



# Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 08:15 pm BST

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](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

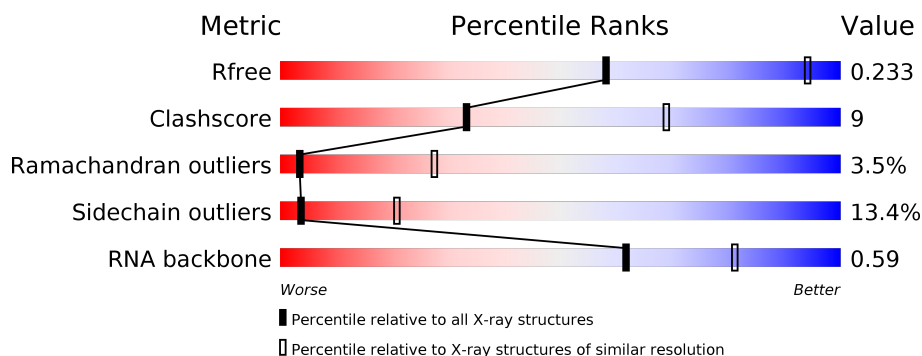
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.50 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.








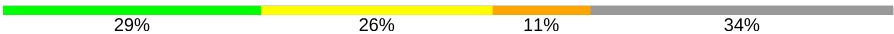

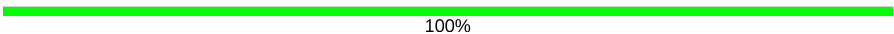

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RNA backbone	3102	1002 (4.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	1732	
2	B	1224	
3	C	318	
4	D	221	
5	E	215	
6	F	155	

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Mol	Chain	Length	Quality of chain
7	G	171	
8	H	146	
9	I	122	
10	J	70	
11	K	120	
12	L	70	
13	N	11	
14	P	7	
15	T	26	

## 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		

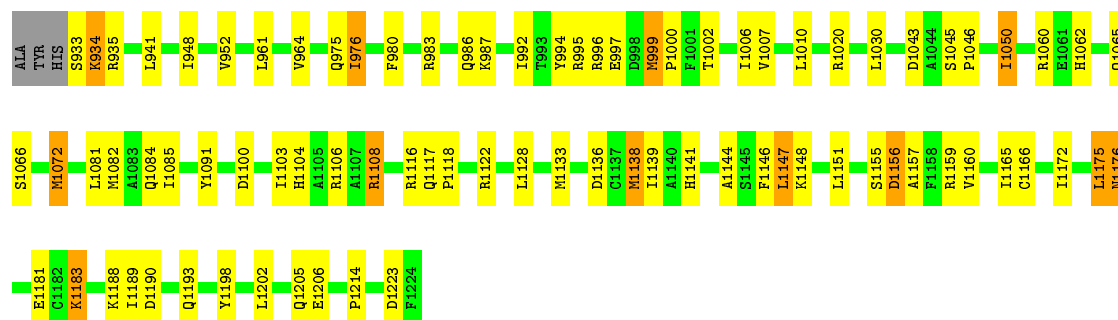


L1348	L1349	K1350	E1351	V1352	V1355	R1366	L1370	L1371	D1373	V1374	M1375	T1376	S1383	R1386	H1387	R1391	C1400	S1401	F1402	E1403	E1404	T1405	V1406	E1407	I1408	A1414	V1424	S1425	E1426	V1427	V1428	M1433	A1434	P1435	I1436	G1437	T1438	G1439	A1440	F1441	D1442	V1443	M1444	I1445	V1451	M1454																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
P1455	GLU	GLN	LYS	ILE	THR	GLU	ILE	GLU	ASP	GLY	ALA	TYR	PRO	GLY	ASN	GLU	LEU	VAL	ASN	ALA	ASP	LEU	ASP	VAL	LYS	ASP	GLU	LEU	PHE	SER	PRO	ALA	LEU	VAL	ASP	SER	GLY	ASN	PRO	ASP	ALA	GLY	GLY	PHE	THR	ALA	GLY	GLY	THR	ALA	GLY	THR	ALA																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
ASP	TYR	GLY	GLU	ALA	THR	SER	SER	PRO	PHE	GLY	ALA	TYR	PRO	GLY	PHE	VAL	SER	PRO	GLY	PHE	ASP	PRO	THR	VAL	LYS	ASP	TYR	SER	PRO	THR	PRO	ALA	THR	SER	PRO	THR	THR	SER	PRO	PRO	ALA	THR	SER	PRO	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

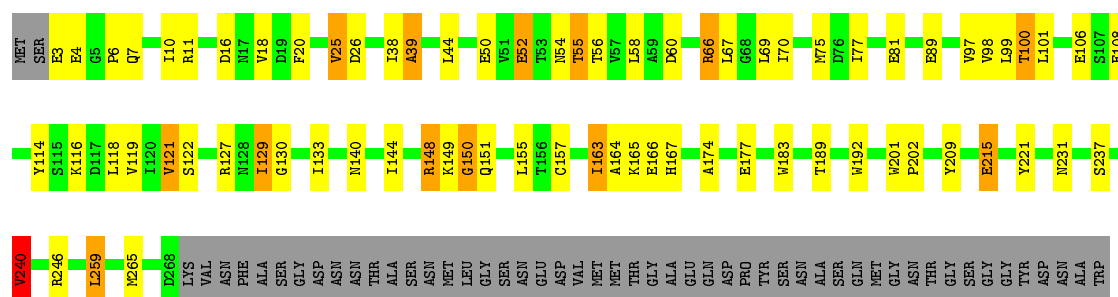
• Molecule 2: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB2

