



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:43 PM GMT

PDB ID : 4A3K
Title : RNA Polymerase II initial transcribing complex with a 7nt DNA-RNA hybrid
Authors : Cheung, A.C.M.; Sainsbury, S.; Cramer, P.
Deposited on : 2011-09-30
Resolution : 3.50 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

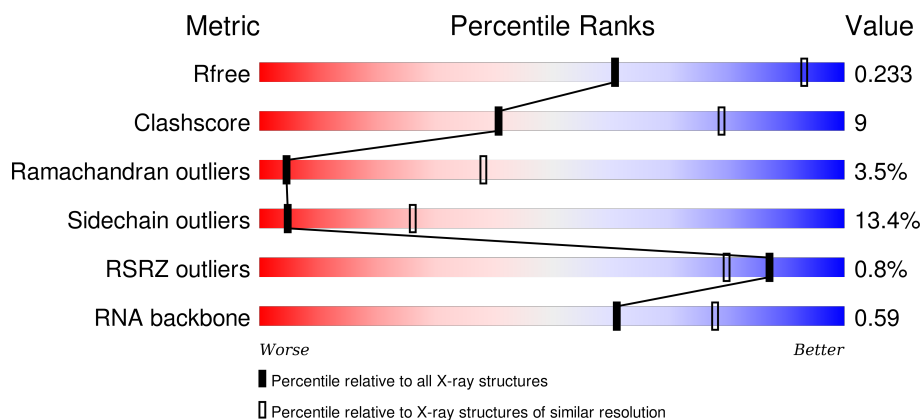
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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}	91344	1051 (3.60-3.40)
Clashscore	102246	1157 (3.60-3.40)
Ramachandran outliers	100387	1120 (3.60-3.40)
Sidechain outliers	100360	1121 (3.60-3.40)
RSRZ outliers	91569	1058 (3.60-3.40)
RNA backbone	2183	1050 (4.20-2.80)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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>%</div> <div> <div></div> <div>59%</div> <div>19%</div> <div>•</div> <div>18%</div> </div> </div>
2	B	1224	<div> <div>%</div> <div> <div></div> <div>63%</div> <div>24%</div> <div>•</div> <div>9%</div> </div> </div>
3	C	318	<div> <div></div> <div> <div>60%</div> <div>19%</div> <div>•</div> <div>16%</div> </div> </div>
4	D	221	<div> <div></div> <div> <div>54%</div> <div>21%</div> <div>5%</div> <div>19%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
5	E	215	 76% 22% •
6	F	155	 36% 14% • 46%
7	G	171	 64% 26% 10%
8	H	146	 65% 19% 7% 9%
9	I	122	 79% 17% • •
10	J	70	 53% 34% 6% 7%
11	K	120	 62% 29% 5% •
12	L	70	 7% 29% 26% 11% 34%
13	N	11	 64% 27% 9%
14	P	7	 100%
15	T	26	 54% 19% 27%

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 31940 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	1115	Total	C	N	O	S	0	0	0
			8859	5609	1554	1641	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)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	N	10	Total	C	N	O	P	0	0	0
			207	99	39	59	10			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	P	7	Total	C	N	O	P	0	0	0
			152	68	31	46	7			

- Molecule 15 is a DNA chain called 5'-D(*AP*GP*CP*TP*CP*AP*AP*GP*TP*AP*CP*TP*TP*DTP*TP*TP*CP*CP*BRU*GP*GP*TP*CP*AP*TP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	T	19	Total	Br	C	N	O	P	0	0
			385	1	185	60	120	19		

- 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		

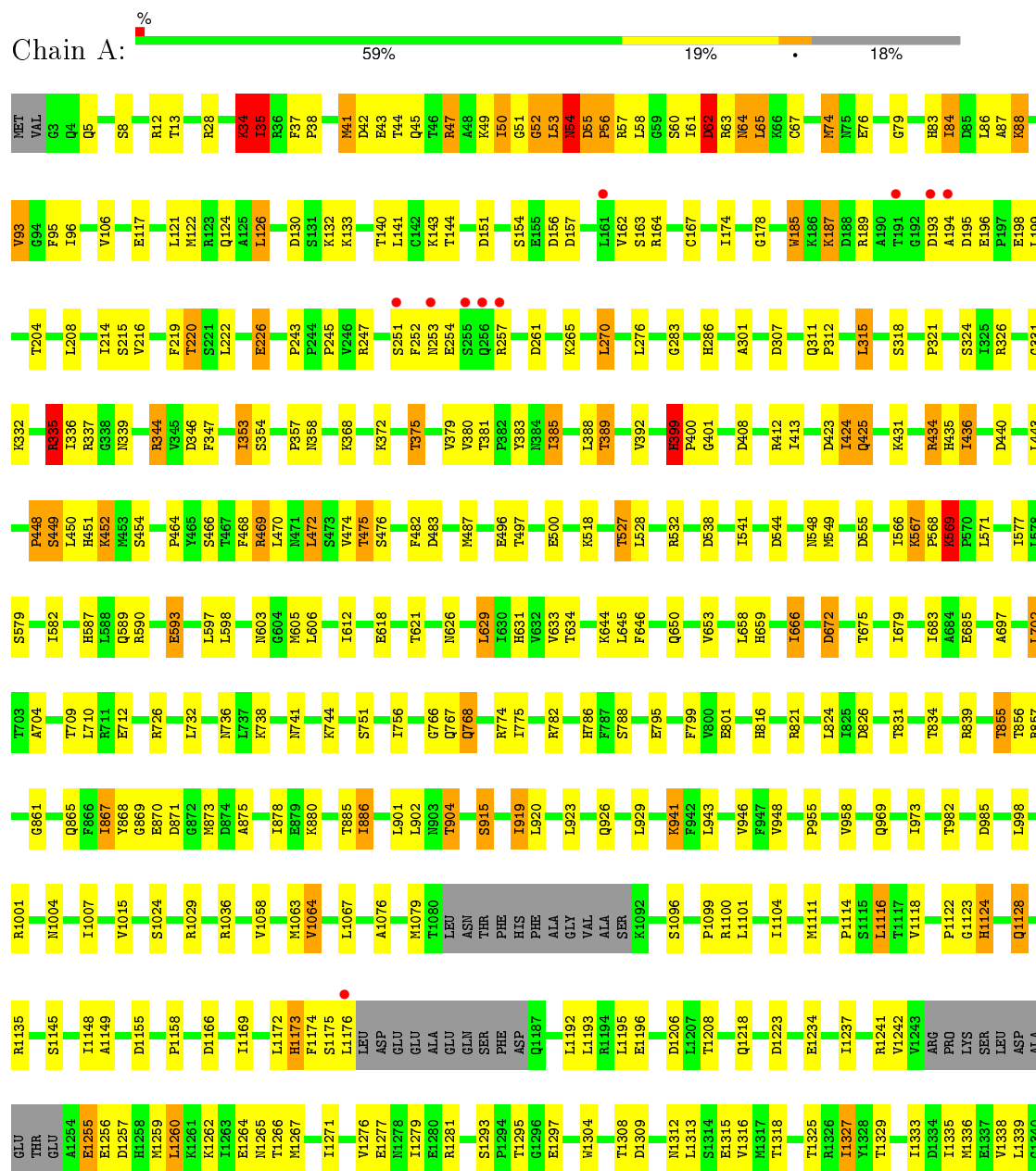
- Molecule 17 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

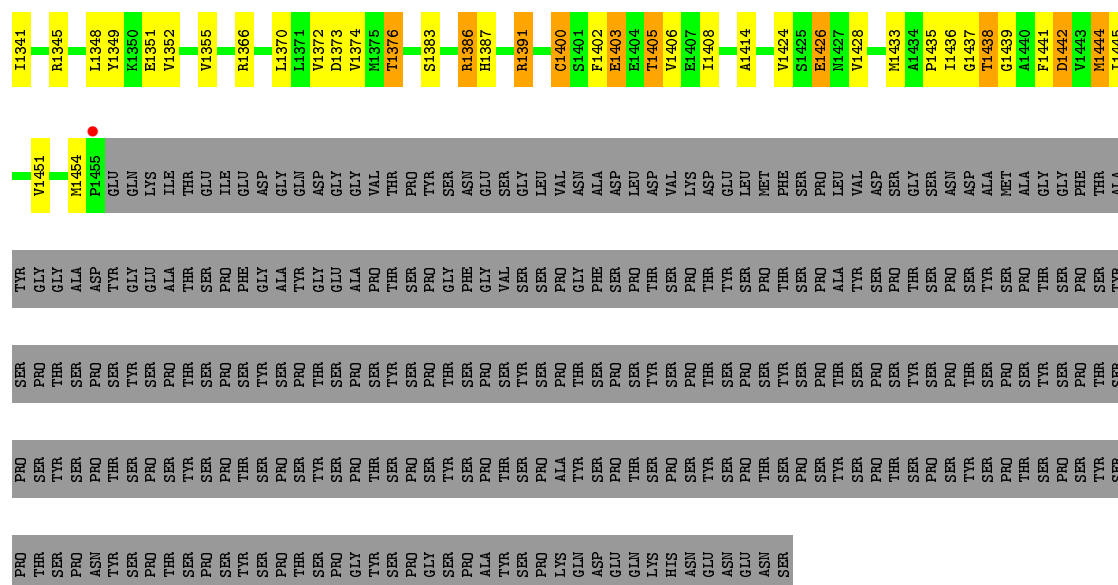
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	1	Total	Mg	0	0
			1	1		

3 Residue-property plots

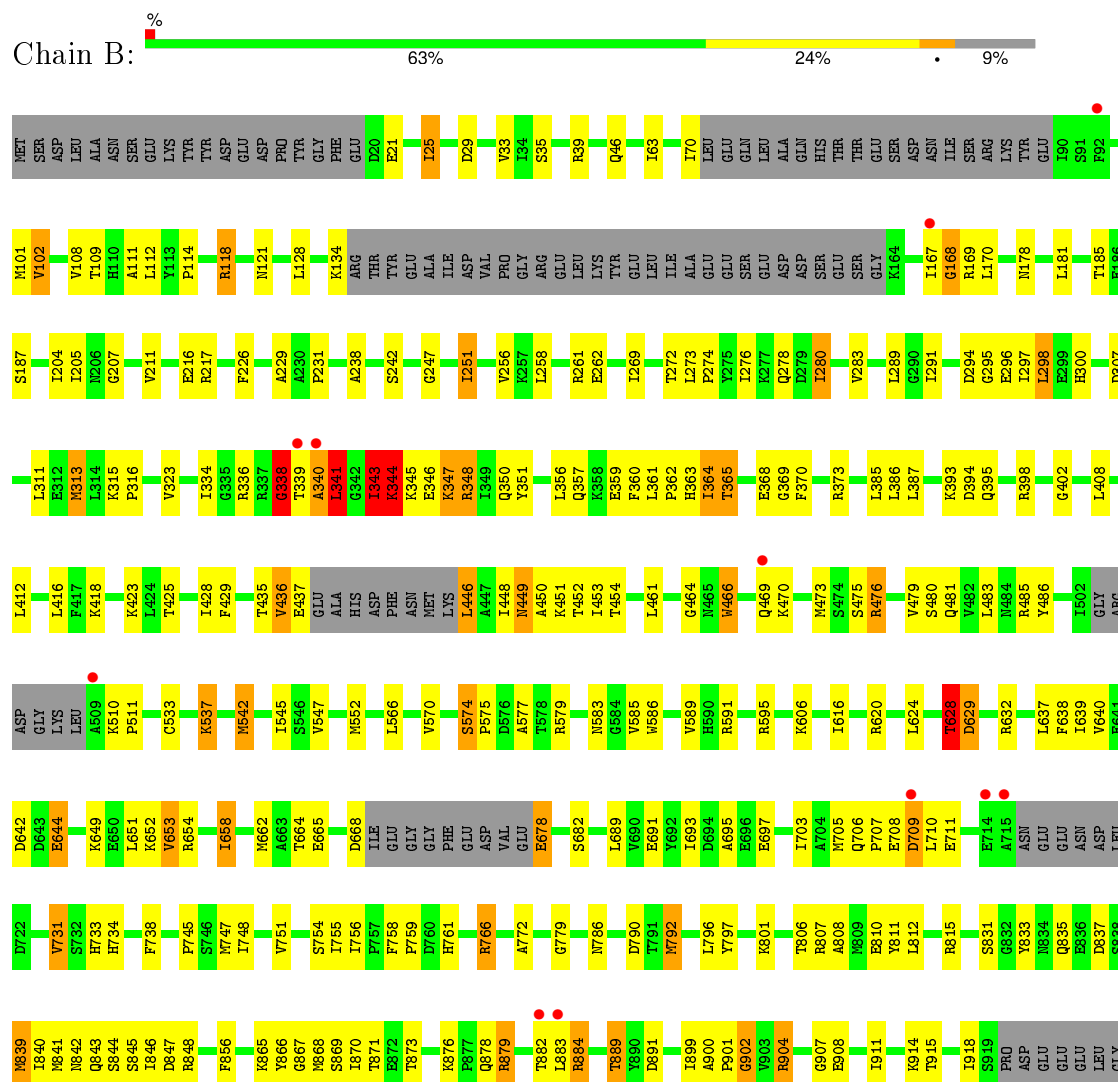
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

