.00	0.42
1:A:219:PHE:HA	1:A:222:LEU:CD1	2.49	0.42
1:A:406:ILE:HB	1:A:431:LYS:HB2	2.02	0.42
1:A:602:ASP:HB3	1:A:616:VAL:HG23	2.02	0.42
4:D:63:LEU:O	4:D:133:THR:HG21	2.20	0.42
5:E:211:TYR:N	5:E:211:TYR:CD1	2.87	0.42
1:A:1100:ARG:O	1:A:1104:ILE:HG13	2.19	0.42
1:A:1223:ASP:HA	1:A:1243:VAL:HB	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:LEU:HD23	1:A:126:LEU:HA	1.87	0.42
2:B:879:ARG:HB3	2:B:880:THR:H	1.56	0.42
3:C:66:ARG:O	3:C:70:ILE:HD12	2.19	0.42
5:E:52:ARG:HA	5:E:53:PRO:HD2	1.66	0.42
8:H:109:LYS:HB3	8:H:110:ASP:H	1.53	0.42
1:A:219:PHE:HA	1:A:222:LEU:HD12	2.00	0.42
1:A:25:GLU:CD	1:A:25:GLU:H	2.20	0.42
1:A:648:ASN:O	1:A:652:VAL:HG23	2.20	0.42
2:B:1167:GLY:H	2:B:1215:ARG:HD3	1.85	0.42
2:B:582:VAL:HG22	2:B:626:ILE:HB	2.01	0.42
5:E:195:VAL:HG22	5:E:213:ILE:HG13	2.00	0.42
1:A:1387:HIS:CE1	13:N:6:DA:H2"	2.55	0.42
1:A:380:VAL:HG13	1:A:385:ILE:HG12	2.01	0.42
1:A:556:TRP:CZ3	1:A:558:GLY:HA2	2.55	0.42
1:A:664:THR:HG22	2:B:1014:PRO:HB3	2.02	0.42
1:A:710:LEU:HD12	1:A:710:LEU:HA	1.83	0.42
2:B:744:HIS:CE1	2:B:746:SER:HG	2.38	0.42
2:B:758:PHE:CZ	2:B:1044:ALA:HA	2.54	0.42
4:D:13:ARG:NH1	4:D:18:VAL:H	2.18	0.42
7:G:46:LEU:HA	7:G:46:LEU:HD23	1.88	0.42
8:H:47:PHE:HB3	8:H:95:TYR:CD2	2.55	0.42
10:J:57:ILE:HA	10:J:60:PHE:HD2	1.82	0.42
1:A:1412:ALA:HA	1:A:1417:GLU:HG3	2.02	0.42
1:A:196:GLU:HA	1:A:197:PRO:HD3	1.90	0.42
1:A:444:PHE:HE2	1:A:470:LEU:HD23	1.83	0.42
1:A:74:MET:O	1:A:76:GLU:N	2.52	0.42
2:B:807:ARG:HG2	2:B:1045:SER:OG	2.20	0.42
2:B:422:LYS:HA	2:B:425:THR:HB	2.02	0.42
2:B:956:THR:HA	2:B:961:LEU:O	2.19	0.42
3:C:41:ILE:HB	3:C:172:PRO:HG3	2.02	0.42
3:C:31:ASN:O	3:C:34:ARG:HB3	2.19	0.42
4:D:24:ALA:HB3	4:D:26:THR:CG2	2.44	0.42
1:A:1318:THR:HG22	5:E:142:VAL:HG23	2.00	0.42
1:A:1377:THR:HG22	5:E:176:PRO:HB3	2.02	0.42
5:E:65:THR:O	5:E:69:ILE:HG13	2.20	0.42
2:B:412:LEU:HA	2:B:412:LEU:HD13	1.84	0.42
2:B:821:GLN:OE1	2:B:850:LEU:HD12	2.20	0.42
5:E:135:PHE:CD2	5:E:140:LEU:HD21	2.55	0.42
11:K:82:ASP:OD2	11:K:84:LYS:HB2	2.20	0.42
14:P:6:C:C2	14:P:7:A:C8	3.08	0.42
1:A:681:GLU:HA	1:A:684:ALA:HB3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:848:ILE:HA	1:A:857:ARG:O	2.20	0.41
2:B:426:LYS:O	2:B:430:ARG:HD2	2.19	0.41
2:B:853:SER:HB3	2:B:1094:ARG:HH11	1.85	0.41
3:C:62:PHE:O	3:C:66:ARG:HG3	2.20	0.41
5:E:4:GLU:HB3	5:E:7:ARG:CZ	2.50	0.41
8:H:15:VAL:HA	8:H:26:ILE:HD12	2.01	0.41
8:H:82:PRO:HB2	8:H:83:GLN:H	1.61	0.41
13:N:6:DA:C2	13:N:7:DC:C2	3.08	0.41
1:A:116:ASP:N	1:A:116:ASP:OD1	2.53	0.41
1:A:928:LEU:HA	1:A:928:LEU:HD23	1.86	0.41
1:A:986:ILE:HG21	1:A:1028:THR:HA	2.01	0.41
2:B:1081:LEU:HA	2:B:1081:LEU:HD23	1.86	0.41
1:A:452:LYS:HG2	2:B:1141:HIS:CE1	2.55	0.41
2:B:336:ARG:HG3	2:B:348:ARG:NH2	2.35	0.41
5:E:35:VAL:O	5:E:37:LEU:N	2.51	0.41
1:A:770:VAL:HG12	1:A:771:GLU:HG3	2.02	0.41
2:B:1065:GLN:HG2	3:C:201:TRP:CZ3	2.55	0.41
2:B:276:ILE:HA	2:B:338:GLY:O	2.20	0.41
2:B:26:THR:OG1	2:B:27:ALA:N	2.54	0.41
2:B:554:ILE:O	2:B:558:LEU:N	2.47	0.41
4:D:54:GLU:O	4:D:58:VAL:HG23	2.19	0.41
2:B:1224:PHE:HD1	5:E:171:LYS:HG3	1.86	0.41
1:A:1004:ASN:ND2	5:E:167:ARG:HD2	2.35	0.41
1:A:11:LEU:HD13	2:B:1193:GLN:HG3	2.03	0.41
1:A:239:LEU:HD12	1:A:239:LEU:HA	1.81	0.41
1:A:335:ARG:HA	1:A:339:ASN:HB2	2.02	0.41
1:A:534:LEU:O	1:A:574:GLY:HA3	2.20	0.41
2:B:246:LYS:HG2	2:B:418:LYS:HZ1	1.85	0.41
2:B:461:LEU:HD12	2:B:461:LEU:H	1.86	0.41
2:B:519:TRP:C	2:B:519:TRP:CD1	2.93	0.41
2:B:770:GLN:HG2	2:B:983:ARG:O	2.20	0.41
2:B:916:THR:HA	2:B:917:PRO:HD3	1.90	0.41
3:C:251:LEU:O	3:C:255:VAL:HG23	2.20	0.41
13:N:4:DG:N2	13:N:5:DT:C2	2.88	0.41
15:T:26:DC:C4	15:T:27:DA:N6	2.89	0.41
1:A:181:LEU:HA	1:A:181:LEU:HD23	1.80	0.41
1:A:43:GLU:OE2	1:A:48:ALA:HB3	2.21	0.41
1:A:568:PRO:HB2	3:C:221:TYR:CE2	2.56	0.41
1:A:49:LYS:NZ	1:A:60:SER:HA	2.35	0.41
2:B:99:LYS:HB3	2:B:180:TYR:CE1	2.56	0.41
2:B:227:LYS:H	2:B:395:GLN:CD	2.24	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:453:ILE:H	2:B:453:ILE:HD12	1.86	0.41
8:H:118:PHE:HB2	8:H:121:LEU:HB2	2.03	0.41
9:I:50:THR:CG2	9:I:52:ILE:HG12	2.49	0.41
9:I:73:ARG:HH12	9:I:112:SER:CB	2.34	0.41
11:K:10:PHE:HA	11:K:37:LYS:HB3	2.01	0.41
1:A:481:ASP:O	1:A:485:ASP:CG	2.59	0.41
1:A:679:ILE:HG23	1:A:729:ALA:HB1	2.03	0.41
1:A:993:LEU:HD12	1:A:993:LEU:O	2.20	0.41
2:B:254:LEU:HD22	2:B:361:LEU:HD13	2.02	0.41
2:B:879:ARG:HA	2:B:879:ARG:HD2	1.58	0.41
3:C:47:ASP:HA	3:C:169:LYS:NZ	2.36	0.41
3:C:92:CYS:O	3:C:96:SER:OG	2.35	0.41
4:D:144:THR:CG2	4:D:148:LEU:HD12	2.50	0.41
9:I:14:LEU:HB3	9:I:27:PHE:HB3	2.01	0.41
10:J:8:PHE:H	10:J:49:MET:CE	2.34	0.41
1:A:1064:VAL:HG12	1:A:1064:VAL:O	2.21	0.41
1:A:1366:ARG:HG2	1:A:1366:ARG:H	1.41	0.41
1:A:41:MET:HA	1:A:50:ILE:H	1.86	0.41
2:B:530:GLY:H	2:B:533:CYS:HB2	1.86	0.41
2:B:680:THR:O	2:B:683:SER:HB2	2.20	0.41
2:B:710:LEU:HA	2:B:733:HIS:HB3	2.03	0.41
2:B:995:ARG:HB3	2:B:997:GLU:OE2	2.21	0.41
5:E:29:PHE:N	5:E:63:ASN:O	2.41	0.41
6:F:74:ILE:HA	6:F:75:PRO:HD2	1.70	0.41
8:H:13:SER:N	8:H:27:GLU:O	2.38	0.41