Chain B:  63% 24% 9%

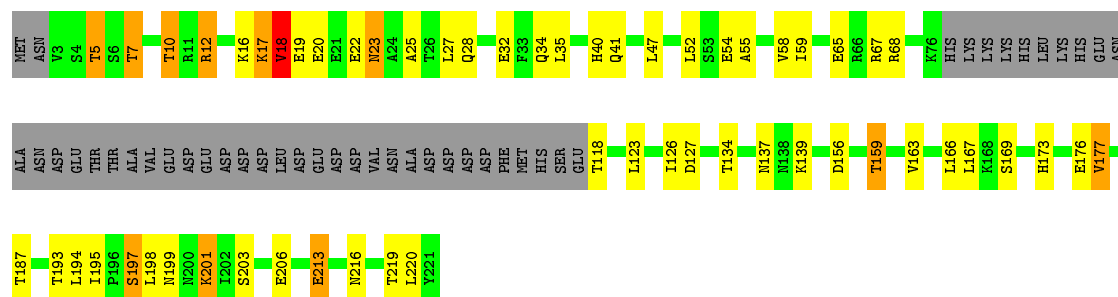
M842	S732	E644	LYS	L416	E312	I204	V108	SER	MET
Q843	H733	K649	LEU	F417	M313	I205	T109	ASP	ASP
S844	H734	E650	K510	K418	L314	M206	H110	LEU	
S845	F738	L651	P511	K423	K315	G207	A111	ALA	
I846	P745	K652	C533	L424	P316	V211	L112	ASN	
D847	S746	V653	R594	T425	V323	E216	Y113	SER	
R848	M747	R654	K537	F428	L334	R217	P114	GLU	
F856	I748	I658	M542	F429	G335	R217	R118	LYS	
K865	V751	M662	T545	T435	R336	F226	M121	TYR	
G866	S754	A663	I546	V436	G337	A229	L128	ASP	
M868	I755	T664	S546	E437	G338	P231	K134	GLU	
S869	I756	E665	V547	GLU	T339	A230	L128	ASP	
I870	I756	E665	V547	GLU	A340	P231	L128	PRO	
T871	F757	D668	M552	ALA	L341	A238	K134	TYR	
E872	F758	I668	M552	HIS	G342	A238	ARG	GLY	
T873	P759	GLU	L566	ASP	L343	S242	THR	GLY	
K876	H761	GLY	V570	PHE	K345	G247	TYR	GLU	
R877	R766	PHE	LYS	MET	K347	E346	ALA	ALA	
Q878	A772	VAL	S574	L446	R348	I251	ILE	ASP	
R879	G779	GLU	P575	A447	I349	R348	VAL	ASP	
T882	H790	ASP	P575	I448	T349	E282	VAL	ASP	
L883	V791	VAL	D576	M449	Y351	V256	PRO	GLY	
R884	G779	GLU	A577	M449	Y351	L258	ARG	GLY	
T889	N786	E678	R579	A450	L361	R261	GLU	GLU	
V890	D790	S682	M583	T452	P362	E282	LEU	LYS	
D891	T791	L689	G584	I453	K358	E282	LYS	TYR	
M792	E691	V690	V585	T454	F360	I269	GLU	GLU	
I899	M792	E691	V586	L461	L361	I269	LEU	TYR	
A900	L796	V692	M589	G464	P362	T272	ILE	ILE	
P901	Y797	I693	V589	M465	R363	L273	ALA	ALA	
G902	E801	D694	H590	R465	I364	P274	GLU	GLU	
V903	K801	A695	R591	M466	T365	Y275	GLU	GLU	
R904	T806	E696	R595	Q469	E368	I276	SER	SER	
G907	R807	E697	R595	K470	G369	K277	GLU	GLU	
E908	A808	I703	K606	K470	Q278	D279	ASP	GLN	
I911	M809	A704	I616	M473	F370	I280	ASP	ALA	
R914	E810	Q706	R620	S475	R373	V283	SER	GLN	
T915	H811	P707	R620	R476	L385	L289	HIS	GLY	
	L812	E708	L624	V479	L386	G290	GLY	THR	
	R815	D709	L624	S480	L387	I291	GLY	THR	
I918	S831	L710	E711	Q481	K393	I291	GLY	GLU	
S919	G832	E711	T628	S481	D394	G168	ASP	SER	
PRO	R833	A715	D629	Q481	L169	R170	ASP	ASN	
GLU	Y833	ASN	R632	L483	Q395	M178	ILE	ASN	
GLY	M834	GLU	R632	M484	E296	M178	ARG	ARG	
GLU	Q835	GLU	L637	R485	I297	L298	LYS	LYS	
LEU	E836	ASN	F638	Y486	E299	H300	TYR	TYR	
GLY	S838	ASP	I639	Y486	G402	T185	GLY	GLY	
GLN	M839	LEU	E641	ARG	L408	E186	GLU	GLN	
ARG	T841	D722	V640	GLY	L412	D307	GLY	ARG	
THR	V841	V724	E642	ASP	L412	I211	S187	M101	
			E642	GLY				V102	



