



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:04 PM UTC

PDB ID : 6BLP / pdb_00006blp
Title : Pol II elongation complex with an abasic lesion at i+1 position, soaking AM-PCPP
Authors : Wang, W.; Wang, D.
Deposited on : 2017-11-11
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

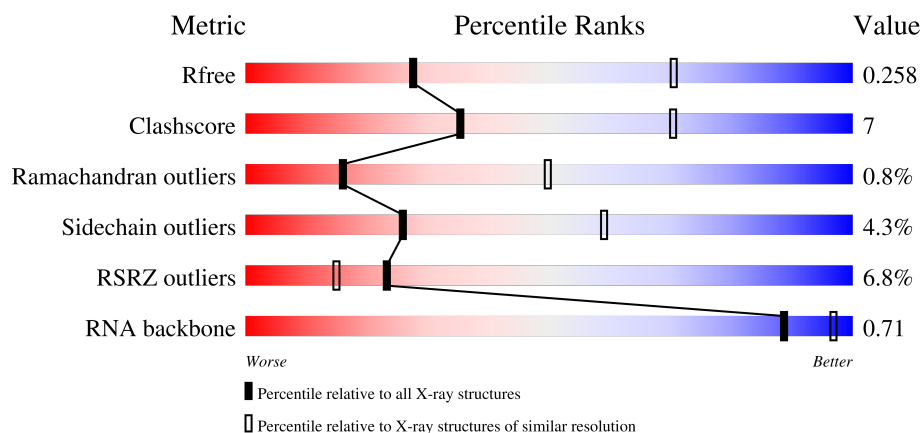
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)
RNA backbone	3983	1222 (3.50-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1733	5% 61% 17% 21%
2	B	1224	6% 67% 21% 10%
3	C	318	2% 64% 18% 16%
4	E	215	9% 86% 13%

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Mol	Chain	Length	Quality of chain
5	F	155	2% 43% 10% 46%
6	H	146	13% 68% 21% 11%
7	I	122	5% 80% 14% 6%
8	J	70	3% 66% 26% 7%
9	K	120	76% 17% 5%
10	L	70	23% 46% 17% 37%
11	T	29	7% 24% 10% 62%
12	R	8	62% 38%

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 28239 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	1372	Total	C	N	O	S	0	0	0
			10784	6802	1887	2034	61			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1097	Total	C	N	O	S	0	0	0
			8726	5526	1530	1615	55			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	213	Total	C	N	O	S	0	0	0
			1744	1107	308	318	11			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	H	130	Total	C	N	O	S	0	0	0
			1043	660	173	206	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	I	115	Total	C	N	O	S	0	0	0
			935	575	170	180	10			

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

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

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

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

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

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

- Molecule 11 is a DNA chain called DNA (5'-D(P*AP*(3DR)P*CP*TP*CP*TP*CP*GP*A P*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	T	11	Total	C	N	O	P	0	0	0
			214	102	35	66	11			

- Molecule 12 is a RNA chain called RNA (5'-R(P*AP*UP*CP*GP*AP*GP*AP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	R	8	Total	C	N	O	P	0	0	0
			175	78	35	54	8			

- Molecule 13 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	2	Total	Zn	0	0
			2	2		