12:L:61:THR:HG21	12:L:63:ARG:NE	2.35	0.41
1:A:1261:LYS:HE3	1:A:1261:LYS:HB2	1.60	0.41
1:A:262:LEU:HD11	1:A:325:ILE:HG12	2.03	0.41
1:A:503:GLN:OE1	6:F:90:ARG:NH2	2.50	0.41
1:A:54:ASN:HB3	1:A:247:ARG:NH2	2.30	0.41
1:A:626:ASN:O	1:A:631:HIS:CD2	2.74	0.41
2:B:95:ILE:HD11	2:B:128:LEU:HD12	2.03	0.41
2:B:221:ASN:OD1	2:B:242:SER:HA	2.21	0.41
2:B:305:VAL:O	2:B:305:VAL:HG12	2.21	0.41
2:B:368:GLU:O	2:B:370:PHE:N	2.50	0.41
2:B:469:GLN:HG2	2:B:470:LYS:HE2	2.03	0.41
2:B:485:ARG:CZ	2:B:782:LEU:HD11	2.51	0.41
2:B:797:TYR:HB3	2:B:798:TYR:CD1	2.56	0.41
2:B:848:ARG:HH22	2:B:996:ARG:HH11	1.69	0.41
5:E:167:ARG:HD3	5:E:167:ARG:HA	1.85	0.41
7:G:138:THR:HG22	7:G:139:ILE:N	2.30	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:63:VAL:HG23	11:K:63:VAL:O	2.21	0.41
11:K:65:HIS:HE1	11:K:67:PHE:CD1	2.38	0.41
1:A:451:HIS:HB2	1:A:454:SER:HB2	2.02	0.41
1:A:871:ASP:O	1:A:873:MET:HE2	2.21	0.41
2:B:283:VAL:HG21	2:B:317:CYS:O	2.21	0.41
2:B:775:LYS:HB2	2:B:775:LYS:HE3	1.94	0.41
3:C:50:GLU:HG3	3:C:156:THR:HB	2.03	0.41
3:C:18:VAL:CG2	3:C:240:VAL:HB	2.51	0.41
5:E:118:PRO:HA	5:E:121:MET:HB2	2.02	0.41
6:F:118:LEU:HD12	6:F:118:LEU:HA	1.85	0.41
13:N:10:DG:H2'	13:N:11:DA:C8	2.56	0.41
1:A:1387:HIS:HE1	13:N:6:DA:H2''	1.86	0.41
1:A:1123:GLY:O	1:A:1125:ALA:N	2.54	0.41
1:A:266:LEU:HD21	1:A:303:TYR:CZ	2.56	0.41
1:A:391:LEU:HA	1:A:394:ASN:HB2	2.03	0.41
2:B:367:LEU:HB2	2:B:368:GLU:H	1.66	0.41
8:H:93:TYR:CD1	8:H:143:LEU:HD23	2.56	0.41
11:K:84:LYS:HB3	11:K:84:LYS:HE3	1.89	0.41
1:A:1116:LEU:HG	1:A:1327:ILE:HD11	2.03	0.41
1:A:265:LYS:O	1:A:269:ILE:HG13	2.21	0.41
1:A:347:PHE:CD1	2:B:1107:ALA:HB1	2.56	0.41
1:A:821:ARG:HB2	1:A:821:ARG:HH11	1.86	0.41
2:B:129:PHE:HA	2:B:165:VAL:O	2.21	0.41
2:B:247:GLY:H	2:B:418:LYS:HZ3	1.69	0.41
8:H:104:PHE:CD1	8:H:114:VAL:HG12	2.56	0.41
8:H:77:ARG:HB2	8:H:77:ARG:HH11	1.85	0.41
15:T:7:DC:H2'	15:T:7:DC:H6	1.70	0.41
1:A:1000:LEU:HD12	1:A:1011:GLN:HA	2.04	0.40
1:A:42:ASP:OD2	1:A:45:GLN:HA	2.21	0.40
1:A:353:ILE:HG13	1:A:482:PHE:HD1	1.86	0.40
1:A:498:ARG:HD3	1:A:498:ARG:HH11	1.74	0.40
2:B:211:VAL:HG23	2:B:481:GLN:O	2.21	0.40
1:A:525:GLN:HG3	2:B:836:GLU:HG2	2.03	0.40
3:C:259:LEU:HD12	3:C:259:LEU:HA	1.92	0.40
8:H:83:GLN:O	8:H:86:ASP:N	2.45	0.40
9:I:70:ARG:HA	9:I:70:ARG:HD3	1.91	0.40
1:A:1313:LEU:HD23	1:A:1338:VAL:HG21	2.02	0.40
1:A:1345:ARG:HG2	1:A:1372:VAL:CG1	2.52	0.40
1:A:767:GLN:NE2	1:A:774:ARG:HD2	2.36	0.40
2:B:128:LEU:HD21	2:B:170:LEU:CB	2.51	0.40
2:B:365:THR:HG21	2:B:370:PHE:CD1	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:116:LYS:HD3	3:C:140:ASN:HA	2.03	0.40
3:C:5:GLY:HA3	3:C:6:PRO:HD2	1.95	0.40
4:D:39:ASN:O	4:D:42:GLY:N	2.44	0.40
4:D:41:GLN:N	4:D:41:GLN:OE1	2.54	0.40
5:E:118:PRO:O	5:E:122:LYS:HG2	2.21	0.40
5:E:156:LEU:HA	5:E:160:GLU:OE1	2.22	0.40
5:E:181:ALA:HA	5:E:186:LEU:HD21	2.03	0.40
5:E:69:ILE:HG13	5:E:69:ILE:H	1.70	0.40
4:D:138:ASN:ND2	7:G:35:GLU:HG2	2.35	0.40
11:K:47:ARG:HD2	11:K:51:LEU:HD22	2.02	0.40
11:K:5:ASP:HB3	11:K:7:PHE:CE2	2.56	0.40
2:B:31:TRP:CZ2	2:B:807:ARG:HB2	2.56	0.40
1:A:804:TYR:OH	2:B:763:GLN:HA	2.21	0.40
4:D:126:ILE:HG21	4:D:145:MET:HB3	2.03	0.40
6:F:136:ARG:O	6:F:143:PHE:HB2	2.21	0.40
11:K:101:LEU:HD23	11:K:101:LEU:HA	1.81	0.40
15:T:14:DA:H1'	15:T:15:DC:H5'	2.01	0.40
1:A:1424:VAL:HG13	1:A:1436:ILE:HG12	2.03	0.40
1:A:567:LYS:HG2	1:A:569:LYS:N	2.35	0.40
2:B:295:GLY:N	2:B:298:LEU:HD12	2.37	0.40
2:B:491:THR:O	2:B:495:LEU:HD12	2.22	0.40
2:B:722:ASP:OD2	2:B:723:VAL:HG23	2.21	0.40
6:F:116:ASP:HA	6:F:117:PRO:HD2	1.91	0.40
8:H:135:LEU:HB2	8:H:137:GLN:HG3	2.03	0.40
8:H:58:THR:HB	8:H:143:LEU:HB2	2.04	0.40
10:J:6:ARG:HA	10:J:12:LYS:O	2.21	0.40
15:T:14:DA:C2	15:T:15:DC:C2	3.10	0.40
1:A:852:TYR:CE1	1:A:1060:PRO:HB2	2.55	0.40
1:A:868:TYR:CZ	1:A:1064:VAL:HG11	2.54	0.40
1:A:134:ARG:NH1	1:A:221:SER:HA	2.36	0.40
1:A:15:LYS:HD3	1:A:15:LYS:HA	1.89	0.40
1:A:443:LEU:HA	1:A:443:LEU:HD23	1.72	0.40
1:A:351:THR:HG22	1:A:468:PHE:CD2	2.57	0.40
1:A:722:LEU:HD11	1:A:794:PRO:HB3	2.04	0.40
1:A:984:LYS:HB3	1:A:988:LEU:HD12	2.04	0.40
2:B:1167:GLY:H	2:B:1215:ARG:HG2	1.87	0.40
2:B:765:PRO:O	2:B:769:TYR:HD1	2.05	0.40
3:C:22:LEU:O	3:C:227:THR:HA	2.20	0.40
3:C:3:GLU:O	3:C:4:GLU:HG3	2.22	0.40
13:N:10:DG:H2'	13:N:11:DA:H8	1.86	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	1414/1732 (82%)	1209 (86%)	145 (10%)	60 (4%)	3	18
2	B	1096/1224 (90%)	945 (86%)	120 (11%)	31 (3%)	5	24
3	C	264/318 (83%)	237 (90%)	23 (9%)	4 (2%)	10	36
4	D	174/221 (79%)	146 (84%)	15 (9%)	13 (8%)	1	7
5	E	212/215 (99%)	193 (91%)	14 (7%)	5 (2%)	6	28
6	F	82/155 (53%)	74 (90%)	7 (8%)	1 (1%)	13	41
7	G	169/171 (99%)	153 (90%)	13 (8%)	3 (2%)	8	32
8	H	129/146 (88%)	102 (79%)	19 (15%)	8 (6%)	1	10
9	I	117/122 (96%)	100 (86%)	12 (10%)	5 (4%)	2	17
10	J	63/70 (90%)	56 (89%)	4 (6%)	3 (5%)	2	15
11	K	113/120 (94%)	104 (92%)	9 (8%)	0	100	100
12	L	44/70 (63%)	31 (70%)	6 (14%)	7 (16%)	0	0
All	All	3877/4564 (85%)	3350 (86%)	387 (10%)	140 (4%)	3	21