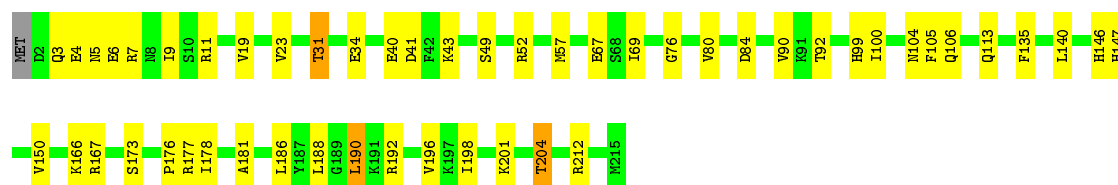
• Molecule 3: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB3



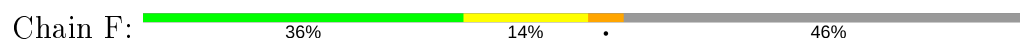
- Molecule 4: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB4

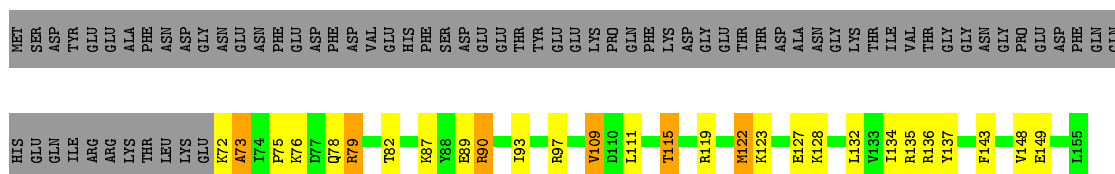


● Molecule 5: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 1

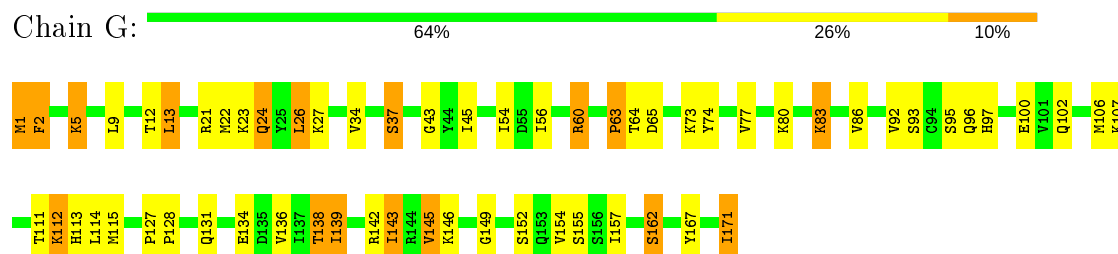


● Molecule 6: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 2

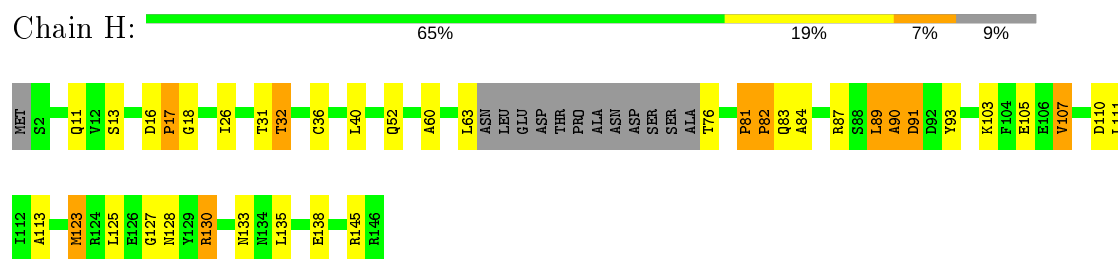




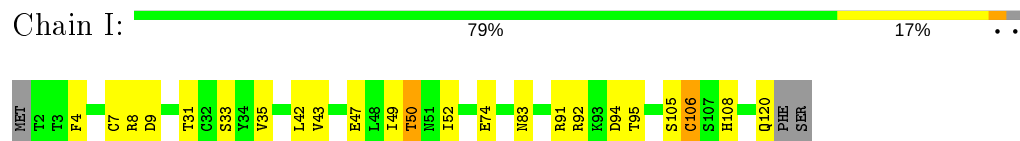
- Molecule 7: RPB7, DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB7



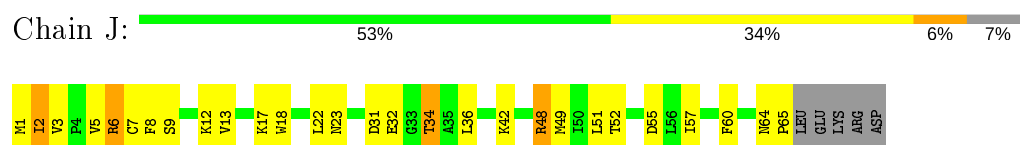
- Molecule 8: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 3