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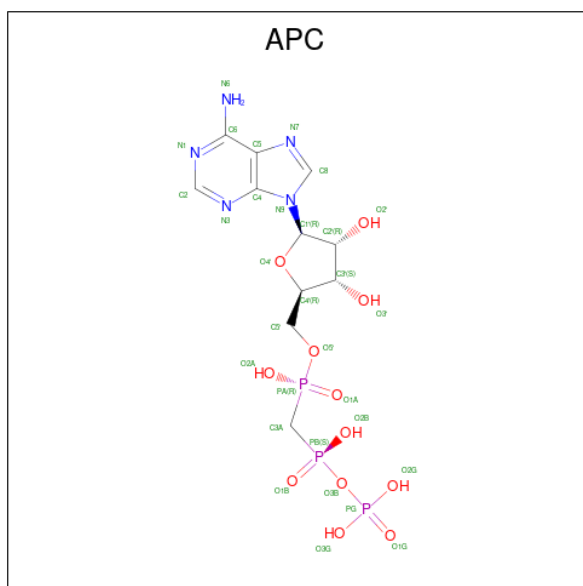
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	B	1	Total	Zn	0	0
			1	1		
13	C	1	Total	Zn	0	0
			1	1		
13	I	2	Total	Zn	0	0
			2	2		
13	J	1	Total	Zn	0	0
			1	1		
13	L	1	Total	Zn	0	0
			1	1		

- Molecule 14 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	2	Total	Mg	0	0
			2	2		

- Molecule 15 is DIPHOSPHOMETHYLPHOSPHONIC ACID ADENOSYL ESTER (CCD ID: APC) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
15	A	1	Total	C	N	O	P	0	0
			31	11	5	12	3		

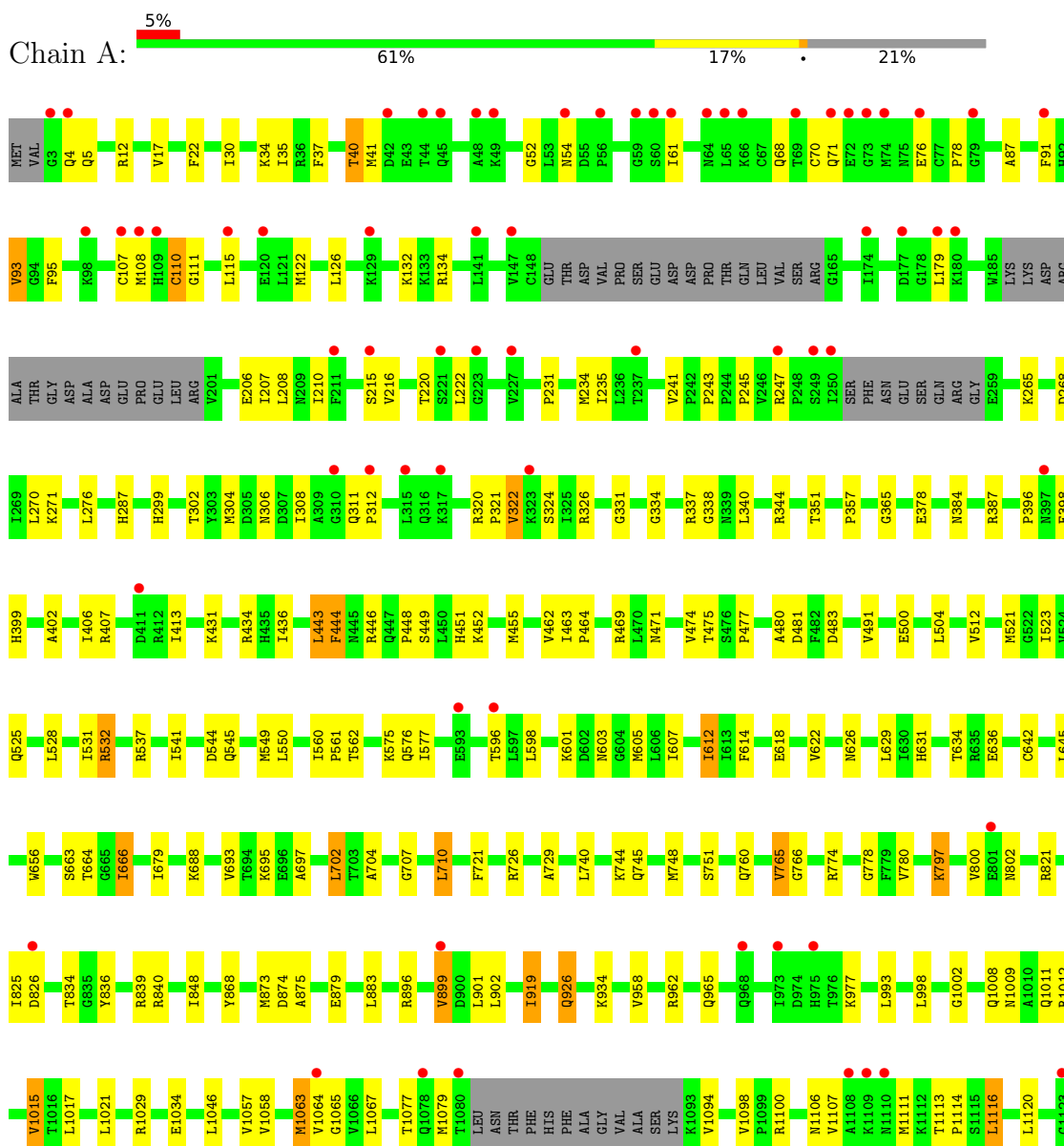
- Molecule 16 is water.