All (140) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	43	GLU
1	A	48	ALA
1	A	57	ARG
1	A	58	LEU
1	A	74	MET
1	A	76	GLU
1	A	169	ASN
1	A	193	ASP
1	A	257	ARG
1	A	286	HIS
1	A	311	GLN
1	A	399	HIS

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Mol	Chain	Res	Type
1	A	556	TRP
1	A	885	THR
1	A	1403	GLU
1	A	1438	THR
2	B	340	ALA
2	B	343	ILE
2	B	367	LEU
2	B	476	ARG
2	B	643	ASP
2	B	707	PRO
2	B	731	VAL
2	B	879	ARG
2	B	881	ASN
2	B	959	ASP
2	B	1046	PRO
2	B	1170	THR
4	D	13	ARG
4	D	15	LEU
4	D	16	LYS
4	D	18	VAL
4	D	53	SER
4	D	119	ARG
4	D	169	SER
4	D	198	LEU
7	G	154	VAL
8	H	83	GLN
9	I	95	THR
10	J	2	ILE
10	J	6	ARG
12	L	39	SER
1	A	97	ALA
1	A	167	CYS
1	A	178	GLY
1	A	223	GLY
1	A	310	GLY
1	A	314	ALA
1	A	318	SER
1	A	628	GLY
1	A	774	ARG
1	A	855	THR
1	A	1123	GLY
1	A	1124	HIS