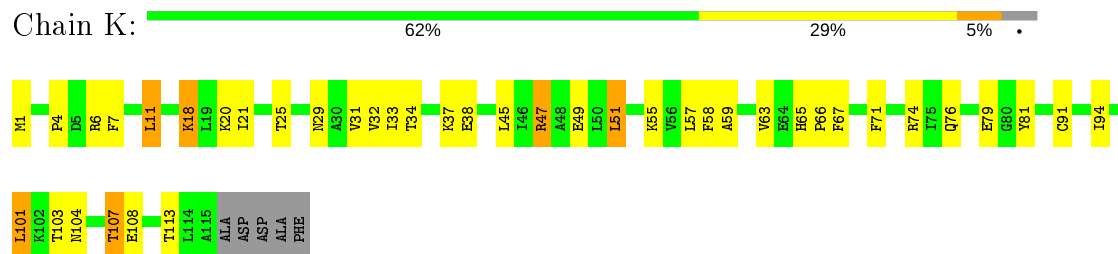
- Molecule 9: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB9



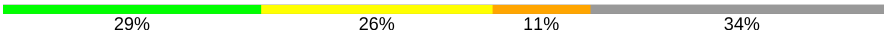
- Molecule 10: DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC 5

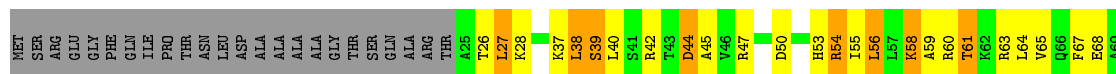


- Molecule 11: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB11



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

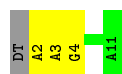
Chain L: 



R70

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

Chain N: 



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

Chain P: 

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\*C  
P\*CP\*BRU\*GP\*GP\*TP\*CP\*AP\*TP\*T)-3'

Chain T: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	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
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	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	3353 reflections (1.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	97.8	Xtriage
Anisotropy	0.391	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 91.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
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
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	31940	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	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.*