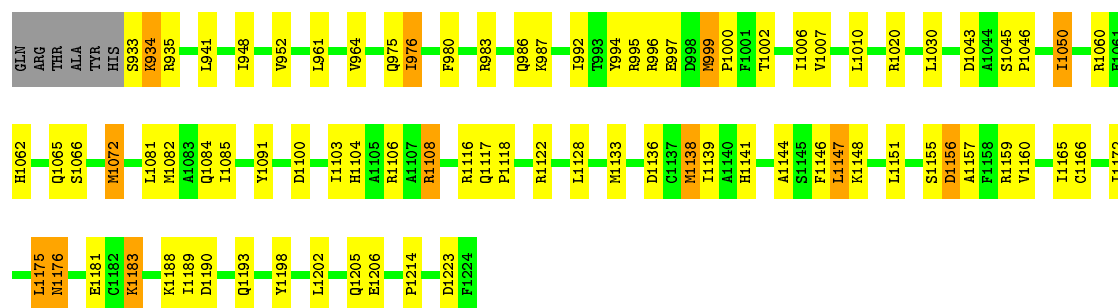
- Molecule 1: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB1



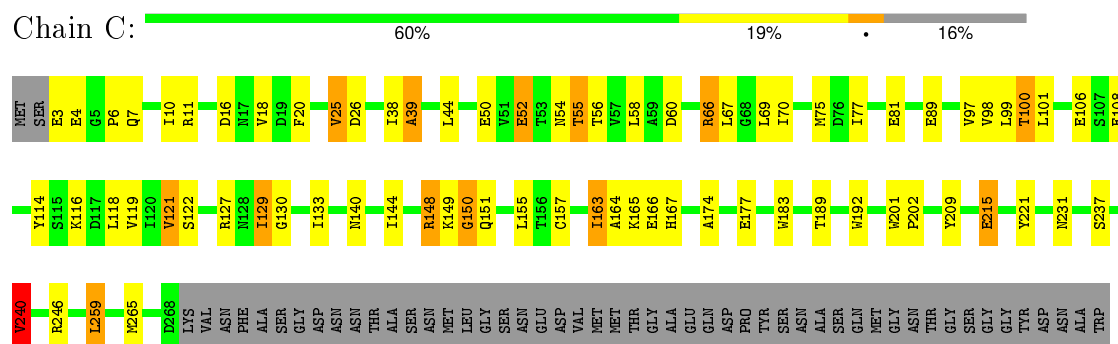


• Molecule 2: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB2

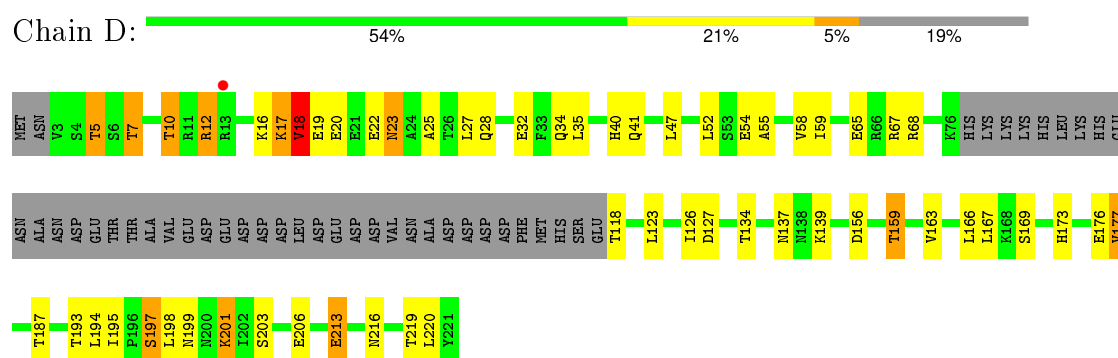




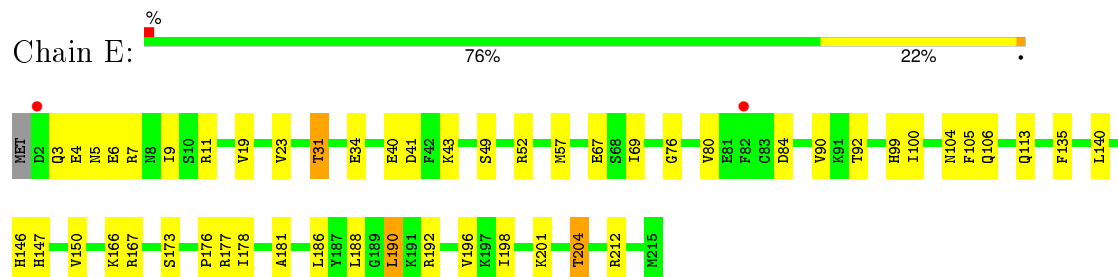
• Molecule 3: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB3



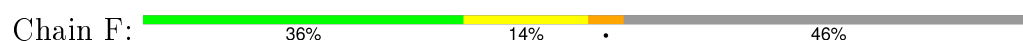
• Molecule 4: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB4



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



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



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

HIS GLN ILE ARG LYS THR LEU LYS K72 K73 K74 K75 K76 K77 K78 K79 T82 K87 K88 K89 K90 R97 R109 R110 R111 T115 R119 M122 K123 E127 K128 L132 V133 I134 R135 R136 Y137 F143 V148 E149 L155

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

Chain G: 


K1 F2 K5 K11 K12 K13 L14 L15 L9 T12 L13 R21 K22 K23 Q24 Y25 L26 K27 T138 T139 V34 S37 T82 K87 K88 K89 K90 R97 R109 R110 R111 T115 R119 M122 K123 E127 K128 L132 V133 I134 R135 R136 Y137 F143 V148 E149 L155

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

Chain H: 

MET S2 Q11 V12 S13 D16 P17 G18 I26 T31 T32 C36 L40 Q52 A60 L63 ASN LEU GLU ASP THR PRO ALA ASN ASP SER SER ALA T76 P81 P82 Q83 A84 R87 S88 L89 A90 D91 D92 Y93 K103 F104 E105 E106 V107 D110 L111

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

Chain I: 

MET T2 T3 F4 C7 R8 D9 T31 C32 S33 V34 V35 L42 V43 E47 L48 L49 T50 N51 Y52 E74 N83 R91 R92 R93 D94 T95 S105 C106 S107 H108 R118 T119 Q120 PHE SER

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

Chain J: 

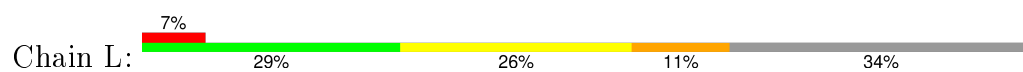
M1 I2 V3 P4 V5 R6 C7 F8 S9 K12 K13 K17 M18 L22 N23 D31 E32 T33 T34 A35 L36 K42 K48 R49 T49 L50 L51 T52 D55 L56 L57 P60 N64 P65 LEU GLU LYS ARG ASP

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

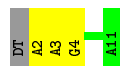
Chain K: 

M1 P4 D5 R6 F7 L11 K18 L19 K20 I21 T25 N29 A30 V31 V32 I33 T34 K37 E38 L45 L46 R47 A48 E49 L50 L51 K55 V56 L57 F58 A59 V63 E64 H65 P66 P67 F71 R74 I75 Q76 E79 G80 Y81 C91 I94

- 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)-3'



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



There are no outlier residues recorded for this chain.

- Molecule 15: 5'-D(*AP*GP*CP*TP*CP*AP*AP*GP*TP*AP*CP*TP*TP*DTP *TP*TP*CP*CP*BRU*GP*GP*TP*CP*AP*TP*T)-3'



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	221.91Å 391.36Å 283.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.95 – 3.50 49.11 – 3.37	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.95-3.50) 98.2 (49.11-3.37)	Depositor EDS
R_{merge}	1.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 3.40Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.158 , 0.185 0.220 , 0.233	Depositor DCC
R_{free} test set	3051 reflections (2.01%)	DCC
Wilson B-factor (Å ²)	97.8	Xtriage
Anisotropy	0.391	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 91.3	EDS
Estimated twinning fraction	0.019 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.028 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 169418 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	31940	wwPDB-VP
Average B, all atoms (Å ²)	112.0	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.*

¹ Intensities estimated from amplitudes.

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

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	0.54	1/11374 (0.0%)	0.84	8/15383 (0.1%)
2	B	0.51	0/9029	0.80	2/12171 (0.0%)
3	C	0.50	0/2133	0.80	2/2891 (0.1%)
4	D	0.52	0/1444	0.82	1/1935 (0.1%)
5	E	0.47	0/1788	0.72	0/2406
6	F	0.61	0/691	0.80	0/933
7	G	0.50	0/1368	0.83	0/1844
8	H	0.50	0/1086	0.80	0/1470
9	I	0.46	0/989	0.80	0/1331
10	J	0.56	0/541	0.83	1/727 (0.1%)
11	K	0.48	0/938	0.73	0/1267
12	L	0.59	0/365	1.04	0/485
13	N	1.15	0/232	1.03	0/356
14	P	1.04	0/170	0.80	0/263
15	T	1.30	0/405	1.13	1/620 (0.2%)
All	All	0.55	1/32553 (0.0%)	0.82	15/44082 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	867	ILE	CG1-CD1	5.19	1.86	1.50

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	34	LYS	C-N-CA	8.15	142.07	121.70
1	A	399	HIS	N-CA-CB	7.04	123.28	110.60
1	A	54	ASN	C-N-CA	6.02	136.75	121.70
1	A	35	ILE	N-CA-CB	5.82	124.19	110.80
1	A	56	PRO	C-N-CA	5.70	135.96	121.70
2	B	628	THR	C-N-CA	5.68	135.90	121.70
1	A	194	ALA	C-N-CA	5.67	135.88	121.70
1	A	53	LEU	N-CA-CB	5.45	121.31	110.40
2	B	338	GLY	C-N-CA	5.27	134.87	121.70
4	D	25	ALA	C-N-CA	5.25	134.81	121.70
1	A	35	ILE	CB-CA-C	5.24	122.09	111.60
15	T	24	DG	O4'-C4'-C3'	-5.20	102.42	104.50
3	C	39	ALA	N-CA-C	5.17	124.97	111.00
3	C	183	TRP	N-CA-C	-5.01	97.48	111.00
10	J	5	VAL	N-CA-C	-5.00	97.49	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	34	LYS	Mainchain,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	201	1
2	B	8859	0	8901	173	0
3	C	2095	0	2051	46	0
4	D	1434	0	1460	24	0
5	E	1752	0	1776	24	0
6	F	679	0	701	21	0
7	G	1340	0	1357	43	1
8	H	1068	0	1040	17	0
9	I	971	0	927	6	1
10	J	532	0	542	15	0
11	K	920	0	929	28	0
12	L	363	0	386	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	N	207	0	114	4	0
14	P	152	0	77	0	0
15	T	385	0	216	5	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	31940	0	31710	547	2

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 9.