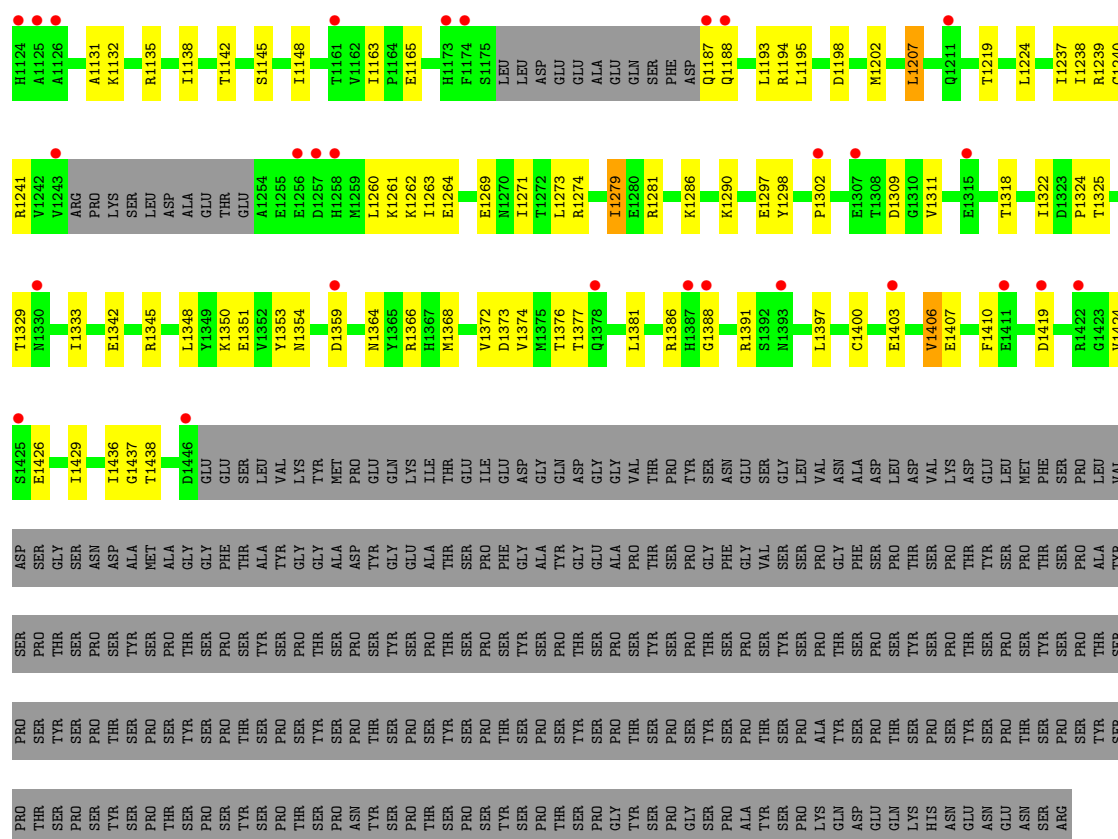
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	B	1	Total	O	0	0
			1	1		