<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

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
3:C:6:PRO:HB3	3:C:25:VAL:HG13	1.49	0.92
7:G:1:MET:CE	7:G:2:PHE:H	1.82	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
2:B:1172:ILE:HD11	2:B:1183:LYS:HE2	1.72	0.71
11:K:51:LEU:HD13	11:K:59:ALA:HB3	1.71	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
2:B:999:MET:HG3	2:B:1000:PRO:HD2	1.79	0.64
3:C:70:ILE:HD11	3:C:144:ILE:HG12	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
1:A:335:ARG:HD2	2:B:1206:GLU:OE1	1.99	0.62
4:D:18:VAL:HG22	4:D:20:GLU:H	1.64	0.62
8:H:82:PRO:C	8:H:84:ALA:H	2.02	0.62
1:A:472:LEU:O	1:A:475:THR:HB	2.00	0.61
1:A:683:ILE:HG21	1:A:801:GLU:HG3	1.82	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:590:ARG:NH2	1:A:621:THR:OG1	2.33	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:1111:MET:HG3	1:A:1114:PRO:HG3	1.82	0.61
1:A:37:PHE:CD2	1:A:52:GLY:HA3	2.35	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
2:B:653:VAL:HG22	2:B:689:LEU:HB3	1.81	0.60
2:B:901:PRO:HD3	12:L:58:LYS:HB3	1.83	0.60
7:G:1:MET:CE	7:G:80:LYS:H	2.13	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
1:A:106:VAL:HG21	1:A:214:ILE:HG12	1.84	0.60
4:D:7:THR:HG21	7:G:5:LYS:HZ1	1.66	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:1279:ILE:HG23	1:A:1308:THR:HG23	1.84	0.59
1:A:1424:VAL:HG22	1:A:1436:ILE:HD11	1.85	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
1:A:1433:MET:HE3	7:G:63:PRO:HB3	1.85	0.58
2:B:639:ILE:HD11	2:B:691:GLU:HB2	1.86	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
1:A:1348:LEU:O	1:A:1352:VAL:HG23	2.03	0.57
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: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
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
3:C:67:LEU:HA	3:C:70:ILE:HD12	1.87	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
1:A:187:LYS:HE3	1:A:198:GLU:HB2	1.89	0.55
10:J:1:MET:HG3	10:J:60:PHE:HE2	1.72	0.55
4:D:59:ILE:HD11	7:G:77:VAL:HG11	1.89	0.55
7:G:1:MET:HE3	7:G:80:LYS:O	2.06	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
1:A:1370:LEU:O	1:A:1374:VAL:HG23	2.07	0.55
2:B:839:MET:CE	2:B:980:PHE:HB2	2.36	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)
1:A:448:PRO:O	1:A:449:SER:HB2	2.07	0.54
2:B:343:ILE:O	2:B:344:LYS:HB2	2.08	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:1312:ASN:O	1:A:1316:VAL:HG23	2.08	0.54
1:A:589:GLN:HG2	1:A:606:LEU:HD13	1.90	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
2:B:402:GLY:HA2	2:B:695:ALA:HB3	1.88	0.53
7:G:138:THR:HG22	7:G:139:ILE:H	1.73	0.53
2:B:996:ARG:HG3	2:B:1007:VAL:HG11	1.90	0.53
2:B:35:SER:HA	2:B:811:TYR:CE1	2.42	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
7:G:1:MET:SD	7:G:2:PHE:N	2.82	0.53
2:B:899:ILE:HD11	2:B:911:ILE:HA	1.90	0.53
1:A:1149:ALA:HB2	9:I:47:GLU: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
2:B:1103:ILE:O	2:B:1122:ARG:NH1	2.41	0.53
3:C:98:VAL:H	3:C:122:SER:HB2	1.74	0.53
1:A:741:ASN:HB3	1:A:744:LYS:HB2	1.90	0.52
2:B:247:GLY:H	2:B:418:LYS:NZ	2.07	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
1:A:130:ASP:HB3	1:A:133:LYS:HB2	1.92	0.52
2:B:274:PRO:HG2	2:B:359:GLU:HB3	1.90	0.52
2:B:705:MET:HA	2:B:705:MET:HE3	1.93	0.52
1:A:1100:ARG:O	1:A:1104:ILE:HG13	2.10	0.51
1:A:326:ARG:HG3	1:A:1406:VAL:HG21	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:100:THR:HB	3:C:121:VAL:HG21	1.91	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
5:E:40:GLU:HA	5:E:43:LYS:HD2	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:258:LEU:HB2	2:B:385:LEU:HD21	1.92	0.51
2:B:882:THR:OG1	2:B:935:ARG:N	2.41	0.51
1:A:1148:ILE:HA	9:I:49:ILE:HD12	1.93	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:1433:MET:HE3	7:G:63:PRO:CB	2.41	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
1:A:1442:ASP:HB2	6:F:137:TYR:HE1	1.76	0.51
11:K:63:VAL:HG12	11:K:71:PHE:HB3	1.93	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
1:A:52:GLY:N	1:A:56:PRO:HB3	2.26	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:857:ARG:HD3	1:A:861:GLY:O	2.11	0.50
1:A:42:ASP:HB3	1:A:45:GLN:HA	1.94	0.50