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Mol	Chain	Res	Type
1	A	1173	HIS
1	A	1175	SER
1	A	1232	ASN
1	A	1233	ASP
1	A	1405	THR
2	B	108	VAL
2	B	867	GLY
2	B	937	ALA
2	B	1155	SER
2	B	1176	ASN
2	B	1181	GLU
3	C	136	ASP
3	C	184	ASN
4	D	218	GLU
5	E	36	GLU
5	E	45	LYS
8	H	81	PRO
8	H	82	PRO
9	I	9	ASP
9	I	78	CYS
9	I	79	HIS
12	L	56	LEU
1	A	51	GLY
1	A	63	ARG
1	A	75	ASN
1	A	189	ARG
1	A	333	GLU
1	A	400	PRO
1	A	449	SER
1	A	958	VAL
1	A	975	HIS
2	B	249	ARG
2	B	363	HIS
2	B	711	GLU
2	B	772	ALA
2	B	883	LEU
2	B	943	SER
2	B	1108	ARG
2	B	1156	ASP
4	D	40	HIS
4	D	138	ASN
4	D	168	LYS

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Mol	Chain	Res	Type
5	E	113	GLN
8	H	128	ASN
12	L	45	ALA
12	L	64	LEU
1	A	44	THR
1	A	65	LEU
1	A	196	GLU
1	A	569	LYS
1	A	1255	GLU
2	B	667	GLN
2	B	708	GLU
2	B	713	ALA
3	C	4	GLU
3	C	214	ASN
4	D	10	THR
5	E	43	LYS
8	H	17	PRO
8	H	60	ALA
8	H	77	ARG
8	H	132	LEU
9	I	47	GLU
12	L	26	THR
12	L	59	ALA
1	A	188	ASP
1	A	191	THR
1	A	510	GLN
1	A	1127	ASP
5	E	140	LEU
6	F	73	ALA
7	G	57	GLN
10	J	64	ASN
12	L	42	ARG
1	A	42	ASP
1	A	54	ASN
1	A	453	MET
1	A	567	LYS
1	A	1448	GLU
7	G	63	PRO
1	A	35	ILE
1	A	1242	VAL
2	B	263	GLY
1	A	52	GLY