All (547) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:867:ILE:CD1	1:A:867:ILE:CG1	1.86	1.53
1:A:53:LEU:HD23	1:A:54:ASN:H	0.97	1.11
4:D:40:HIS:HB3	7:G:73:LYS:HE3	1.34	1.08
7:G:1:MET:HE2	7:G:2:PHE:H	1.19	1.06
1:A:53:LEU:CD2	1:A:54:ASN:H	1.78	0.97
1:A:868:TYR:CE1	1:A:1064:VAL:HG11	1.99	0.96
1:A:53:LEU:HD23	1:A:54:ASN:N	1.81	0.94
7:G:1:MET:CE	7:G:2:PHE:H	1.82	0.92
3:C:6:PRO:HB3	3:C:25:VAL:HG13	1.49	0.92
1:A:855:THR:HG21	1:A:857:ARG:HE	1.36	0.88
6:F:76:LYS:HA	6:F:79:ARG:HD3	1.55	0.86
7:G:1:MET:HE1	7:G:80:LYS:H	1.43	0.84
1:A:41:MET:HB3	1:A:49:LYS:HA	1.59	0.83
1:A:902:LEU:HG	1:A:926:GLN:HG3	1.58	0.82
1:A:868:TYR:CZ	1:A:1064:VAL:HG11	2.15	0.82
2:B:882:THR:HG1	2:B:935:ARG:N	1.78	0.82
1:A:63:ARG:HA	1:A:74:MET:HG3	1.62	0.82
2:B:815:ARG:HH11	2:B:815:ARG:HG3	1.43	0.81
6:F:93:ILE:HD11	6:F:134:ILE:HD11	1.62	0.81
1:A:61:ILE:HG22	1:A:62:ASP:H	1.43	0.80
1:A:869:GLY:O	5:E:204:THR:HG21	1.83	0.79
1:A:1100:ARG:HH21	1:A:1351:GLU:HG2	1.47	0.79
7:G:34:VAL:O	7:G:37:SER:HB3	1.82	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:40:HIS:HB3	7:G:73:LYS:CE	2.12	0.78
2:B:976:ILE:HD11	2:B:992:ILE:HA	1.67	0.77
7:G:111:THR:HG22	7:G:113:HIS:H	1.48	0.77
3:C:10:ILE:HD12	11:K:108:GLU:HB3	1.67	0.76
1:A:254:GLU:HB3	2:B:935:ARG:HH21	1.52	0.74
12:L:28:LYS:HB2	12:L:39:SER:HA	1.70	0.74
10:J:48:ARG:O	10:J:52:THR:HG22	1.88	0.73
1:A:383:TYR:HB3	6:F:115:THR:HG22	1.70	0.73
2:B:705:MET:H	2:B:710:LEU:HD12	1.53	0.73
4:D:203:SER:HB3	4:D:206:GLU:HB2	1.70	0.72
2:B:114:PRO:HG3	2:B:181:LEU:HD11	1.72	0.71
11:K:51:LEU:HD13	11:K:59:ALA:HB3	1.71	0.71
2:B:1172:ILE:HD11	2:B:1183:LYS:HE2	1.72	0.71
3:C:66:ARG:NH2	10:J:3:VAL:O	2.23	0.70
2:B:662:MET:HA	2:B:665:GLU:HB2	1.72	0.70
1:A:1438:THR:HG22	2:B:1144:ALA:HB3	1.74	0.69
12:L:27:LEU:HD13	12:L:37:LYS:HG2	1.73	0.69
2:B:638:PHE:HB3	2:B:651:LEU:HD21	1.75	0.69
1:A:34:LYS:HB3	1:A:83:HIS:CE1	2.27	0.69
1:A:64:ASN:O	1:A:65:LEU:HB3	1.93	0.68
2:B:952:VAL:HB	12:L:58:LYS:HB2	1.73	0.68
3:C:56:THR:HG22	3:C:58:LEU:H	1.57	0.68
3:C:163:ILE:HD12	3:C:165:LYS:HB2	1.74	0.67
1:A:219:PHE:HA	1:A:222:LEU:HD12	1.77	0.67
1:A:497:THR:HG22	2:B:1146:PHE:HA	1.76	0.67
2:B:446:LEU:HD12	2:B:448:ILE:HD11	1.77	0.67
7:G:1:MET:HE2	7:G:2:PHE:N	2.01	0.67
1:A:37:PHE:HD2	1:A:52:GLY:HA3	1.60	0.66
2:B:466:TRP:HB2	2:B:479:VAL:HG21	1.77	0.66
1:A:873:MET:HB3	1:A:878:ILE:HD11	1.77	0.65
12:L:61:THR:HG21	12:L:63:ARG:HG2	1.78	0.65
2:B:296:GLU:O	2:B:300:HIS:HD2	1.80	0.65
2:B:269:ILE:HD11	2:B:386:LEU:HD21	1.78	0.65
1:A:871:ASP:OD1	1:A:1366:ARG:NH2	2.30	0.65
1:A:868:TYR:CD2	1:A:1058:VAL:HG11	2.31	0.65
2:B:779:GLY:HA2	2:B:796:LEU:HB2	1.79	0.65
1:A:368:LYS:HE2	1:A:399:HIS:HB2	1.79	0.64
1:A:855:THR:HG23	1:A:857:ARG:HG3	1.79	0.64
1:A:1444:MET:HG3	7:G:60:ARG:HA	1.79	0.64
3:C:70:ILE:HD11	3:C:144:ILE:HG12	1.79	0.64
2:B:999:MET:HG3	2:B:1000:PRO:HD2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:363:HIS:HD2	2:B:585:VAL:HG22	1.62	0.64
2:B:356:LEU:HA	2:B:360:PHE:HB3	1.78	0.64
2:B:865:LYS:HE2	2:B:869:SER:HA	1.80	0.64
6:F:90:ARG:HG3	6:F:90:ARG:HH11	1.61	0.63
9:I:106:CYS:SG	9:I:108:HIS:HB3	2.38	0.63
2:B:882:THR:HB	2:B:934:LYS:O	1.99	0.63
2:B:642:ASP:HA	2:B:649:LYS:HA	1.81	0.63
7:G:26:LEU:HD13	7:G:56:ILE:HD11	1.80	0.63
11:K:21:ILE:HG12	11:K:33:ILE:HG12	1.81	0.62
1:A:41:MET:CB	1:A:49:LYS:HA	2.29	0.62
5:E:135:PHE:HB3	5:E:140:LEU:HD11	1.81	0.62
13:N:2:DA:H4'	13:N:3:DA:OP1	1.98	0.62
4:D:18:VAL:HG22	4:D:20:GLU:H	1.64	0.62
1:A:335:ARG:HD2	2:B:1206:GLU:OE1	1.99	0.62
8:H:82:PRO:C	8:H:84:ALA:H	2.02	0.62
1:A:683:ILE:HG21	1:A:801:GLU:HG3	1.82	0.61
1:A:472:LEU:O	1:A:475:THR:HB	2.00	0.61
2:B:35:SER:HA	2:B:811:TYR:HE1	1.65	0.61
3:C:116:LYS:HD3	3:C:140:ASN:HA	1.82	0.61
1:A:855:THR:CG2	1:A:857:ARG:HE	2.11	0.61
2:B:238:ALA:HB3	2:B:256:VAL:HB	1.83	0.61
1:A:590:ARG:NH2	1:A:621:THR:OG1	2.33	0.61
1:A:37:PHE:CD2	1:A:52:GLY:HA3	2.35	0.61
1:A:1111:MET:HG3	1:A:1114:PRO:HG3	1.82	0.61
1:A:666:ILE:HD11	2:B:1030:LEU:HD13	1.83	0.61
1:A:49:LYS:HD2	1:A:55:ASP:HB3	1.82	0.61
3:C:98:VAL:H	3:C:122:SER:CB	2.13	0.61
7:G:143:ILE:HG22	7:G:145:VAL:HG22	1.82	0.61
7:G:111:THR:HB	7:G:114:LEU:HD23	1.83	0.61
12:L:61:THR:CG2	12:L:63:ARG:HG2	2.30	0.61
7:G:1:MET:CE	7:G:80:LYS:H	2.13	0.60
2:B:901:PRO:HD3	12:L:58:LYS:HB3	1.83	0.60
2:B:653:VAL:HG22	2:B:689:LEU:HB3	1.81	0.60
12:L:47:ARG:HH21	12:L:54:ARG:HE	1.48	0.60
2:B:996:ARG:NH2	3:C:174:ALA:O	2.32	0.60
6:F:89:GLU:O	6:F:93:ILE:HD12	2.01	0.60
4:D:7:THR:HG21	7:G:5:LYS:HZ1	1.66	0.60
1:A:106:VAL:HG21	1:A:214:ILE:HG12	1.84	0.60
3:C:97:VAL:HG21	3:C:129:ILE:HG23	1.83	0.59
3:C:55:THR:HB	3:C:151:GLN:HA	1.84	0.59
12:L:60:ARG:HH22	12:L:65:VAL:HG22	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:815:ARG:HH11	2:B:815:ARG:CG	2.14	0.59
1:A:1424:VAL:HG22	1:A:1436:ILE:HD11	1.85	0.59
1:A:1279:ILE:HG23	1:A:1308:THR:HG23	1.84	0.59
1:A:726:ARG:HD3	1:A:766:GLY:HA3	1.84	0.58
7:G:27:LYS:HE2	7:G:54:ILE:HB	1.85	0.58
1:A:346:ASP:HB3	2:B:1108:ARG:H	1.68	0.58
2:B:639:ILE:HD11	2:B:691:GLU:HB2	1.86	0.58
1:A:1433:MET:HE3	7:G:63:PRO:HB3	1.85	0.58
11:K:55:LYS:HB3	11:K:81:TYR:CD2	2.39	0.58
2:B:902:GLY:O	12:L:65:VAL:HG11	2.03	0.58
7:G:114:LEU:HD12	7:G:162:SER:HB2	1.85	0.57
11:K:58:PHE:HB3	11:K:76:GLN:HB3	1.86	0.57
1:A:1348:LEU:O	1:A:1352:VAL:HG23	2.03	0.57
1:A:62:ASP:HB2	1:A:65:LEU:HD22	1.86	0.57
2:B:344:LYS:HB3	2:B:347:LYS:HB2	1.84	0.57
1:A:1155:ASP:HB3	1:A:1241:ARG:HH21	1.70	0.57
1:A:1402:PHE:CE2	1:A:1403:GLU:HG2	2.40	0.57
1:A:379:VAL:HG22	1:A:431:LYS:HG2	1.87	0.56
3:C:177:GLU:HB2	3:C:231:ASN:HB3	1.87	0.56
1:A:253:ASN:HA	2:B:884:ARG:HH22	1.70	0.56
1:A:871:ASP:HB3	5:E:204:THR:HG23	1.86	0.56
3:C:67:LEU:HA	3:C:70:ILE:HD12	1.87	0.56
1:A:1259:MET:HA	1:A:1262:LYS:HD2	1.86	0.56
1:A:392:VAL:HG11	1:A:424:ILE:HG21	1.88	0.56
5:E:147:HIS:HB3	5:E:150:VAL:HG23	1.88	0.56
4:D:167:LEU:HB3	4:D:177:VAL:HG22	1.88	0.56
1:A:646:PHE:O	1:A:650:GLN:HG2	2.05	0.55
1:A:1433:MET:CE	7:G:63:PRO:HB3	2.36	0.55
3:C:39:ALA:HA	3:C:164:ALA:HB3	1.88	0.55
10:J:1:MET:HG3	10:J:60:PHE:HE2	1.72	0.55
1:A:187:LYS:HE3	1:A:198:GLU:HB2	1.89	0.55
7:G:1:MET:HE3	7:G:80:LYS:O	2.06	0.55
4:D:59:ILE:HD11	7:G:77:VAL:HG11	1.89	0.55
2:B:311:LEU:HB3	9:I:4:PHE:HE1	1.70	0.55
2:B:25:ILE:HD11	2:B:658:ILE:HD13	1.89	0.55
2:B:1172:ILE:HD11	2:B:1183:LYS:CE	2.37	0.55
2:B:33:VAL:HG21	2:B:638:PHE:HZ	1.69	0.55
2:B:839:MET:CE	2:B:980:PHE:HB2	2.36	0.55
1:A:1370:LEU:O	1:A:1374:VAL:HG23	2.07	0.55
1:A:392:VAL:CG1	1:A:424:ILE:HG21	2.37	0.55
6:F:75:PRO:HG2	6:F:78:GLN:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:343:ILE:O	2:B:344:LYS:HB2	2.08	0.54
1:A:448:PRO:O	1:A:449:SER:HB2	2.07	0.54
1:A:315:LEU:HA	1:A:321:PRO:HA	1.89	0.54
8:H:130:ARG:HA	8:H:133:ASN:HD22	1.72	0.54
1:A:589:GLN:HG2	1:A:606:LEU:HD13	1.90	0.54
1:A:1312:ASN:O	1:A:1316:VAL:HG23	2.08	0.54
13:N:2:DA:H61	15:T:16:DT:H3	1.55	0.54
7:G:127:PRO:HB2	7:G:139:ILE:HD12	1.90	0.54
7:G:138:THR:HG22	7:G:139:ILE:H	1.73	0.53
2:B:402:GLY:HA2	2:B:695:ALA:HB3	1.88	0.53
2:B:35:SER:HA	2:B:811:TYR:CE1	2.42	0.53
2:B:996:ARG:HG3	2:B:1007:VAL:HG11	1.90	0.53
7:G:1:MET:SD	7:G:2:PHE:N	2.82	0.53
2:B:629:ASP:HB3	2:B:632:ARG:HE	1.73	0.53
1:A:568:PRO:HB2	3:C:221:TYR:CZ	2.44	0.53
2:B:899:ILE:HD11	2:B:911:ILE:HA	1.90	0.53
1:A:1345:ARG:HD2	1:A:1373:ASP:OD1	2.08	0.53
1:A:579:SER:HA	1:A:582:ILE:HD12	1.91	0.53
1:A:1149:ALA:HB2	9:I:47:GLU:HA	1.90	0.53
3:C:98:VAL:H	3:C:122:SER:HB2	1.74	0.53
2:B:1103:ILE:O	2:B:1122:ARG:NH1	2.41	0.53
2:B:247:GLY:H	2:B:418:LYS:NZ	2.07	0.52
1:A:741:ASN:HB3	1:A:744:LYS:HB2	1.90	0.52
2:B:577:ALA:HB1	2:B:589:VAL:HB	1.91	0.52
1:A:49:LYS:NZ	1:A:60:SER:HA	2.24	0.52
4:D:55:ALA:O	4:D:59:ILE:HD12	2.08	0.52
1:A:1386:ARG:HB3	1:A:1403:GLU:HG3	1.92	0.52
1:A:915:SER:HB2	1:A:919:ILE:HD13	1.91	0.52
1:A:339:ASN:HB3	2:B:1117:GLN:HE22	1.73	0.52
1:A:982:THR:HB	1:A:985:ASP:H	1.75	0.52
2:B:706:GLN:HB3	2:B:709:ASP:OD1	2.10	0.52
2:B:848:ARG:HD2	10:J:8:PHE:O	2.08	0.52
1:A:704:ALA:HB2	1:A:710:LEU:HD12	1.92	0.52
2:B:1159:ARG:HD3	2:B:1193:GLN:HB2	1.90	0.52
1:A:1435:PRO:HA	1:A:1439:GLY:O	2.10	0.52
2:B:1165:ILE:HG21	4:D:17:LYS:HB3	1.91	0.52
2:B:705:MET:HA	2:B:705:MET:HE3	1.93	0.52