1:A:679:ILE:HG13	1:A:732:LEU:HD12	1.94	0.50
1:A:1400:CYS:HA	1:A:1408:ILE:HD12	1.94	0.49
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:380:VAL:HG13	1:A:385:ILE:HG12	1.94	0.49
2:B:242:SER:OG	2:B:362:PRO:HD2	2.12	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:216:VAL:O	1:A:220:THR:HB	2.13	0.49
1:A:448:PRO:O	1:A:449:SER:CB	2.60	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:768:GLN:HG2	1:A:816:HIS:HA	1.95	0.49
1:A:870:GLU:HB2	5:E:204:THR:HG21	1.95	0.49
1:A:452:LYS:HG2	2:B:1141:HIS:CE1	2.47	0.49
2:B:276:ILE:HA	2:B:338:GLY:O	2.13	0.49
2:B:425:THR:HA	2:B:428:ILE:HD12	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
1:A:154:SER:HB3	1:A:162:VAL:HG23	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
2:B:918:ILE:HG12	2:B:935:ARG:HH22	1.78	0.48
8:H:105:GLU:HB3	8:H:113:ALA:HB3	1.94	0.48
8:H:125:LEU:HG	8:H:130:ARG:NH2	2.28	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:1428:VAL:HG13	2:B:1151:LEU:HD21	1.96	0.48
1:A:54:ASN:HB3	1:A:247:ARG:HH12	1.78	0.48
1:A:353:ILE:HD12	1:A:482:PHE:CD1	2.48	0.48
2:B:33:VAL:HG21	2:B:638:PHE:CZ	2.48	0.48
2:B:899:ILE:CD1	2:B:911:ILE:HA	2.44	0.48
4:D:23:ASN:HA	4:D:28:GLN:O	2.14	0.48
4:D:34:GLN:O	4:D:47:LEU:HD12	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
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
11:K:103:THR:O	11:K:107:THR:HB	2.14	0.47
11:K:57:LEU:HB2	11:K:76:GLN:HG2	1.95	0.47
1:A:185:TRP:HE3	1:A:185:TRP:H	1.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:GLY:HA3	1:A:243:PRO:CG	2.44	0.47
2:B:866:TYR:HB2	2:B:870:ILE:HB	1.95	0.47
2:B:904:ARG:HG3	2:B:948:ILE:HG13	1.97	0.47
3:C:165:LYS:O	11:K:6:ARG:NH1	2.40	0.47
7:G:34:VAL:HG13	7:G:45:ILE:HG21	1.96	0.47
1:A:1338:VAL:HG12	1:A:1339:LEU:HG	1.95	0.47
1:A:347:PHE:HE1	1:A:375:THR:HG22	1.79	0.47
1:A:358:ASN:HB2	11:K:65:HIS:HD2	1.79	0.47
2:B:983:ARG:HD2	2:B:1091:TYR:HB3	1.94	0.47
4:D:194:LEU:HD22	7:G:86:VAL:HG11	1.96	0.47
1:A:548:ASN:HD21	11:K:47:ARG:HE	1.62	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
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
1:A:399:HIS:HB3	1:A:400:PRO:HD3	1.96	0.47
1:A:528:LEU:HD23	1:A:751:SER:HA	1.96	0.47
3:C:77:ILE:HA	3:C:129:ILE:HD11	1.97	0.47
10:J:36:LEU:HD11	10:J:51:LEU:HB2	1.96	0.47
11:K:49:GLU:HG3	11:K:94:ILE:CG1	2.45	0.47
2:B:865:LYS:HB2	2:B:961:LEU:HD21	1.97	0.47
6:F:73:ALA:HB2	6:F:143:PHE:CZ	2.50	0.47
8:H:63:LEU:HB3	8:H:90:ALA:CB	2.45	0.47
1:A:1329:THR:H	1:A:1335:ILE:HD11	1.79	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:61:ILE:HG22	1:A:62:ASP:N	2.23	0.47
1:A:886:ILE:HG12	1:A:943:LEU:HB3	1.97	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
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
8:H:84:ALA:HA	8:H:87:ARG:HB2	1.97	0.46
1:A:1004:ASN:HD21	1:A:1007:ILE:HG12	1.80	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:B:649:LYS:HE2	2:B:738:PHE:O	2.15	0.46
1:A:497:THR:CG2	2:B:1146:PHE:HA	2.46	0.46
2:B:579:ARG:HB2	2:B:586:TRP:NE1	2.31	0.46
6:F:90:ARG:CG	6:F:90:ARG:HH11	2.29	0.46
1:A:1063:MET:SD	1:A:1436:ILE:HG13	2.55	0.46
1:A:941:LYS:O	1:A:941:LYS:HE3	2.15	0.46
2:B:652:LYS:HB3	2:B:689:LEU:HD23	1.97	0.46
11:K:49:GLU:HG3	11:K:94:ILE:HG13	1.98	0.46
1:A:672:ASP:HB3	1:A:736:ASN:OD1	2.16	0.46
3:C:259:LEU:HD22	11:K:91:CYS:HB3	1.97	0.46
1:A:79:GLY:H	2:B:1205:GLN:HE22	1.63	0.46
3:C:98:VAL:H	3:C:122:SER:HB3	1.79	0.46
8:H:81:PRO:HB2	8:H:82:PRO:HD3	1.97	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:587:HIS:HB2	1:A:969:GLN:HE22	1.80	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
5:E:31:THR:HG23	5:E:34:GLU:HB2	1.98	0.46
1:A:1444:MET:HE1	6:F:135:ARG:NE	2.31	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
2:B:226:PHE:HA	2:B:395:GLN:HG3	1.98	0.45
7:G:106:MET:HG3	7:G:157:ILE:O	2.16	0.45
5:E:19:VAL:HG22	5:E:140:LEU:HD22	1.97	0.45
1:A:425:GLN:NE2	1:A:425:GLN:HA	2.31	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
7:G:23:LYS:HA	7:G:56:ILE:HD12	1.99	0.45
2:B:363:HIS:O	2:B:364:ILE:HB	2.16	0.45
2:B:810:GLU:HA	2:B:815:ARG:HH12	1.82	0.45
1:A:1349:TYR:HA	1:A:1372:VAL:HG21	1.99	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