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Mol	Chain	Res	Type
1	A	61	ILE
2	B	369	GLY

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	1240/1519 (82%)	1057 (85%)	183 (15%)	3	12
2	B	964/1061 (91%)	816 (85%)	148 (15%)	2	11
3	C	234/274 (85%)	206 (88%)	28 (12%)	5	19
4	D	160/200 (80%)	136 (85%)	24 (15%)	3	12
5	E	196/197 (100%)	178 (91%)	18 (9%)	9	31
6	F	74/137 (54%)	65 (88%)	9 (12%)	5	18
7	G	152/152 (100%)	128 (84%)	24 (16%)	2	10
8	H	117/128 (91%)	100 (86%)	17 (14%)	3	12
9	I	113/116 (97%)	101 (89%)	12 (11%)	6	24
10	J	60/65 (92%)	53 (88%)	7 (12%)	5	20
11	K	99/102 (97%)	88 (89%)	11 (11%)	6	22
12	L	40/57 (70%)	28 (70%)	12 (30%)	0	1
All	All	3449/4008 (86%)	2956 (86%)	493 (14%)	3	13

All (493) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	THR
1	A	32	VAL
1	A	35	ILE
1	A	36	ARG
1	A	39	GLU
1	A	41	MET
1	A	47	ARG
1	A	50	ILE

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Mol	Chain	Res	Type
1	A	62	ASP
1	A	67	CYS
1	A	84	ILE
1	A	93	VAL
1	A	113	LEU
1	A	117	GLU
1	A	132	LYS
1	A	147	VAL
1	A	160	GLN
1	A	173	THR
1	A	175	ARG
1	A	182	VAL
1	A	188	ASP
1	A	191	THR
1	A	193	ASP
1	A	199	LEU
1	A	204	THR
1	A	208	LEU
1	A	215	SER
1	A	220	THR
1	A	232	GLU
1	A	237	THR
1	A	251	SER
1	A	270	LEU
1	A	277	GLU
1	A	287	HIS
1	A	293	GLU
1	A	307	ASP
1	A	315	LEU
1	A	320	ARG
1	A	322	VAL
1	A	323	LYS
1	A	324	SER
1	A	333	GLU
1	A	335	ARG
1	A	337	ARG
1	A	344	ARG
1	A	354	SER
1	A	369	SER
1	A	375	THR
1	A	381	THR
1	A	385	ILE

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Mol	Chain	Res	Type
1	A	386	ASP
1	A	394	ASN
1	A	398	GLU
1	A	412	ARG
1	A	425	GLN
1	A	434	ARG
1	A	436	ILE
1	A	443	LEU
1	A	444	PHE
1	A	445	ASN
1	A	449	SER
1	A	454	SER
1	A	461	LYS
1	A	469	ARG
1	A	472	LEU
1	A	474	VAL
1	A	475	THR
1	A	479	ASN
1	A	485	ASP
1	A	498	ARG
1	A	505	CYS
1	A	513	SER
1	A	521	MET
1	A	528	LEU
1	A	538	ASP
1	A	566	ILE
1	A	571	LEU
1	A	588	LEU
1	A	593	GLU
1	A	596	THR
1	A	598	LEU
1	A	602	ASP
1	A	618	GLU
1	A	622	VAL
1	A	629	LEU
1	A	635	ARG
1	A	644	LYS
1	A	666	ILE
1	A	670	ILE
1	A	672	ASP
1	A	676	MET
1	A	719	VAL

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Mol	Chain	Res	Type
1	A	738	LYS
1	A	764	CYS
1	A	768	GLN
1	A	769	SER
1	A	773	LYS
1	A	782	ARG
1	A	788	SER
1	A	801	GLU
1	A	816	HIS
1	A	821	ARG
1	A	834	THR
1	A	837	ILE
1	A	851	HIS
1	A	855	THR
1	A	865	GLN
1	A	871	ASP
1	A	881	GLN
1	A	882	SER
1	A	896	ARG
1	A	904	THR
1	A	906	HIS
1	A	918	GLU
1	A	919	ILE
1	A	920	LEU
1	A	932	GLU
1	A	934	LYS
1	A	948	VAL
1	A	964	ILE
1	A	969	GLN
1	A	973	ILE
1	A	976	THR
1	A	982	THR
1	A	993	LEU
1	A	1001	ARG
1	A	1036	ARG
1	A	1058	VAL
1	A	1062	GLU
1	A	1067	LEU
1	A	1078	GLN
1	A	1112	LYS
1	A	1113	THR
1	A	1116	LEU

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Mol	Chain	Res	Type
1	A	1120	LEU
1	A	1124	HIS
1	A	1133	LEU
1	A	1135	ARG
1	A	1165	GLU
1	A	1170	ILE
1	A	1172	LEU
1	A	1173	HIS
1	A	1174	PHE
1	A	1176	LEU
1	A	1199	ARG
1	A	1215	ARG
1	A	1222	ASN
1	A	1223	ASP
1	A	1234	GLU
1	A	1242	VAL
1	A	1255	GLU
1	A	1257	ASP
1	A	1260	LEU
1	A	1264	GLU
1	A	1270	ASN
1	A	1273	LEU
1	A	1280	GLU
1	A	1291	VAL
1	A	1293	SER
1	A	1295	THR
1	A	1297	GLU
1	A	1301	GLU
1	A	1315	GLU
1	A	1327	ILE
1	A	1341	ILE
1	A	1366	ARG
1	A	1376	THR
1	A	1387	HIS
1	A	1391	ARG
1	A	1394	THR
1	A	1400	CYS
1	A	1403	GLU
1	A	1407	GLU
1	A	1420	ASP
1	A	1426	GLU
1	A	1436	ILE