3 Residue-property plots

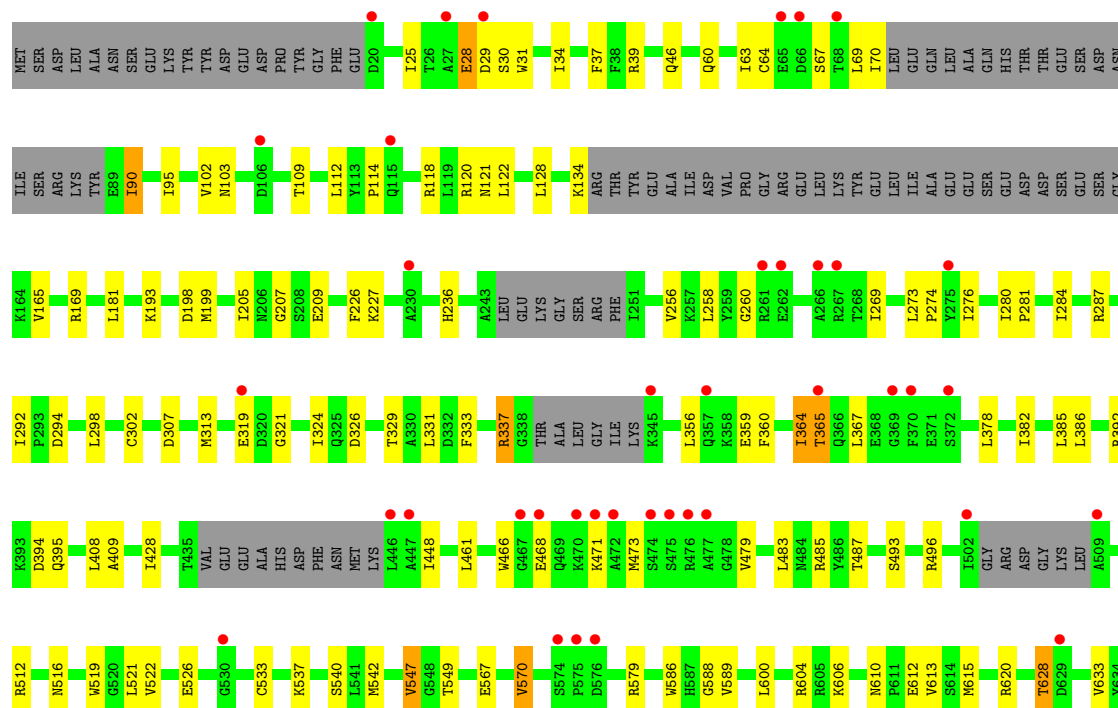
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