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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
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
10:J:3:VAL:HG21	10:J:18:TRP:CB	2.47	0.45
1:A:121:LEU:O	1:A:124:GLN:HB3	2.16	0.45
3:C:97:VAL:HG11	3:C:130:GLY:HA3	1.99	0.45
2:B:995:ARG:NH1	2:B:997:GLU:OE1	2.50	0.45
5:E:4:GLU:HB3	5:E:7:ARG:HE	1.81	0.45
6:F:109:VAL:HG11	6:F:123:LYS:HG2	2.00	0.45
7:G:106:MET:HG2	7:G:107:LYS:N	2.32	0.45
10:J:7:CYS:HA	10:J:49:MET:HG2	1.99	0.45
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
10:J:3:VAL:HG11	10:J:18:TRP:HB2	1.98	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:801:LYS:O	10:J:52:THR:OG1	2.35	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
2:B:792:MET:HA	2:B:856:PHE:O	2.18	0.44
8:H:125:LEU:HG	8:H:130:ARG:HH22	1.82	0.44
2:B:900:ALA:HB3	12:L:61:THR:HG23	2.00	0.44
1:A:1402:PHE:CD2	1:A:1403:GLU:HG2	2.53	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:873:THR:O	2:B:914:LYS:HA	2.17	0.44
1:A:1313:LEU:HD23	1:A:1338:VAL:HB	2.00	0.44
1:A:880:LYS:HA	1:A:955:PRO:HA	1.99	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
2:B:839:MET:HE1	2:B:980:PHE:HB2	1.99	0.44
10:J:32:GLU:CD	10:J:32:GLU:H	2.20	0.44
1:A:388:LEU:O	1:A:392:VAL:HG23	2.18	0.44
2:B:338:GLY:HA3	2:B:340:ALA:H	1.83	0.44
2:B:831:SER:HG	2:B:994:TYR:HE2	1.65	0.44
6:F:97:ARG:HD2	6:F:97:ARG:HA	1.90	0.44
7:G:128:PRO:O	7:G:138:THR:HG23	2.18	0.44
11:K:7:PHE:HB2	11:K:11:LEU:HD22	1.99	0.44
11:K:45:LEU:HG	11:K:94:ILE:HD13	2.00	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
1:A:5:GLN:O	2:B:1159:ARG:NH2	2.51	0.44
2:B:475:SER:O	2:B:476:ARG:HB3	2.18	0.44
6:F:134:ILE:HG22	6:F:136:ARG:HG3	2.00	0.44
7:G:21:ARG:NH1	7:G:24:GLN:OE1	2.51	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
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
1:A:464:PRO:HB2	11:K:4:PRO:HD3	2.01	0.43
1:A:1376:THR:HG23	5:E:212:ARG:HH22	1.82	0.43
2:B:283:VAL:HG13	2:B:297:ILE:HD13	1.99	0.43
3:C:54:ASN:OD1	3:C:56:THR:HB	2.19	0.43
4:D:176:GLU:OE2	4:D:197:SER:HB2	2.19	0.43
5:E:76:GLY:H	5:E:106:GLN:CD	2.22	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
1:A:767:GLN:HA	1:A:799:PHE:HA	2.01	0.43
2:B:1122:ARG:HB3	15:T:23:DG:OP1	2.19	0.43
3:C:18:VAL:HG12	3:C:20:PHE:HD1	1.83	0.43
3:C:75:MET:O	3:C:246:ARG:NH2	2.50	0.43
4:D:18:VAL:HG13	4:D:19:GLU:HA	2.00	0.43
5:E:19:VAL:O	5:E:23:VAL:HG23	2.19	0.43
2:B:766:ARG:NH2	2:B:1020:ARG:HD3	2.33	0.43
2:B:128:LEU:HB2	2:B:167:ILE:O	2.18	0.43
5:E:19:VAL:HG11	5:E:80:VAL:HG11	2.01	0.43
1:A:1076:ALA:HA	1:A:1079:MET:HG3	2.01	0.43
2:B:754:SER:HB2	2:B:812:LEU:HD11	2.01	0.43
1:A:567:LYS:HA	1:A:568:PRO:C	2.38	0.43
1:A:658:LEU:HD23	1:A:659:HIS:NE2	2.33	0.43
2:B:995:ARG:HB3	2:B:997:GLU:OE2	2.18	0.43
11:K:51:LEU:HD12	11:K:51:LEU:HA	1.87	0.43
2:B:847:ASP:HB3	3:C:167:HIS:CE1	2.53	0.43
1:A:1096:SER:O	1:A:1099:PRO:HG2	2.18	0.43
1:A:901:LEU:HD22	1:A:919:ILE:HG23	2.00	0.43
2:B:1138:MET:HB3	2:B:1147:LEU:HG	2.01	0.42
6:F:90:ARG:NH1	6:F:90:ARG:HG3	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:50:THR:HG22	9:I:52:ILE:H	1.83	0.42
13:N:2:DA:N6	15:T:16:DT:H3	2.16	0.42
1:A:434:ARG:NH2	1:A:440:ASP:OD2	2.52	0.42
4:D:65:GLU:HA	4:D:68:ARG:HG3	2.00	0.42
8:H:63:LEU:HB3	8:H:90:ALA:HB2	2.01	0.42
3:C:58:LEU:HD21	10:J:57:ILE:HD12	2.01	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
3:C:52:GLU:HG2	12:L:64:LEU:HD11	2.01	0.42
4:D:213:GLU:HA	4:D:216:ASN:HD22	1.84	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:464:GLY:HA2	2:B:480:SER:HB3	2.02	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
13:N:4:DG:N2	15:T:15:DT:O2	2.53	0.42
1:A:95:PHE:CE1	1:A:1414:ALA:HB2	2.55	0.42
1:A:243:PRO:HB2	1:A:245:PRO:HD2	2.02	0.42
2:B:168:GLY:H	2:B:450:ALA:HB1	1.85	0.42
2:B:216:GLU:OE1	2:B:537:LYS:HD2	2.20	0.42
4:D:10:THR:O	4:D:12:ARG:NH2	2.53	0.42
4:D:195:ILE:HG22	4:D:198:LEU:HG	2.01	0.42
11:K:65:HIS:HE1	11:K:67:PHE:CG	2.37	0.42
1:A:868:TYR:HD2	1:A:1058:VAL:HG11	1.83	0.41
2:B:70:ILE:HD12	2:B:70:ILE:H	1.85	0.41
2:B:542:MET:HG3	2:B:747:MET:HB3	2.02	0.41
3:C:4:GLU:HB2	11:K:104:ASN:HD21	1.84	0.41
5:E:167:ARG:HA	5:E:167:ARG:HD3	1.79	0.41
11:K:51:LEU:CD1	11:K:59:ALA:HB3	2.45	0.41
2:B:435:THR:C	2:B:437:GLU:H	2.24	0.41
2:B:637:LEU:HD12	2:B:693:ILE:HD13	2.01	0.41
2:B:876:LYS:NZ	2:B:891:ASP:HA	2.35	0.41