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Mol	Chain	Res	Type
1	A	1438	THR
1	A	1442	ASP
1	A	1444	MET
1	A	1445	ILE
1	A	1451	VAL
1	A	1453	TYR
1	A	1454	MET
2	B	44	VAL
2	B	46	GLN
2	B	66	ASP
2	B	101	MET
2	B	102	VAL
2	B	105	SER
2	B	112	LEU
2	B	131	ASP
2	B	134	LYS
2	B	165	VAL
2	B	185	THR
2	B	211	VAL
2	B	217	ARG
2	B	218	SER
2	B	225	VAL
2	B	228	LYS
2	B	248	SER
2	B	251	ILE
2	B	261	ARG
2	B	265	SER
2	B	272	THR
2	B	278	GLN
2	B	313	MET
2	B	325	GLN
2	B	337	ARG
2	B	343	ILE
2	B	344	LYS
2	B	346	GLU
2	B	348	ARG
2	B	350	GLN
2	B	357	GLN
2	B	361	LEU
2	B	365	THR
2	B	367	LEU
2	B	371	GLU

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Mol	Chain	Res	Type
2	B	387	LEU
2	B	394	ASP
2	B	401	PHE
2	B	412	LEU
2	B	416	LEU
2	B	423	LYS
2	B	425	THR
2	B	429	PHE
2	B	430	ARG
2	B	434	ARG
2	B	448	ILE
2	B	453	ILE
2	B	455	SER
2	B	470	LYS
2	B	475	SER
2	B	476	ARG
2	B	480	SER
2	B	481	GLN
2	B	485	ARG
2	B	490	SER
2	B	498	THR
2	B	502	ILE
2	B	529	GLU
2	B	552	MET
2	B	559	SER
2	B	570	VAL
2	B	574	SER
2	B	598	GLU
2	B	603	LEU
2	B	608	ASP
2	B	613	VAL
2	B	615	MET
2	B	620	ARG
2	B	628	THR
2	B	641	GLU
2	B	642	ASP
2	B	648	HIS
2	B	653	VAL
2	B	658	ILE
2	B	678	GLU
2	B	690	VAL
2	B	706	GLN

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Mol	Chain	Res	Type
2	B	722	ASP
2	B	730	ARG
2	B	734	HIS
2	B	737	THR
2	B	754	SER
2	B	764	SER
2	B	766	ARG
2	B	773	MET
2	B	786	ASN
2	B	788	ARG
2	B	790	ASP
2	B	830	TYR
2	B	831	SER
2	B	835	GLN
2	B	837	ASP
2	B	843	GLN
2	B	844	SER
2	B	857	ARG
2	B	858	SER
2	B	878	GLN
2	B	879	ARG
2	B	882	THR
2	B	884	ARG
2	B	887	HIS
2	B	889	THR
2	B	904	ARG
2	B	915	THR
2	B	916	THR
2	B	944	THR
2	B	945	GLU
2	B	953	LEU
2	B	956	THR
2	B	959	ASP
2	B	964	VAL
2	B	970	THR
2	B	986	GLN
2	B	987	LYS
2	B	997	GLU
2	B	999	MET
2	B	1002	THR
2	B	1007	VAL
2	B	1045	SER

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Mol	Chain	Res	Type
2	B	1048	THR
2	B	1050	ILE
2	B	1051	THR
2	B	1060	ARG
2	B	1065	GLN
2	B	1072	MET
2	B	1106	ARG
2	B	1112	GLN
2	B	1122	ARG
2	B	1129	ARG
2	B	1147	LEU
2	B	1148	LYS
2	B	1150	ARG
2	B	1151	LEU
2	B	1156	ASP
2	B	1159	ARG
2	B	1160	VAL
2	B	1166	CYS
2	B	1169	MET
2	B	1170	THR
2	B	1172	ILE
2	B	1175	LEU
2	B	1182	CYS
2	B	1183	LYS
2	B	1188	LYS
2	B	1196	ILE
2	B	1202	LEU
2	B	1220	ARG
2	B	1221	SER
3	C	16	ASP
3	C	22	LEU
3	C	23	SER
3	C	25	VAL
3	C	27	LEU
3	C	50	GLU
3	C	55	THR
3	C	56	THR
3	C	57	VAL
3	C	81	GLU
3	C	89	GLU
3	C	108	GLU
3	C	111	THR

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Mol	Chain	Res	Type
3	C	119	VAL
3	C	124	LEU
3	C	127	ARG
3	C	129	ILE
3	C	136	ASP
3	C	148	ARG
3	C	200	GLU
3	C	204	SER
3	C	215	GLU
3	C	224	GLN
3	C	238	ILE
3	C	240	VAL
3	C	259	LEU
3	C	265	MET
3	C	268	ASP
4	D	5	THR
4	D	7	THR
4	D	11	ARG
4	D	17	LYS
4	D	18	VAL
4	D	23	ASN
4	D	34	GLN
4	D	51	ASN
4	D	52	LEU
4	D	63	LEU
4	D	73	SER
4	D	118	THR
4	D	121	LYS
4	D	126	ILE
4	D	139	LYS
4	D	141	LEU
4	D	146	GLN
4	D	159	THR
4	D	186	ASP
4	D	187	THR
4	D	197	SER
4	D	213	GLU
4	D	217	LEU
4	D	219	THR
5	E	2	ASP
5	E	5	ASN
5	E	6	GLU