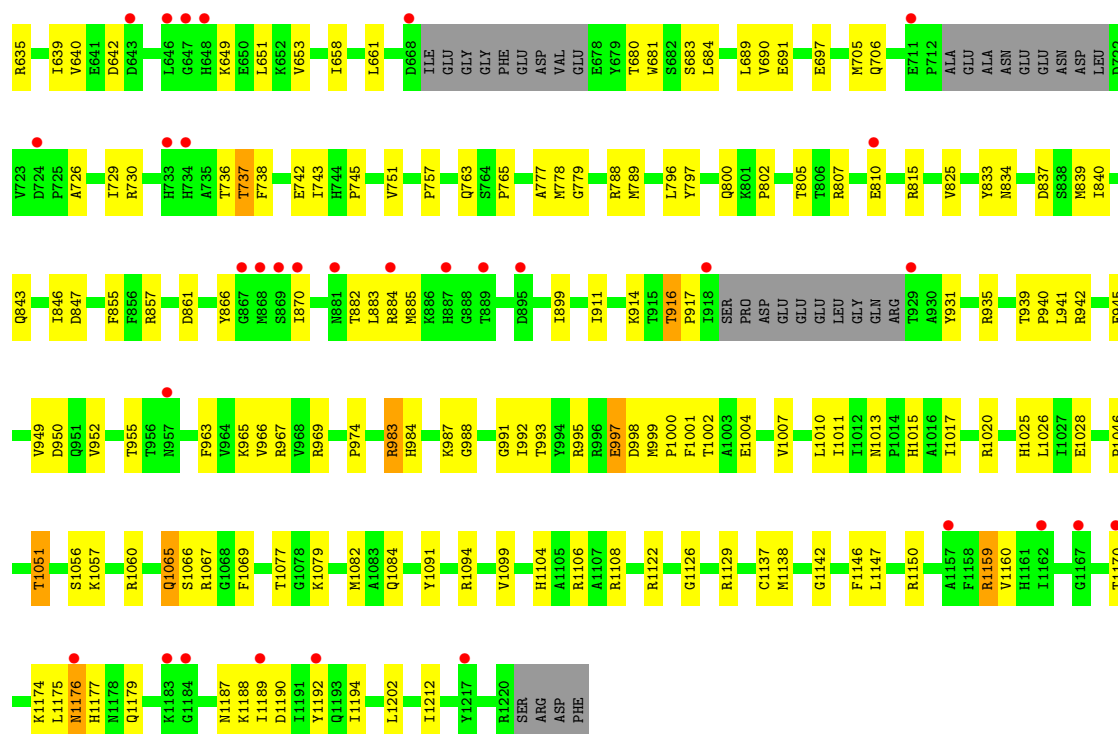
- Molecule 1: DNA-directed RNA polymerase II subunit RPB1



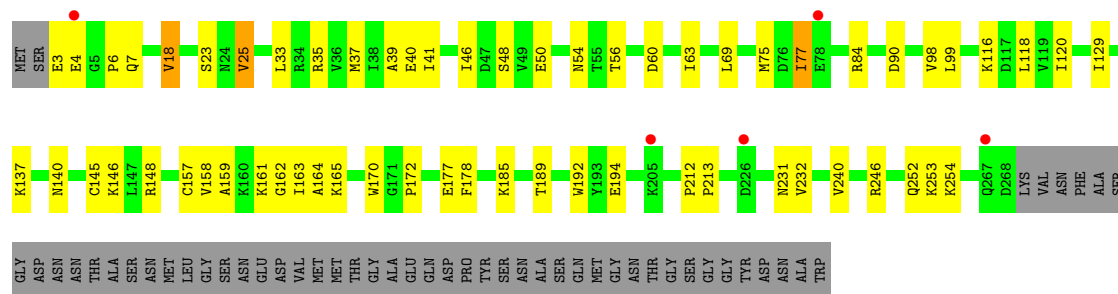


● Molecule 2: DNA-directed RNA polymerase II subunit RPB2

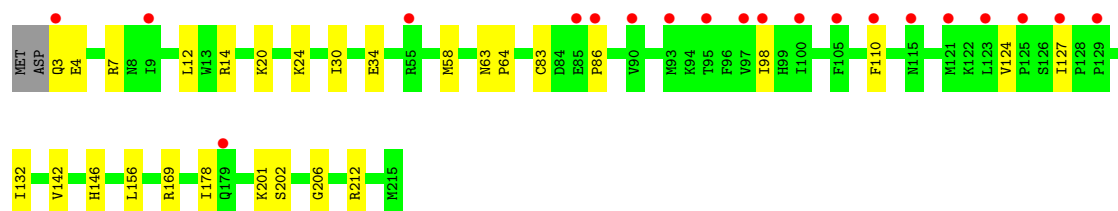
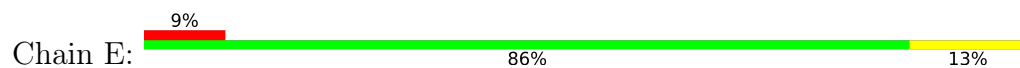