2:B:274:PRO:HG2	2:B:359:GLU:HB3	1.90	0.52
1:A:130:ASP:HB3	1:A:133:LYS:HB2	1.92	0.52
1:A:1100:ARG:O	1:A:1104:ILE:HG13	2.10	0.51
3:C:100:THR:HB	3:C:121:VAL:HG21	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:326:ARG:HG3	1:A:1406:VAL:HG21	1.93	0.51
5:E:40:GLU:HA	5:E:43:LYS:HD2	1.93	0.51
1:A:1193:LEU:HB2	1:A:1260:LEU:HD21	1.91	0.51
1:A:140:THR:HA	1:A:143:LYS:HE2	1.93	0.51
2:B:296:GLU:O	2:B:300:HIS:CD2	2.61	0.51
3:C:44:LEU:HB2	3:C:77:ILE:HD13	1.92	0.51
5:E:4:GLU:HB3	5:E:7:ARG:NE	2.26	0.51
3:C:149:LYS:HG3	3:C:150:GLY:H	1.75	0.51
2:B:882:THR:OG1	2:B:935:ARG:N	2.41	0.51
2:B:258:LEU:HB2	2:B:385:LEU:HD21	1.92	0.51
1:A:1433:MET:HE3	7:G:63:PRO:CB	2.41	0.51
1:A:709:THR:HB	1:A:712:GLU:H	1.75	0.51
2:B:345:LYS:HA	2:B:348:ARG:HD2	1.93	0.51
1:A:1148:ILE:HA	9:I:49:ILE:HD12	1.93	0.51
1:A:79:GLY:HA3	1:A:243:PRO:HG3	1.93	0.51
5:E:5:ASN:HD21	5:E:52:ARG:HE	1.57	0.51
11:K:63:VAL:HG12	11:K:71:PHE:HB3	1.93	0.51
1:A:1442:ASP:HB2	6:F:137:TYR:HE1	1.76	0.51
1:A:483:ASP:HB2	2:B:987:LYS:HG3	1.92	0.50
4:D:193:THR:HG21	7:G:167:TYR:HD2	1.76	0.50
2:B:313:MET:HG2	2:B:386:LEU:HD22	1.94	0.50
1:A:697:ALA:HB2	1:A:702:LEU:HD13	1.94	0.50
2:B:1100:ASP:OD2	11:K:1:MET:HB3	2.12	0.50
2:B:280:ILE:HD13	2:B:334:ILE:HG12	1.93	0.50
1:A:1148:ILE:HD12	1:A:1196:GLU:HG2	1.93	0.50
6:F:76:LYS:HA	6:F:79:ARG:CD	2.34	0.50
10:J:48:ARG:NE	10:J:49:MET:HE2	2.26	0.50
1:A:52:GLY:N	1:A:56:PRO:HB3	2.26	0.50
1:A:857:ARG:HD3	1:A:861:GLY:O	2.11	0.50
1:A:679:ILE:HG13	1:A:732:LEU:HD12	1.94	0.50
1:A:42:ASP:HB3	1:A:45:GLN:HA	1.94	0.50
2:B:29:ASP:HB3	2:B:658:ILE:HG12	1.93	0.49
2:B:758:PHE:HB3	2:B:761:HIS:CD2	2.47	0.49
1:A:1400:CYS:HA	1:A:1408:ILE:HD12	1.94	0.49
2:B:242:SER:OG	2:B:362:PRO:HD2	2.12	0.49
1:A:380:VAL:HG13	1:A:385:ILE:HG12	1.94	0.49
2:B:843:GLN:HA	2:B:846:ILE:HD12	1.93	0.49
1:A:353:ILE:HG22	1:A:468:PHE:HB2	1.94	0.49
3:C:4:GLU:H	3:C:7:GLN:HE22	1.59	0.49
1:A:448:PRO:O	1:A:449:SER:CB	2.60	0.49
1:A:216:VAL:O	1:A:220:THR:HB	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:875:ALA:HB2	1:A:1366:ARG:HD2	1.94	0.49
10:J:9:SER:OG	10:J:48:ARG:NH2	2.45	0.49
1:A:870:GLU:HB2	5:E:204:THR:HG21	1.95	0.49
2:B:425:THR:HA	2:B:428:ILE:HD12	1.95	0.49
2:B:276:ILE:HA	2:B:338:GLY:O	2.13	0.49
1:A:452:LYS:HG2	2:B:1141:HIS:CE1	2.47	0.49
1:A:768:GLN:HG2	1:A:816:HIS:HA	1.95	0.49
1:A:449:SER:HA	1:A:454:SER:CB	2.42	0.49
8:H:107:VAL:HG23	8:H:111:LEU:HB3	1.95	0.49
1:A:49:LYS:HG2	1:A:61:ILE:HD12	1.95	0.49
2:B:1072:MET:HE3	2:B:1085:ILE:HB	1.94	0.49
2:B:664:THR:HG1	2:B:678:GLU:N	2.10	0.49
3:C:6:PRO:HB2	11:K:101:LEU:HD23	1.95	0.48
3:C:99:LEU:HD12	3:C:118:LEU:HB3	1.94	0.48
2:B:882:THR:C	2:B:884:ARG:H	2.16	0.48
3:C:99:LEU:HB2	3:C:157:CYS:HB2	1.95	0.48
11:K:32:VAL:HG22	11:K:74:ARG:HG3	1.94	0.48
2:B:918:ILE:HG12	2:B:935:ARG:HH22	1.78	0.48
8:H:125:LEU:HG	8:H:130:ARG:NH2	2.28	0.48
1:A:154:SER:HB3	1:A:162:VAL:HG23	1.94	0.48
8:H:105:GLU:HB3	8:H:113:ALA:HB3	1.94	0.48
2:B:745:PRO:O	2:B:748:ILE:HG12	2.13	0.48
2:B:842:ASN:HB3	2:B:845:SER:HB2	1.95	0.48
8:H:82:PRO:O	8:H:84:ALA:N	2.45	0.48
2:B:542:MET:HE2	2:B:747:MET:HG3	1.94	0.48
1:A:54:ASN:HB3	1:A:247:ARG:HH12	1.78	0.48
2:B:33:VAL:HG21	2:B:638:PHE:CZ	2.48	0.48
1:A:353:ILE:HD12	1:A:482:PHE:CD1	2.48	0.48
1:A:1428:VAL:HG13	2:B:1151:LEU:HD21	1.96	0.48
2:B:899:ILE:CD1	2:B:911:ILE:HA	2.44	0.48
4:D:34:GLN:O	4:D:47:LEU:HD12	2.14	0.48
4:D:23:ASN:HA	4:D:28:GLN:O	2.14	0.48
3:C:11:ARG:HD3	3:C:209:TYR:CE2	2.49	0.48
7:G:93:SER:OG	7:G:100:GLU:HB2	2.13	0.48
1:A:1101:LEU:HB2	1:A:1355:VAL:HG11	1.95	0.47
7:G:142:ARG:HB3	7:G:171:ILE:HD12	1.95	0.47
11:K:57:LEU:HB2	11:K:76:GLN:HG2	1.95	0.47
11:K:103:THR:O	11:K:107:THR:HB	2.14	0.47
1:A:1267:MET:HA	1:A:1271:ILE:HD12	1.96	0.47
2:B:128:LEU:HD21	2:B:170:LEU:HB2	1.96	0.47
7:G:34:VAL:HG13	7:G:45:ILE:HG21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:165:LYS:O	11:K:6:ARG:NH1	2.40	0.47
1:A:79:GLY:HA3	1:A:243:PRO:CG	2.44	0.47
2:B:904:ARG:HG3	2:B:948:ILE:HG13	1.97	0.47
1:A:185:TRP:HE3	1:A:185:TRP:H	1.61	0.47
2:B:866:TYR:HB2	2:B:870:ILE:HB	1.95	0.47
1:A:347:PHE:HE1	1:A:375:THR:HG22	1.79	0.47
1:A:1338:VAL:HG12	1:A:1339:LEU:HG	1.95	0.47
2:B:983:ARG:HD2	2:B:1091:TYR:HB3	1.94	0.47
1:A:358:ASN:HB2	11:K:65:HIS:HD2	1.79	0.47
1:A:548:ASN:HD21	11:K:47:ARG:HE	1.62	0.47
4:D:194:LEU:HD22	7:G:86:VAL:HG11	1.96	0.47
1:A:84:ILE:HD11	1:A:86:LEU:HD23	1.97	0.47
3:C:114:TYR:CD1	3:C:140:ASN:HB3	2.49	0.47
3:C:148:ARG:HG2	3:C:149:LYS:HG2	1.97	0.47
1:A:1100:ARG:NH2	1:A:1351:GLU:HG2	2.25	0.47
1:A:399:HIS:HB3	1:A:400:PRO:HD3	1.96	0.47
3:C:77:ILE:HA	3:C:129:ILE:HD11	1.97	0.47
2:B:839:MET:HE2	2:B:980:PHE:HB2	1.97	0.47
1:A:358:ASN:HB2	11:K:65:HIS:CD2	2.50	0.47
11:K:49:GLU:HG3	11:K:94:ILE:CG1	2.45	0.47
1:A:528:LEU:HD23	1:A:751:SER:HA	1.96	0.47
10:J:36:LEU:HD11	10:J:51:LEU:HB2	1.96	0.47
2:B:865:LYS:HB2	2:B:961:LEU:HD21	1.97	0.47
8:H:63:LEU:HB3	8:H:90:ALA:CB	2.45	0.47
6:F:73:ALA:HB2	6:F:143:PHE:CZ	2.50	0.47
1:A:1329:THR:H	1:A:1335:ILE:HD11	1.79	0.47
1:A:61:ILE:HG22	1:A:62:ASP:N	2.23	0.47
2:B:710:LEU:HA	2:B:733:HIS:HB3	1.97	0.47
2:B:806:THR:HG22	2:B:808:ALA:H	1.79	0.47
3:C:166:GLU:HG2	12:L:70:ARG:HH22	1.80	0.47
7:G:92:VAL:HG21	7:G:102:GLN:HB2	1.97	0.47
1:A:1426:GLU:HG2	1:A:1426:GLU:H	1.48	0.47
1:A:88:LYS:HB2	1:A:276:LEU:HD21	1.97	0.47
1:A:886:ILE:HG12	1:A:943:LEU:HB3	1.97	0.47
8:H:84:ALA:HA	8:H:87:ARG:HB2	1.97	0.46
6:F:128:LYS:HD3	6:F:149:GLU:O	2.15	0.46
8:H:40:LEU:HD13	8:H:123:MET:HG3	1.97	0.46
1:A:62:ASP:HB3	1:A:64:ASN:O	2.15	0.46
2:B:1072:MET:HB3	2:B:1081:LEU:HD12	1.96	0.46
10:J:64:ASN:HB2	10:J:65:PRO:HD3	1.96	0.46
1:A:1004:ASN:HD21	1:A:1007:ILE:HG12	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:649:LYS:HE2	2:B:738:PHE:O	2.15	0.46
1:A:1172:LEU:C	1:A:1174:PHE:H	2.18	0.46
2:B:449:ASN:HD21	2:B:451:LYS:HB2	1.80	0.46
1:A:497:THR:CG2	2:B:1146:PHE:HA	2.46	0.46
6:F:90:ARG:CG	6:F:90:ARG:HH11	2.29	0.46
2:B:579:ARG:HB2	2:B:586:TRP:NE1	2.31	0.46
2:B:652:LYS:HB3	2:B:689:LEU:HD23	1.97	0.46
1:A:1063:MET:SD	1:A:1436:ILE:HG13	2.55	0.46
11:K:49:GLU:HG3	11:K:94:ILE:HG13	1.98	0.46
1:A:941:LYS:O	1:A:941:LYS:HE3	2.15	0.46
3:C:259:LEU:HD22	11:K:91:CYS:HB3	1.97	0.46
1:A:672:ASP:HB3	1:A:736:ASN:OD1	2.16	0.46
8:H:81:PRO:HB2	8:H:82:PRO:HD3	1.97	0.46
3:C:98:VAL:H	3:C:122:SER:HB3	1.79	0.46
1:A:79:GLY:H	2:B:1205:GLN:HE22	1.63	0.46
1:A:1441:PHE:CZ	6:F:89:GLU:HA	2.51	0.46
5:E:198:ILE:HD13	5:E:212:ARG:HG3	1.97	0.46
5:E:6:GLU:HA	5:E:9:ILE:HD12	1.98	0.46
1:A:51:GLY:HA2	1:A:56:PRO:HA	1.97	0.46
1:A:1444:MET:HE1	6:F:135:ARG:NE	2.31	0.46
2:B:341:LEU:HD12	2:B:343:ILE:H	1.81	0.46
2:B:756:ILE:O	2:B:759:PRO:HD3	2.16	0.46
1:A:587:HIS:HB2	1:A:969:GLN:HE22	1.80	0.46
5:E:31:THR:HG23	5:E:34:GLU:HB2	1.98	0.46
12:L:38:LEU:HD22	12:L:56:LEU:HD21	1.97	0.45
1:A:1428:VAL:HG13	2:B:1151:LEU:CD2	2.46	0.45
6:F:132:LEU:O	6:F:148:VAL:HG22	2.15	0.45
7:G:131:GLN:HG2	7:G:136:VAL:HG22	1.97	0.45
1:A:38:PRO:HD3	1:A:270:LEU:HD12	1.98	0.45
7:G:106:MET:HG3	7:G:157:ILE:O	2.16	0.45
2:B:226:PHE:HA	2:B:395:GLN:HG3	1.98	0.45
5:E:19:VAL:HG22	5:E:140:LEU:HD22	1.97	0.45
7:G:23:LYS:HA	7:G:56:ILE:HD12	1.99	0.45
1:A:527:THR:HG23	1:A:653:VAL:HB	1.97	0.45
2:B:365:THR:HG21	2:B:370:PHE:CD2	2.52	0.45
1:A:425:GLN:NE2	1:A:425:GLN:HA	2.31	0.45
2:B:810:GLU:HA	2:B:815:ARG:HH12	1.82	0.45
2:B:363:HIS:O	2:B:364:ILE:HB	2.16	0.45
1:A:35:ILE:HG22	1:A:84:ILE:HG22	1.99	0.45
1:A:380:VAL:CG1	1:A:385:ILE:HG12	2.46	0.45
1:A:1349:TYR:HA	1:A:1372:VAL:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:583:ASN:HD21	2:B:628:THR:HB	1.81	0.45
10:J:3:VAL:HG21	10:J:18:TRP:CB	2.47	0.45
1:A:385:ILE:O	1:A:389:THR:OG1	2.34	0.45
2:B:1175:LEU:O	2:B:1176:ASN:HB2	2.16	0.45
3:C:97:VAL:HG11	3:C:130:GLY:HA3	1.99	0.45
1:A:121:LEU:O	1:A:124:GLN:HB3	2.16	0.45
10:J:7:CYS:HA	10:J:49:MET:HG2	1.99	0.45
5:E:4:GLU:HB3	5:E:7:ARG:HE	1.81	0.45
7:G:106:MET:HG2	7:G:107:LYS:N	2.32	0.45
2:B:995:ARG:NH1	2:B:997:GLU:OE1	2.50	0.45
6:F:109:VAL:HG11	6:F:123:LYS:HG2	2.00	0.45
10:J:3:VAL:HG11	10:J:18:TRP:HB2	1.98	0.44
3:C:149:LYS:C	3:C:151:GLN:H	2.20	0.44
5:E:176:PRO:O	5:E:212:ARG:HA	2.16	0.44
2:B:801:LYS:O	10:J:52:THR:OG1	2.35	0.44