4:D:173:HIS:CE1	4:D:201:LYS:HE3	2.56	0.41
1:A:871:ASP:CG	1:A:1366:ARG:HH22	2.24	0.41
1:A:53:LEU:O	1:A:54:ASN:C	2.59	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:118:ARG:HH11	2:B:204:ILE:HD11	1.85	0.41
2:B:211:VAL:HG23	2:B:483:LEU:HB2	2.01	0.41
1:A:122:MET:HG3	1:A:126:LEU:HD12	2.02	0.41
1:A:55:ASP:O	1:A:55:ASP:CG	2.59	0.41
1:A:786:HIS:CD2	2:B:703:ILE:HB	2.54	0.41
4:D:54:GLU:O	4:D:58:VAL:HG23	2.21	0.41
11:K:18:LYS:HE3	11:K:38:GLU:HG2	2.03	0.41
1:A:270:LEU:HD22	1:A:270:LEU:HA	1.89	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
2:B:1104:HIS:HB2	2:B:1122:ARG:HG3	2.03	0.41
5:E:188:LEU:HB2	5:E:190:LEU:HD23	2.02	0.41
12:L:47:ARG:HG3	12:L:54:ARG:HG3	2.02	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
2:B:315:LYS:N	2:B:316:PRO:HD2	2.35	0.41
4:D:18:VAL:HG22	4:D:19:GLU:HA	2.03	0.41
5:E:181:ALA:HA	5:E:186:LEU:HD21	2.02	0.41
8:H:89:LEU:C	8:H:91:ASP:H	2.24	0.41
1:A:436:ILE:HD13	1:A:436:ILE:HA	1.60	0.41
4:D:159:THR:O	4:D:163:VAL:HG23	2.20	0.41
12:L:40:LEU:HB2	12:L:44:ASP:HB3	2.01	0.41
1:A:1116:LEU:HD21	1:A:1327:ILE:HD11	2.03	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
1:A:856:THR:HB	1:A:865:GLN:HB2	2.02	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:1166:CYS:O	2:B:1166:CYS:SG	2.79	0.41
2:B:169:ARG:HB2	2:B:454:THR:HG23	2.02	0.41
2:B:889:THR:HG22	2:B:891:ASP:OD1	2.20	0.41
15:T:19:DT:H2'	15:T:19:DT:O2	2.21	0.41
2:B:273:LEU:HD23	2:B:273:LEU:HA	1.92	0.41
2:B:640:VAL:HA	2:B:651:LEU:HA	2.02	0.41
2:B:644:GLU:HG2	2:B:654:ARG:HH22	1.86	0.41
1:A:87:ALA:HB3	1:A:276:LEU:HD23	2.03	0.41
3:C:201:TRP:HA	3:C:202:PRO:HD3	1.95	0.41
6:F:90:ARG:NH1	6:F:90:ARG:CG	2.84	0.41
10:J:31:ASP:OD1	10:J:34:THR:OG1	2.37	0.41
1:A:1166:ASP:HA	1:A:1169:ILE:HD12	2.03	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
7:G:73:LYS:HA	7:G:73:LYS:HD2	1.93	0.41
11:K:65:HIS:CE1	11:K:67:PHE:CG	3.08	0.41
1:A:354:SER:O	1:A:469:ARG:HA	2.21	0.40
1:A:629:LEU:O	1:A:633:VAL:HG23	2.20	0.40
2:B:840:ILE:HG21	2:B:994:TYR:HD2	1.85	0.40
1:A:1318:THR:HB	5:E:11:ARG:HH12	1.86	0.40
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:101:MET:HG2	2:B:111:ALA:HA	2.02	0.40
12:L:60:ARG:NH2	12:L:65:VAL:HG22	2.33	0.40
1:A:399:HIS:O	1:A:401:GLY:N	2.54	0.40
1:A:41:MET:HA	1:A:50:ILE:HB	2.02	0.40
2:B:1082:MET:HA	3:C:189:THR:HA	2.04	0.40
2:B:121:ASN:HA	2:B:207:GLY:HA3	2.03	0.40
2:B:280:ILE:H	2:B:280:ILE:HG13	1.78	0.40
2:B:373:ARG:HA	2:B:566:LEU:HD23	2.03	0.40
2:B:39:ARG:NE	2:B:665:GLU:HG2	2.37	0.40
2:B:915:THR:HG21	2:B:934:LYS:HB2	2.02	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
7:G:13:LEU:HA	7:G:13:LEU:HD23	1.92	0.40
1:A:709:THR:HG23	9:I:94:ASP:HA	2.03	0.40
1:A:93:VAL:HG13	1:A:301:ALA:HB1	2.03	0.40
2:B:1043:ASP:O	2:B:1050:ILE:HD13	2.22	0.40
2:B:39:ARG:HE	2:B:665:GLU:HG2	1.85	0.40
7:G:9:LEU:HD22	7:G:34:VAL:HG23	2.04	0.40
1:A:151:ASP:HA	1:A:163:SER:HA	2.02	0.40
1:A:353:ILE:HD13	1:A:487:MET:CE	2.51	0.40
1:A:567:LYS:HA	1:A:569:LYS:N	2.36	0.40
7:G:83:LYS:HD2	7:G:149:GLY:HA2	2.04	0.40
2:B:992:ILE:HD11	11:K:66:PRO:HB2	2.03	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%)	3	27
2	B	1095/1224 (90%)	969 (88%)	82 (8%)	44 (4%)	3	24
3	C	264/318 (83%)	236 (89%)	24 (9%)	4 (2%)	10	45
4	D	174/221 (79%)	154 (88%)	14 (8%)	6 (3%)	3	28
5	E	212/215 (99%)	186 (88%)	24 (11%)	2 (1%)	17	56
6	F	82/155 (53%)	77 (94%)	4 (5%)	1 (1%)	13	50
7	G	169/171 (99%)	160 (95%)	6 (4%)	3 (2%)	8	41
8	H	129/146 (88%)	101 (78%)	19 (15%)	9 (7%)	1	12
9	I	117/122 (96%)	96 (82%)	18 (15%)	3 (3%)	5	33
10	J	63/70 (90%)	55 (87%)	4 (6%)	4 (6%)	1	14
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%)	3	27

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

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	15,21,22	1.24	2 (13%)	17,30,33	3.13	3 (17%)

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	-	0/4/21/22	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	3.19	1.42	1.38
15	T	22	BRU	C2-N3	-2.55	1.33	1.38

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	T	22	BRU	C4-N3-C2	11.36	124.73	115.14
15	T	22	BRU	C5-C4-N3	-4.26	118.54	123.64
15	T	22	BRU	C2'-C1'-N1	-4.10	104.82	114.27

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	934:LYS	C	935:ARG	N	5.38
1	B	351:TYR	C	352:ALA	N	3.05

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.