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Mol	Chain	Res	Type
5	E	10	SER
5	E	18	THR
5	E	31	THR
5	E	49	SER
5	E	65	THR
5	E	72	PHE
5	E	84	ASP
5	E	95	THR
5	E	114	ASN
5	E	131	THR
5	E	173	SER
5	E	174	GLN
5	E	191	LYS
5	E	192	ARG
5	E	203	GLU
6	F	72	LYS
6	F	82	THR
6	F	92	ARG
6	F	109	VAL
6	F	111	LEU
6	F	115	THR
6	F	128	LYS
6	F	148	VAL
6	F	153	VAL
7	G	2	PHE
7	G	13	LEU
7	G	22	MET
7	G	34	VAL
7	G	37	SER
7	G	60	ARG
7	G	64	THR
7	G	75	ARG
7	G	83	LYS
7	G	92	VAL
7	G	95	SER
7	G	106	MET
7	G	114	LEU
7	G	118	ASP
7	G	134	GLU
7	G	135	ASP
7	G	136	VAL
7	G	143	ILE

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Mol	Chain	Res	Type
7	G	145	VAL
7	G	151	ILE
7	G	152	SER
7	G	154	VAL
7	G	155	SER
7	G	162	SER
8	H	14	GLU
8	H	26	ILE
8	H	32	THR
8	H	42	ILE
8	H	46	LEU
8	H	76	THR
8	H	86	ASP
8	H	89	LEU
8	H	91	ASP
8	H	106	GLU
8	H	107	VAL
8	H	108	SER
8	H	114	VAL
8	H	124	ARG
8	H	130	ARG
8	H	138	GLU
8	H	145	ARG
9	I	5	ARG
9	I	7	CYS
9	I	8	ARG
9	I	31	THR
9	I	43	VAL
9	I	50	THR
9	I	55	THR
9	I	62	ILE
9	I	94	ASP
9	I	111	THR
9	I	113	ASP
9	I	120	GLN
10	J	7	CYS
10	J	13	VAL
10	J	14	VAL
10	J	23	ASN
10	J	34	THR
10	J	42	LYS
10	J	48	ARG

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Mol	Chain	Res	Type
11	K	6	ARG
11	K	12	LEU
11	K	18	LYS
11	K	22	ASP
11	K	25	THR
11	K	41	THR
11	K	47	ARG
11	K	51	LEU
11	K	95	ILE
11	K	101	LEU
11	K	107	THR
12	L	27	LEU
12	L	37	LYS
12	L	38	LEU
12	L	44	ASP
12	L	50	ASP
12	L	51	CYS
12	L	55	ILE
12	L	58	LYS
12	L	61	THR
12	L	64	LEU
12	L	65	VAL
12	L	68	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1387	HIS
2	B	103	ASN
2	B	395	GLN
2	B	481	GLN
2	B	986	GLN
4	D	37	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	P	9/12 (75%)	2 (22%)	2 (22%)

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
14	P	4	A
14	P	11	A

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
14	P	3	G
14	P	10	A

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
15	BRU	T	22	15,14	15,21,22	2.10	2 (13%)	17,30,33	2.23	3 (17%)
15	TT	T	17	15	40,43,44	1.27	5 (12%)	59,69,72	2.09	15 (25%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	BRU	T	22	15,14	-	2/4/21/22	0/2/2/2
15	TT	T	17	15	-	9/18/105/106	0/5/6/6

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	T	22	BRU	C4-C5	7.38	1.47	1.38
15	T	17	TT	C2-N3	-3.21	1.32	1.38
15	T	17	TT	C1R-N1T	3.04	1.49	1.45
15	T	17	TT	C4-N3	-2.98	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	T	17	TT	C2-N1	2.85	1.42	1.36
15	T	22	BRU	C2-N3	-2.32	1.33	1.38
15	T	17	TT	C4T-N3T	-2.04	1.34	1.37

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	T	17	TT	O4R-C1R-N1T	8.05	118.19	108.65
15	T	17	TT	C4-N3-C2	-6.30	116.98	126.67
15	T	22	BRU	C4-N3-C2	6.20	120.37	115.14
15	T	22	BRU	C2'-C1'-N1	-4.71	103.41	114.27
15	T	17	TT	O4T-C4T-C5T	-4.03	119.66	122.88
15	T	17	TT	C2'-C1'-N1	-3.84	110.39	115.59
15	T	17	TT	O4-C4-C5	-3.81	119.83	122.88
15	T	22	BRU	C5-C4-N3	-3.09	119.95	123.64
15	T	17	TT	C4T-N3T-C2T	-2.94	122.15	126.67
15	T	17	TT	C2R-C1R-N1T	-2.91	111.66	115.59
15	T	17	TT	N3T-C2T-N1T	2.84	119.64	116.69
15	T	17	TT	O2-C2-N1	-2.52	119.58	123.49
15	T	17	TT	O5R-C5R-C4R	2.49	114.84	109.27
15	T	17	TT	O4R-C4R-C5R	2.48	117.52	109.37
15	T	17	TT	C5'-C4'-C3'	-2.44	108.95	114.53
15	T	17	TT	O2T-C2T-N1T	-2.13	120.18	123.49
15	T	17	TT	N3-C2-N1	2.10	118.87	116.69
15	T	17	TT	C3'-C2'-C1'	2.06	106.85	102.91