2:B:402:GLY:CA	2:B:695:ALA:HB3	2.46	0.44
2:B:693:ILE:HG23	2:B:697:GLU:HB3	1.99	0.44
2:B:900:ALA:HB3	12:L:61:THR:HG23	2.00	0.44
8:H:125:LEU:HG	8:H:130:ARG:HH22	1.82	0.44
2:B:792:MET:HA	2:B:856:PHE:O	2.18	0.44
1:A:626:ASN:O	1:A:631:HIS:ND1	2.48	0.44
2:B:295:GLY:HA2	2:B:298:LEU:HB2	2.00	0.44
1:A:1402:PHE:CD2	1:A:1403:GLU:HG2	2.53	0.44
2:B:873:THR:O	2:B:914:LYS:HA	2.17	0.44
2:B:1084:GLN:NE2	3:C:192:TRP:H	2.15	0.44
2:B:408:LEU:HD21	2:B:545:ILE:HD13	1.99	0.44
2:B:839:MET:HE1	2:B:980:PHE:HB2	1.99	0.44
1:A:1313:LEU:HD23	1:A:1338:VAL:HB	2.00	0.44
1:A:344:ARG:HB3	2:B:1118:PRO:HB2	2.00	0.44
2:B:510:LYS:N	2:B:511:PRO:HD3	2.32	0.44
10:J:32:GLU:CD	10:J:32:GLU:H	2.20	0.44
1:A:880:LYS:HA	1:A:955:PRO:HA	1.99	0.44
1:A:388:LEU:O	1:A:392:VAL:HG23	2.18	0.44
7:G:128:PRO:O	7:G:138:THR:HG23	2.18	0.44
2:B:338:GLY:HA3	2:B:340:ALA:H	1.83	0.44
11:K:45:LEU:HG	11:K:94:ILE:HD13	2.00	0.44
2:B:831:SER:HG	2:B:994:TYR:HE2	1.65	0.44
11:K:7:PHE:HB2	11:K:11:LEU:HD22	1.99	0.44
6:F:97:ARG:HD2	6:F:97:ARG:HA	1.90	0.44
1:A:1444:MET:HE1	6:F:135:ARG:HE	1.83	0.44
2:B:574:SER:HB3	2:B:591:ARG:HE	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:100:ILE:HA	5:E:105:PHE:HD2	1.83	0.44
6:F:119:ARG:HA	6:F:122:MET:HG3	2.00	0.44
6:F:134:ILE:HG22	6:F:136:ARG:HG3	2.00	0.44
1:A:5:GLN:O	2:B:1159:ARG:NH2	2.51	0.44
7:G:21:ARG:NH1	7:G:24:GLN:OE1	2.51	0.44
2:B:475:SER:O	2:B:476:ARG:HB3	2.18	0.44
1:A:1276:VAL:HB	1:A:1279:ILE:HD13	2.00	0.44
2:B:291:ILE:HD12	2:B:291:ILE:H	1.83	0.44
1:A:1158:PRO:HA	1:A:1241:ARG:NH1	2.33	0.43
2:B:807:ARG:HG2	2:B:1045:SER:OG	2.17	0.43
2:B:1116:ARG:HB2	2:B:1198:TYR:CD2	2.53	0.43
1:A:464:PRO:HB2	11:K:4:PRO:HD3	2.01	0.43
3:C:60:ASP:HB3	12:L:67:PHE:CE2	2.54	0.43
7:G:112:LYS:HA	7:G:115:MET:HE3	2.00	0.43
3:C:54:ASN:OD1	3:C:56:THR:HB	2.19	0.43
1:A:1376:THR:HG23	5:E:212:ARG:HH22	1.82	0.43
7:G:43:GLY:HA2	7:G:157:ILE:HD11	2.00	0.43
8:H:16:ASP:HA	8:H:17:PRO:HD3	1.90	0.43
5:E:76:GLY:H	5:E:106:GLN:CD	2.22	0.43
2:B:283:VAL:HG13	2:B:297:ILE:HD13	1.99	0.43
4:D:176:GLU:OE2	4:D:197:SER:HB2	2.19	0.43
5:E:19:VAL:O	5:E:23:VAL:HG23	2.19	0.43
4:D:18:VAL:HG13	4:D:19:GLU:HA	2.00	0.43
2:B:1122:ARG:HB3	15:T:23:DG:OP1	2.19	0.43
3:C:75:MET:O	3:C:246:ARG:NH2	2.50	0.43
3:C:18:VAL:HG12	3:C:20:PHE:HD1	1.83	0.43
1:A:767:GLN:HA	1:A:799:PHE:HA	2.01	0.43
5:E:19:VAL:HG11	5:E:80:VAL:HG11	2.01	0.43
2:B:128:LEU:HB2	2:B:167:ILE:O	2.18	0.43
2:B:766:ARG:NH2	2:B:1020:ARG:HD3	2.33	0.43
2:B:754:SER:HB2	2:B:812:LEU:HD11	2.01	0.43
1:A:1076:ALA:HA	1:A:1079:MET:HG3	2.01	0.43
11:K:51:LEU:HD12	11:K:51:LEU:HA	1.87	0.43
1:A:567:LYS:HA	1:A:568:PRO:C	2.38	0.43
2:B:995:ARG:HB3	2:B:997:GLU:OE2	2.18	0.43
1:A:658:LEU:HD23	1:A:659:HIS:NE2	2.33	0.43
2:B:847:ASP:HB3	3:C:167:HIS:CE1	2.53	0.43
1:A:901:LEU:HD22	1:A:919:ILE:HG23	2.00	0.43
1:A:1096:SER:O	1:A:1099:PRO:HG2	2.18	0.43
6:F:90:ARG:HG3	6:F:90:ARG:NH1	2.31	0.42
13:N:2:DA:N6	15:T:16:DT:H3	2.16	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1138:MET:HB3	2:B:1147:LEU:HG	2.01	0.42
9:I:50:THR:HG22	9:I:52:ILE:H	1.83	0.42
3:C:58:LEU:HD21	10:J:57:ILE:HD12	2.01	0.42
8:H:63:LEU:HB3	8:H:90:ALA:HB2	2.01	0.42
4:D:65:GLU:HA	4:D:68:ARG:HG3	2.00	0.42
1:A:434:ARG:NH2	1:A:440:ASP:OD2	2.52	0.42
1:A:868:TYR:CE2	1:A:1058:VAL:HG11	2.54	0.42
2:B:911:ILE:HD11	2:B:941:LEU:HD13	2.01	0.42
1:A:372:LYS:HA	1:A:435:HIS:CD2	2.55	0.42
1:A:1155:ASP:HB3	1:A:1241:ARG:NH2	2.32	0.42
1:A:605:MET:HE1	1:A:612:ILE:HG23	2.00	0.42
1:A:357:PRO:HD2	2:B:833:TYR:CZ	2.54	0.42
4:D:213:GLU:HA	4:D:216:ASN:HD22	1.84	0.42
3:C:52:GLU:HG2	12:L:64:LEU:HD11	2.01	0.42
1:A:1128:GLN:HG3	1:A:1304:TRP:CE2	2.54	0.42
8:H:93:TYR:HA	8:H:145:ARG:HB3	2.01	0.42
1:A:216:VAL:HG13	1:A:226:GLU:HB3	2.00	0.42
2:B:766:ARG:HH21	2:B:1020:ARG:HH11	1.68	0.42
2:B:848:ARG:HA	3:C:69:LEU:HD21	2.01	0.42
4:D:5:THR:HG21	7:G:74:TYR:OH	2.20	0.42
2:B:464:GLY:HA2	2:B:480:SER:HB3	2.02	0.42
13:N:4:DG:N2	15:T:15:DT:O2	2.53	0.42
1:A:243:PRO:HB2	1:A:245:PRO:HD2	2.02	0.42
11:K:65:HIS:HE1	11:K:67:PHE:CG	2.37	0.42
2:B:168:GLY:H	2:B:450:ALA:HB1	1.85	0.42
4:D:10:THR:O	4:D:12:ARG:NH2	2.53	0.42
1:A:95:PHE:CE1	1:A:1414:ALA:HB2	2.55	0.42
4:D:195:ILE:HG22	4:D:198:LEU:HG	2.01	0.42
2:B:216:GLU:OE1	2:B:537:LYS:HD2	2.20	0.42
1:A:868:TYR:HD2	1:A:1058:VAL:HG11	1.83	0.41
11:K:51:LEU:CD1	11:K:59:ALA:HB3	2.45	0.41
3:C:4:GLU:HB2	11:K:104:ASN:HD21	1.84	0.41
2:B:542:MET:HG3	2:B:747:MET:HB3	2.02	0.41
5:E:167:ARG:HA	5:E:167:ARG:HD3	1.79	0.41
2:B:70:ILE:HD12	2:B:70:ILE:H	1.85	0.41
2:B:637:LEU:HD12	2:B:693:ILE:HD13	2.01	0.41
4:D:173:HIS:CE1	4:D:201:LYS:HE3	2.56	0.41
2:B:876:LYS:NZ	2:B:891:ASP:HA	2.35	0.41
2:B:435:THR:C	2:B:437:GLU:H	2.24	0.41
1:A:53:LEU:O	1:A:54:ASN:C	2.59	0.41
1:A:871:ASP:CG	1:A:1366:ARG:HH22	2.24	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1050:ILE:H	2:B:1050:ILE:HG13	1.73	0.41
2:B:211:VAL:HG23	2:B:483:LEU:HB2	2.01	0.41
2:B:118:ARG:HH11	2:B:204:ILE:HD11	1.85	0.41
1:A:55:ASP:CG	1:A:55:ASP:O	2.59	0.41
4:D:54:GLU:O	4:D:58:VAL:HG23	2.21	0.41
1:A:122:MET:HG3	1:A:126:LEU:HD12	2.02	0.41
1:A:786:HIS:CD2	2:B:703:ILE:HB	2.54	0.41
11:K:18:LYS:HE3	11:K:38:GLU:HG2	2.03	0.41
12:L:47:ARG:HG3	12:L:54:ARG:HG3	2.02	0.41
2:B:1104:HIS:HB2	2:B:1122:ARG:HG3	2.03	0.41
1:A:270:LEU:HD22	1:A:270:LEU:HA	1.89	0.41
5:E:188:LEU:HB2	5:E:190:LEU:HD23	2.02	0.41
1:A:629:LEU:HD13	1:A:645:LEU:HD21	2.03	0.41
2:B:102:VAL:HG13	2:B:112:LEU:HD22	2.03	0.41
4:D:18:VAL:HG22	4:D:19:GLU:HA	2.03	0.41
1:A:1387:HIS:O	1:A:1391:ARG:HG2	2.21	0.41
2:B:205:ILE:HD13	2:B:461:LEU:HB3	2.02	0.41
8:H:89:LEU:C	8:H:91:ASP:H	2.24	0.41
5:E:181:ALA:HA	5:E:186:LEU:HD21	2.02	0.41
2:B:315:LYS:N	2:B:316:PRO:HD2	2.35	0.41
12:L:40:LEU:HB2	12:L:44:ASP:HB3	2.01	0.41
4:D:159:THR:O	4:D:163:VAL:HG23	2.20	0.41
1:A:436:ILE:HD13	1:A:436:ILE:HA	1.60	0.41
1:A:35:ILE:HA	1:A:52:GLY:O	2.20	0.41
1:A:605:MET:CE	1:A:612:ILE:HG23	2.51	0.41
2:B:889:THR:HG22	2:B:891:ASP:OD1	2.20	0.41
2:B:169:ARG:HB2	2:B:454:THR:HG23	2.02	0.41
1:A:1116:LEU:HD21	1:A:1327:ILE:HD11	2.03	0.41
1:A:856:THR:HB	1:A:865:GLN:HB2	2.02	0.41
15:T:19:DT:H2'	15:T:19:DT:O2	2.21	0.41
2:B:1166:CYS:O	2:B:1166:CYS:SG	2.79	0.41
1:A:923:LEU:HD12	1:A:923:LEU:H	1.86	0.41
2:B:1136:ASP:HA	2:B:1139:ILE:HD12	2.03	0.41
2:B:640:VAL:HA	2:B:651:LEU:HA	2.02	0.41
6:F:90:ARG:CG	6:F:90:ARG:NH1	2.84	0.41
1:A:87:ALA:HB3	1:A:276:LEU:HD23	2.03	0.41
2:B:644:GLU:HG2	2:B:654:ARG:HH22	1.86	0.41
2:B:273:LEU:HD23	2:B:273:LEU:HA	1.92	0.41
10:J:31:ASP:OD1	10:J:34:THR:OG1	2.37	0.41
3:C:201:TRP:HA	3:C:202:PRO:HD3	1.95	0.41
7:G:73:LYS:HA	7:G:73:LYS:HD2	1.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:413:ILE:HD13	1:A:424:ILE:HD11	2.02	0.41
11:K:65:HIS:CE1	11:K:67:PHE:CG	3.08	0.41
1:A:1166:ASP:HA	1:A:1169:ILE:HD12	2.03	0.41
8:H:127:GLY:N	8:H:130:ARG:HH21	2.19	0.40
8:H:63:LEU:CB	8:H:90:ALA:CB	2.99	0.40
2:B:840:ILE:HG21	2:B:994:TYR:HD2	1.85	0.40
1:A:629:LEU:O	1:A:633:VAL:HG23	2.20	0.40
1:A:354:SER:O	1:A:469:ARG:HA	2.21	0.40
1:A:1318:THR:HB	5:E:11:ARG:HH12	1.86	0.40
12:L:60:ARG:NH2	12:L:65:VAL:HG22	2.33	0.40
2:B:101:MET:HG2	2:B:111:ALA:HA	2.02	0.40
1:A:41:MET:HA	1:A:50:ILE:HB	2.02	0.40
2:B:915:THR:HG21	2:B:934:LYS:HB2	2.02	0.40
2:B:39:ARG:NE	2:B:665:GLU:HG2	2.37	0.40
1:A:399:HIS:O	1:A:401:GLY:N	2.54	0.40
1:A:709:THR:HG23	9:I:94:ASP:HA	2.03	0.40
2:B:280:ILE:H	2:B:280:ILE:HG13	1.78	0.40
3:C:18:VAL:HG23	3:C:240:VAL:HB	2.04	0.40
1:A:946:VAL:HG22	5:E:201:LYS:HD2	2.04	0.40
2:B:373:ARG:HA	2:B:566:LEU:HD23	2.03	0.40
2:B:1082:MET:HA	3:C:189:THR:HA	2.04	0.40
7:G:13:LEU:HA	7:G:13:LEU:HD23	1.92	0.40
2:B:121:ASN:HA	2:B:207:GLY:HA3	2.03	0.40
7:G:9:LEU:HD22	7:G:34:VAL:HG23	2.04	0.40
2:B:39:ARG:HE	2:B:665:GLU:HG2	1.85	0.40
2:B:1043:ASP:O	2:B:1050:ILE:HD13	2.22	0.40
1:A:93:VAL:HG13	1:A:301:ALA:HB1	2.03	0.40
2:B:992:ILE:HD11	11:K:66:PRO:HB2	2.03	0.40
1:A:567:LYS:HA	1:A:569:LYS:N	2.36	0.40
1:A:353:ILE:HD13	1:A:487:MET:CE	2.51	0.40
1:A:151:ASP:HA	1:A:163:SER:HA	2.02	0.40
7:G:83:LYS:HD2	7:G:149:GLY:HA2	2.04	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:904:THR:N	9:I:33:SER:O[8_555]	2.18	0.02
7:G:95:SER:OG	7:G:97:HIS:CD2[3_654]	2.18	0.02

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%)	1252 (88%)	112 (8%)	50 (4%)	4	38
2	B	1095/1224 (90%)	969 (88%)	82 (8%)	44 (4%)	4	33
3	C	264/318 (83%)	236 (89%)	24 (9%)	4 (2%)	13	56
4	D	174/221 (79%)	154 (88%)	14 (8%)	6 (3%)	5	39
5	E	212/215 (99%)	186 (88%)	24 (11%)	2 (1%)	21	68
6	F	82/155 (53%)	77 (94%)	4 (5%)	1 (1%)	16	61
7	G	169/171 (99%)	160 (95%)	6 (4%)	3 (2%)	11	53
8	H	129/146 (88%)	101 (78%)	19 (15%)	9 (7%)	1	18
9	I	117/122 (96%)	96 (82%)	18 (15%)	3 (3%)	7	45
10	J	63/70 (90%)	55 (87%)	4 (6%)	4 (6%)	2	21
11	K	113/120 (94%)	108 (96%)	5 (4%)	0	100	100
12	L	44/70 (63%)	27 (61%)	9 (20%)	8 (18%)	0	2
All	All	3876/4564 (85%)	3421 (88%)	321 (8%)	134 (4%)	4	38

All (134) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	47	ARG
1	A	57	ARG
1	A	58	LEU
1	A	74	MET
1	A	193	ASP
1	A	257	ARG
1	A	286	HIS
1	A	318	SER
1	A	332	LYS
1	A	335	ARG
1	A	399	HIS
1	A	448	PRO