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	T	22	BRU	C3'-C4'-C5'-O5'
15	T	22	BRU	O4'-C4'-C5'-O5'
15	T	17	TT	O4'-C4'-C5'-O5'
15	T	17	TT	C3'-C4'-C5'-O5'
15	T	17	TT	C2R-C1R-N1T-C6T
15	T	17	TT	O3'-C7-O5R-C5R
15	T	17	TT	O4R-C1R-N1T-C6T
15	T	17	TT	C2R-C1R-N1T-C2T
15	T	17	TT	O4R-C1R-N1T-C2T
15	T	17	TT	C4'-C5'-O5'-P
15	T	17	TT	O4'-C1'-N1-C2

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	T	17	TT	5	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	1422/1732 (82%)	-0.07	21 (1%) 73 72	56, 101, 162, 298	0
2	B	1113/1224 (90%)	0.04	24 (2%) 62 60	53, 113, 185, 237	0
3	C	266/318 (83%)	-0.14	0 100 100	72, 102, 141, 189	0
4	D	178/221 (80%)	0.03	0 100 100	80, 116, 180, 211	0
5	E	214/215 (99%)	0.05	8 (3%) 41 40	77, 137, 188, 195	0
6	F	84/155 (54%)	-0.36	0 100 100	59, 80, 109, 134	0
7	G	171/171 (100%)	-0.06	0 100 100	63, 100, 139, 166	0
8	H	133/146 (91%)	0.47	6 (4%) 33 33	106, 151, 194, 218	0
9	I	119/122 (97%)	0.10	7 (5%) 22 23	107, 141, 182, 219	0
10	J	65/70 (92%)	-0.19	0 100 100	77, 106, 146, 157	0
11	K	115/120 (95%)	-0.13	1 (0%) 84 83	66, 101, 137, 163	0
12	L	46/70 (65%)	0.19	4 (8%) 10 12	91, 154, 198, 202	0
13	N	12/14 (85%)	-0.19	0 100 100	164, 177, 260, 301	0
14	P	9/12 (75%)	-0.27	0 100 100	132, 150, 197, 204	0
15	T	21/25 (84%)	-0.20	1 (4%) 30 31	125, 177, 286, 307	0
All	All	3968/4615 (85%)	-0.02	72 (1%) 68 67	53, 110, 179, 307	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	883	LEU	5.3
9	I	119	THR	4.9
2	B	250	PHE	4.6
8	H	139	ASN	4.4
9	I	120	GLN	4.1
1	A	1455	PRO	4.1
9	I	118	ARG	4.0

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Mol	Chain	Res	Type	RSRZ
2	B	468	GLU	3.9
11	K	115	ALA	3.8
1	A	194	ALA	3.7
5	E	93	MET	3.6
1	A	193	ASP	3.5
2	B	708	GLU	3.4
2	B	431	TYR	3.4
5	E	110	PHE	3.4
2	B	340	ALA	3.3
2	B	709	ASP	3.3
1	A	155	GLU	3.2
1	A	152	VAL	3.1
2	B	341	LEU	3.1
1	A	114	LEU	3.1
1	A	1176	LEU	3.1
5	E	82	PHE	3.1
2	B	715	ALA	3.0
2	B	342	GLY	3.0
2	B	339	THR	2.9
2	B	92	PHE	2.9
12	L	27	LEU	2.9
2	B	343	ILE	2.9
5	E	123	LEU	2.9
2	B	733	HIS	2.8
1	A	255	SER	2.8
15	T	5	DA	2.7
1	A	161	LEU	2.7
1	A	1169	ILE	2.6
12	L	25	ALA	2.5
9	I	116	ASN	2.5
5	E	127	ILE	2.4
2	B	469	GLN	2.4
9	I	117	LYS	2.4
8	H	146	ARG	2.4
1	A	191	THR	2.4
1	A	164	ARG	2.4
1	A	192	GLY	2.3
1	A	145	LYS	2.3
8	H	134	ASN	2.3
8	H	36	CYS	2.3
5	E	58	MET	2.3
9	I	97	MET	2.3

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Mol	Chain	Res	Type	RSRZ
8	H	140	ALA	2.3
9	I	102	VAL	2.2
1	A	147	VAL	2.2
1	A	162	VAL	2.2
2	B	435	THR	2.2
2	B	167	ILE	2.1
1	A	166	GLY	2.1
2	B	69	LEU	2.1
2	B	246	LYS	2.1
5	E	42	PHE	2.1
2	B	90	ILE	2.1
1	A	1188	GLN	2.1
1	A	195	ASP	2.1
2	B	722	ASP	2.1
12	L	38	LEU	2.0
2	B	868	MET	2.0
12	L	46	VAL	2.0
2	B	918	ILE	2.0
1	A	115	LEU	2.0
8	H	59	ILE	2.0
2	B	871	THR	2.0
1	A	1305	VAL	2.0
5	E	126	SER	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
15	TT	T	17	38/39	0.88	0.24	112,230,240,242	0
15	BRU	T	22	20/21	0.91	0.14	161,193,214,215	0

## 6.3 Carbohydrates [i](#)

There are no carbohydrates 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
17	MG	A	2458	1/1	0.89	0.09	124,124,124,124	0
16	ZN	I	1122	1/1	0.99	0.05	196,196,196,196	0
16	ZN	A	2456	1/1	0.99	0.05	127,127,127,127	0
16	ZN	I	1121	1/1	1.00	0.12	120,120,120,120	0
16	ZN	L	1071	1/1	1.00	0.07	187,187,187,187	0
16	ZN	J	1066	1/1	1.00	0.21	90,90,90,90	0
16	ZN	C	1269	1/1	1.00	0.13	75,75,75,75	0
16	ZN	B	2225	1/1	1.00	0.18	75,75,75,75	0
16	ZN	A	2457	1/1	1.00	0.14	70,70,70,70	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.