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Mol	Chain	Res	Type
1	A	449	SER
1	A	1175	SER
1	A	1403	GLU
1	A	1405	THR
2	B	229	ALA
2	B	307	ASP
2	B	344	LYS
2	B	473	MET
2	B	629	ASP
2	B	707	PRO
2	B	731	VAL
2	B	751	VAL
2	B	879	ARG
2	B	1066	SER
2	B	1157	ALA
2	B	1176	ASN
3	C	215	GLU
3	C	240	VAL
4	D	18	VAL
9	I	9	ASP
10	J	6	ARG
12	L	53	HIS
12	L	56	LEU
1	A	54	ASN
1	A	76	GLU
1	A	178	GLY
1	A	187	LYS
1	A	189	ARG
1	A	195	ASP
1	A	311	GLN
1	A	312	PRO
1	A	1124	HIS
1	A	1206	ASP
1	A	1281	ARG
2	B	340	ALA
2	B	341	LEU
2	B	466	TRP
2	B	867	GLY
2	B	1046	PRO
2	B	1156	ASP
2	B	1181	GLU
2	B	1190	ASP

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Mol	Chain	Res	Type
4	D	169	SER
8	H	17	PRO
8	H	81	PRO
8	H	83	GLN
9	I	95	THR
10	J	2	ILE
10	J	55	ASP
12	L	39	SER
12	L	50	ASP
1	A	43	GLU
1	A	167	CYS
1	A	251	SER
1	A	336	ILE
1	A	593	GLU
1	A	1173	HIS
1	A	1255	GLU
2	B	343	ILE
2	B	575	PRO
2	B	883	LEU
2	B	1223	ASP
4	D	16	LYS
4	D	52	LEU
4	D	199	ASN
5	E	3	GLN
7	G	154	VAL
8	H	52	GLN
8	H	60	ALA
8	H	82	PRO
10	J	17	LYS
12	L	45	ALA
1	A	35	ILE
1	A	62	ASP
1	A	283	GLY
1	A	331	GLY
1	A	423	ASP
1	A	567	LYS
1	A	569	LYS
1	A	775	ILE
1	A	1122	PRO
2	B	262	GLU
2	B	338	GLY
2	B	449	ASN

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Mol	Chain	Res	Type
2	B	533	CYS
2	B	711	GLU
3	C	150	GLY
4	D	220	LEU
7	G	63	PRO
8	H	18	GLY
8	H	90	ALA
9	I	105	SER
12	L	38	LEU
12	L	59	ALA
1	A	52	GLY
1	A	156	ASP
1	A	958	VAL
1	A	1437	GLY
2	B	368	GLU
2	B	772	ALA
2	B	792	MET
2	B	1155	SER
6	F	73	ALA
7	G	139	ILE
8	H	32	THR
12	L	26	THR
2	B	1108	ARG
3	C	38	ILE
2	B	108	VAL
5	E	90	VAL
1	A	196	GLU
2	B	168	GLY
2	B	251	ILE
2	B	436	VAL
2	B	902	GLY
2	B	907	GLY
2	B	369	GLY
1	A	1123	GLY
2	B	1214	PRO
1	A	55	ASP
2	B	231	PRO
2	B	364	ILE

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%)	1070 (86%)	170 (14%)	4	25
2	B	966/1061 (91%)	845 (88%)	121 (12%)	6	29
3	C	234/274 (85%)	207 (88%)	27 (12%)	7	33
4	D	160/200 (80%)	131 (82%)	29 (18%)	2	12
5	E	196/197 (100%)	176 (90%)	20 (10%)	9	40
6	F	74/137 (54%)	64 (86%)	10 (14%)	5	26
7	G	152/152 (100%)	128 (84%)	24 (16%)	3	19
8	H	117/128 (91%)	100 (86%)	17 (14%)	4	23
9	I	113/116 (97%)	100 (88%)	13 (12%)	7	33
10	J	60/65 (92%)	51 (85%)	9 (15%)	3	21
11	K	99/102 (97%)	85 (86%)	14 (14%)	4	24
12	L	40/57 (70%)	32 (80%)	8 (20%)	1	9
All	All	3451/4008 (86%)	2989 (87%)	462 (13%)	5	26

All (462) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	SER
1	A	12	ARG
1	A	13	THR
1	A	28	ARG
1	A	34	LYS
1	A	41	MET
1	A	44	THR
1	A	47	ARG
1	A	50	ILE
1	A	62	ASP
1	A	64	ASN
1	A	65	LEU
1	A	67	CYS
1	A	84	ILE

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Mol	Chain	Res	Type
1	A	88	LYS
1	A	93	VAL
1	A	96	ILE
1	A	117	GLU
1	A	126	LEU
1	A	132	LYS
1	A	141	LEU
1	A	144	THR
1	A	157	ASP
1	A	164	ARG
1	A	174	ILE
1	A	185	TRP
1	A	199	LEU
1	A	204	THR
1	A	208	LEU
1	A	215	SER
1	A	220	THR
1	A	226	GLU
1	A	252	PHE
1	A	261	ASP
1	A	265	LYS
1	A	270	LEU
1	A	307	ASP
1	A	315	LEU
1	A	324	SER
1	A	335	ARG
1	A	337	ARG
1	A	344	ARG
1	A	353	ILE
1	A	375	THR
1	A	381	THR
1	A	385	ILE
1	A	389	THR
1	A	408	ASP
1	A	412	ARG
1	A	424	ILE
1	A	425	GLN
1	A	434	ARG
1	A	436	ILE
1	A	443	LEU
1	A	450	LEU
1	A	451	HIS

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Mol	Chain	Res	Type
1	A	452	LYS
1	A	466	SER
1	A	469	ARG
1	A	470	LEU
1	A	472	LEU
1	A	474	VAL
1	A	475	THR
1	A	476	SER
1	A	496	GLU
1	A	500	GLU
1	A	518	LYS
1	A	527	THR
1	A	532	ARG
1	A	538	ASP
1	A	541	ILE
1	A	544	ASP
1	A	549	MET
1	A	555	ASP
1	A	566	ILE
1	A	569	LYS
1	A	571	LEU
1	A	577	ILE
1	A	593	GLU
1	A	597	LEU
1	A	598	LEU
1	A	603	ASN
1	A	618	GLU
1	A	629	LEU
1	A	634	THR
1	A	644	LYS
1	A	666	ILE
1	A	672	ASP
1	A	675	THR
1	A	685	GLU
1	A	702	LEU
1	A	738	LYS
1	A	756	ILE
1	A	768	GLN
1	A	774	ARG
1	A	782	ARG
1	A	788	SER
1	A	795	GLU

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Mol	Chain	Res	Type
1	A	821	ARG
1	A	824	LEU
1	A	826	ASP
1	A	831	THR
1	A	834	THR
1	A	839	ARG
1	A	855	THR
1	A	885	THR
1	A	886	ILE
1	A	904	THR
1	A	915	SER
1	A	919	ILE
1	A	920	LEU
1	A	929	LEU
1	A	941	LYS
1	A	948	VAL
1	A	973	ILE
1	A	998	LEU
1	A	1001	ARG
1	A	1015	VAL
1	A	1024	SER
1	A	1029	ARG
1	A	1036	ARG
1	A	1064	VAL
1	A	1067	LEU
1	A	1116	LEU
1	A	1118	VAL
1	A	1124	HIS
1	A	1128	GLN
1	A	1135	ARG
1	A	1145	SER
1	A	1173	HIS
1	A	1176	LEU
1	A	1192	LEU
1	A	1195	LEU
1	A	1208	THR
1	A	1218	GLN
1	A	1223	ASP
1	A	1234	GLU
1	A	1237	ILE
1	A	1242	VAL
1	A	1255	GLU

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Mol	Chain	Res	Type
1	A	1256	GLU
1	A	1257	ASP
1	A	1260	LEU
1	A	1264	GLU
1	A	1265	ASN
1	A	1266	THR
1	A	1277	GLU
1	A	1293	SER
1	A	1295	THR
1	A	1297	GLU
1	A	1309	ASP
1	A	1315	GLU
1	A	1325	THR
1	A	1327	ILE
1	A	1333	ILE
1	A	1336	MET
1	A	1341	ILE
1	A	1376	THR
1	A	1383	SER
1	A	1386	ARG
1	A	1391	ARG
1	A	1400	CYS
1	A	1405	THR
1	A	1426	GLU
1	A	1438	THR
1	A	1442	ASP
1	A	1444	MET
1	A	1445	ILE
1	A	1451	VAL
1	A	1454	MET
2	B	21	GLU
2	B	25	ILE
2	B	46	GLN
2	B	63	ILE
2	B	102	VAL
2	B	109	THR
2	B	118	ARG
2	B	134	LYS
2	B	178	ASN
2	B	185	THR
2	B	187	SER
2	B	217	ARG

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Mol	Chain	Res	Type
2	B	251	ILE
2	B	261	ARG
2	B	272	THR
2	B	278	GLN
2	B	280	ILE
2	B	289	LEU
2	B	294	ASP
2	B	298	LEU
2	B	313	MET
2	B	323	VAL
2	B	336	ARG
2	B	339	THR
2	B	341	LEU
2	B	343	ILE
2	B	344	LYS
2	B	346	GLU
2	B	347	LYS
2	B	348	ARG
2	B	350	GLN
2	B	351	TYR
2	B	357	GLN
2	B	361	LEU
2	B	365	THR
2	B	387	LEU
2	B	393	LYS
2	B	394	ASP
2	B	398	ARG
2	B	412	LEU
2	B	416	LEU
2	B	423	LYS
2	B	429	PHE
2	B	436	VAL
2	B	446	LEU
2	B	452	THR
2	B	453	ILE
2	B	469	GLN
2	B	470	LYS
2	B	476	ARG
2	B	481	GLN
2	B	485	ARG
2	B	486	TYR
2	B	537	LYS

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Mol	Chain	Res	Type
2	B	542	MET
2	B	547	VAL
2	B	552	MET
2	B	570	VAL
2	B	574	SER
2	B	595	ARG
2	B	606	LYS
2	B	616	ILE
2	B	620	ARG
2	B	624	LEU
2	B	628	THR
2	B	644	GLU
2	B	653	VAL
2	B	658	ILE
2	B	668	ASP
2	B	678	GLU
2	B	682	SER
2	B	708	GLU
2	B	709	ASP
2	B	731	VAL
2	B	734	HIS
2	B	755	ILE
2	B	766	ARG
2	B	786	ASN
2	B	790	ASP
2	B	797	TYR
2	B	835	GLN
2	B	837	ASP
2	B	839	MET
2	B	841	MET
2	B	844	SER
2	B	868	MET
2	B	871	THR
2	B	878	GLN
2	B	879	ARG
2	B	884	ARG
2	B	889	THR
2	B	904	ARG
2	B	908	GLU
2	B	933	SER
2	B	934	LYS
2	B	964	VAL

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Mol	Chain	Res	Type
2	B	975	GLN
2	B	976	ILE
2	B	986	GLN
2	B	999	MET
2	B	1002	THR
2	B	1006	ILE
2	B	1010	LEU
2	B	1050	ILE
2	B	1060	ARG
2	B	1062	HIS
2	B	1065	GLN
2	B	1072	MET
2	B	1106	ARG
2	B	1128	LEU
2	B	1133	MET
2	B	1138	MET
2	B	1147	LEU
2	B	1148	LYS
2	B	1156	ASP
2	B	1160	VAL
2	B	1175	LEU
2	B	1183	LYS
2	B	1188	LYS
2	B	1189	ILE
2	B	1202	LEU
3	C	3	GLU
3	C	16	ASP
3	C	25	VAL
3	C	26	ASP
3	C	50	GLU
3	C	52	GLU
3	C	55	THR
3	C	66	ARG
3	C	81	GLU
3	C	89	GLU
3	C	100	THR
3	C	101	LEU
3	C	106	GLU
3	C	108	GLU
3	C	119	VAL
3	C	121	VAL
3	C	127	ARG

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Mol	Chain	Res	Type
3	C	129	ILE
3	C	133	ILE
3	C	148	ARG
3	C	155	LEU
3	C	163	ILE
3	C	215	GLU
3	C	237	SER
3	C	240	VAL
3	C	259	LEU
3	C	265	MET
4	D	5	THR
4	D	7	THR
4	D	10	THR
4	D	12	ARG
4	D	17	LYS
4	D	18	VAL
4	D	22	GLU
4	D	23	ASN
4	D	27	LEU
4	D	32	GLU
4	D	35	LEU
4	D	41	GLN
4	D	67	ARG
4	D	118	THR
4	D	123	LEU
4	D	126	ILE
4	D	127	ASP
4	D	134	THR
4	D	137	ASN
4	D	139	LYS
4	D	156	ASP
4	D	159	THR
4	D	166	LEU
4	D	177	VAL
4	D	187	THR
4	D	197	SER
4	D	201	LYS
4	D	213	GLU
4	D	219	THR
5	E	31	THR
5	E	41	ASP
5	E	49	SER

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Mol	Chain	Res	Type
5	E	57	MET
5	E	67	GLU
5	E	69	ILE
5	E	84	ASP
5	E	92	THR
5	E	99	HIS
5	E	104	ASN
5	E	113	GLN
5	E	146	HIS
5	E	166	LYS
5	E	173	SER
5	E	177	ARG
5	E	178	ILE
5	E	190	LEU
5	E	192	ARG
5	E	196	VAL
5	E	204	THR
6	F	72	LYS
6	F	79	ARG
6	F	82	THR
6	F	87	LYS
6	F	90	ARG
6	F	109	VAL
6	F	111	LEU
6	F	115	THR
6	F	122	MET
6	F	127	GLU
7	G	1	MET
7	G	2	PHE
7	G	5	LYS
7	G	12	THR
7	G	13	LEU
7	G	22	MET
7	G	24	GLN
7	G	26	LEU
7	G	37	SER
7	G	60	ARG
7	G	64	THR
7	G	65	ASP
7	G	83	LYS
7	G	96	GLN
7	G	112	LYS

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Mol	Chain	Res	Type
7	G	134	GLU
7	G	138	THR
7	G	143	ILE
7	G	145	VAL
7	G	146	LYS
7	G	152	SER
7	G	155	SER
7	G	162	SER
7	G	171	ILE
8	H	11	GLN
8	H	13	SER
8	H	26	ILE
8	H	31	THR
8	H	32	THR
8	H	36	CYS
8	H	76	THR
8	H	89	LEU
8	H	91	ASP
8	H	103	LYS
8	H	107	VAL
8	H	110	ASP
8	H	123	MET
8	H	128	ASN
8	H	130	ARG
8	H	135	LEU
8	H	138	GLU
9	I	7	CYS
9	I	8	ARG
9	I	31	THR
9	I	35	VAL
9	I	42	LEU
9	I	43	VAL
9	I	50	THR
9	I	74	GLU
9	I	83	ASN
9	I	91	ARG
9	I	92	ARG
9	I	106	CYS
9	I	120	GLN
10	J	2	ILE
10	J	6	ARG
10	J	12	LYS

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Mol	Chain	Res	Type
10	J	13	VAL
10	J	22	LEU
10	J	23	ASN
10	J	34	THR
10	J	42	LYS
10	J	48	ARG
11	K	11	LEU
11	K	18	LYS
11	K	20	LYS
11	K	25	THR
11	K	29	ASN
11	K	31	VAL
11	K	34	THR
11	K	37	LYS
11	K	47	ARG
11	K	51	LEU
11	K	79	GLU
11	K	101	LEU
11	K	107	THR
11	K	113	THR
12	L	27	LEU
12	L	42	ARG
12	L	44	ASP
12	L	54	ARG
12	L	55	ILE
12	L	58	LYS
12	L	61	THR
12	L	68	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (42) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	109	HIS
1	A	363	GLN
1	A	399	HIS
1	A	425	GLN
1	A	439	ASN
1	A	445	ASN
1	A	966	ASN
1	A	969	GLN
1	A	1106	ASN

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Mol	Chain	Res	Type
1	A	1128	GLN
1	A	1140	HIS
1	A	1203	ASN
1	A	1393	ASN
2	B	46	GLN
2	B	255	GLN
2	B	300	HIS
2	B	449	ASN
2	B	465	ASN
2	B	572	HIS
2	B	842	ASN
2	B	975	GLN
2	B	1025	HIS
2	B	1084	GLN
2	B	1117	GLN
2	B	1205	GLN
3	C	7	GLN
4	D	37	GLN
4	D	132	GLN
4	D	137	ASN
4	D	143	ASN
4	D	216	ASN
5	E	3	GLN
5	E	5	ASN
7	G	57	GLN
7	G	71	ASN
7	G	102	GLN
8	H	133	ASN
8	H	137	GLN
8	H	139	ASN
9	I	46	HIS
9	I	83	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	P	6/7 (85%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
15	BRU	T	22	15,14	13,21,22	1.48	2 (15%)	16,30,33	3.51	4 (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	-	0/3/21/22	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	T	22	BRU	C4-C5	3.18	1.42	1.38
15	T	22	BRU	C6-N1	3.77	1.40	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	T	22	BRU	C5-C4-N3	-5.11	118.54	124.00
15	T	22	BRU	C2'-C1'-N1	-3.84	104.82	114.16
15	T	22	BRU	O4'-C1'-N1	5.88	117.89	107.72
15	T	22	BRU	C4-N3-C2	10.97	124.73	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	1422/1732 (82%)	-0.15	11 (0%) 87 80	52, 99, 156, 225	0
2	B	1115/1224 (91%)	-0.12	11 (0%) 84 76	59, 109, 169, 210	0
3	C	266/318 (83%)	-0.21	0 100 100	71, 97, 136, 170	0
4	D	178/221 (80%)	0.04	1 (0%) 90 85	75, 111, 171, 186	0
5	E	214/215 (99%)	-0.04	2 (0%) 85 78	75, 132, 177, 194	0
6	F	84/155 (54%)	-0.29	0 100 100	58, 79, 110, 126	0
7	G	171/171 (100%)	-0.03	0 100 100	67, 98, 134, 153	0
8	H	133/146 (91%)	0.23	0 100 100	109, 140, 177, 200	0
9	I	119/122 (97%)	-0.06	2 (1%) 73 64	105, 136, 174, 191	0
10	J	65/70 (92%)	-0.29	0 100 100	79, 94, 139, 159	0
11	K	115/120 (95%)	-0.14	1 (0%) 85 78	69, 96, 132, 148	0
12	L	46/70 (65%)	0.57	5 (10%) 7 7	85, 165, 184, 194	0
13	N	10/11 (90%)	0.21	0 100 100	173, 193, 239, 248	0
14	P	7/7 (100%)	-0.16	0 100 100	101, 108, 155, 173	0
15	T	18/26 (69%)	0.13	0 100 100	125, 160, 250, 251	0
All	All	3963/4608 (86%)	-0.10	33 (0%) 87 80	52, 105, 169, 251	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	883	LEU	5.4
12	L	27	LEU	5.1
2	B	340	ALA	4.7
12	L	25	ALA	4.3
1	A	1455	PRO	4.2
11	K	115	ALA	3.8
1	A	257	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	194	ALA	3.5
4	D	13	ARG	3.4
1	A	1176	LEU	3.4
1	A	251	SER	3.1
9	I	119	THR	3.0
1	A	256	GLN	3.0
12	L	26	THR	2.9
2	B	339	THR	2.7
1	A	253	ASN	2.7
12	L	50	ASP	2.5
9	I	118	ARG	2.4
1	A	255	SER	2.4
2	B	469	GLN	2.4
2	B	709	ASP	2.4
2	B	167	ILE	2.4
1	A	191	THR	2.3
1	A	193	ASP	2.3
12	L	32	ALA	2.2
5	E	82	PHE	2.2
5	E	2	ASP	2.1
2	B	882	THR	2.1
2	B	509	ALA	2.1
2	B	715	ALA	2.1
1	A	161	LEU	2.1
2	B	714	GLU	2.1
2	B	92	PHE	2.1

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
15	BRU	T	22	20/21	0.93	0.13	-	123,129,133,134	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
16	ZN	I	1121	1/1	0.93	0.13	-0.17	125,125,125,125	0
16	ZN	B	2225	1/1	0.92	0.16	-1.04	82,82,82,82	0
16	ZN	A	2457	1/1	0.96	0.16	-1.09	72,72,72,72	0
16	ZN	C	1269	1/1	0.96	0.09	-1.63	84,84,84,84	0
16	ZN	I	1122	1/1	0.96	0.06	-1.76	175,175,175,175	0
16	ZN	A	2456	1/1	0.89	0.07	-1.77	127,127,127,127	0
16	ZN	J	1066	1/1	0.95	0.20	-1.87	82,82,82,82	0
16	ZN	L	1071	1/1	0.97	0.05	-3.52	192,192,192,192	0
17	MG	A	2458	1/1	0.94	0.13	-	78,78,78,78	0

6.5 Other polymers

There are no such residues in this entry.