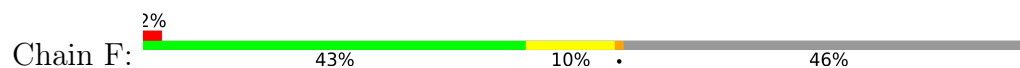
• Molecule 3: DNA-directed RNA polymerase II subunit RPB3

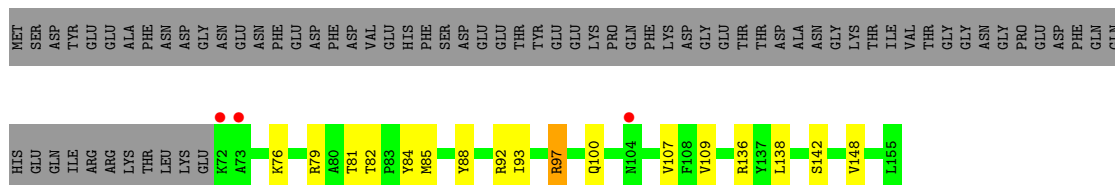


• Molecule 4: DNA-directed RNA polymerases I, II, and III subunit RPABC1

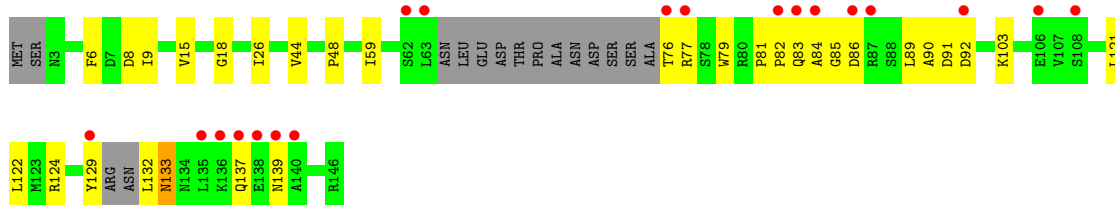


• Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC2

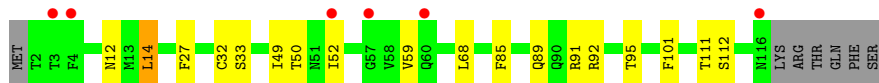
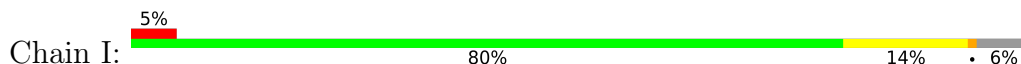




- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC3



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



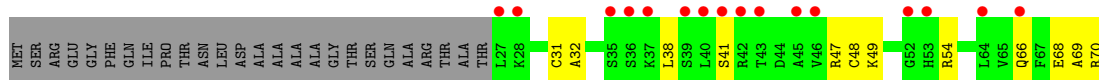
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC5



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

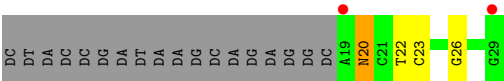


- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC4



- Molecule 11: DNA (5'-D(P*AP*(3DR)P*CP*TP*CP*TP*CP*GP*AP*TP*G)-3')





● Molecule 12: RNA (5'-R(P*AP*UP*CP*GP*AP*GP*AP*G)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	169.06Å 222.18Å 193.20Å 90.00° 101.34° 90.00°	Depositor
Resolution (Å)	82.88 – 3.20 82.88 – 3.20	Depositor EDS
% Data completeness (in resolution range)	87.0 (82.88-3.20) 87.0 (82.88-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.214 , 0.257 0.216 , 0.258	Depositor DCC
R_{free} test set	4883 reflections (4.26%)	wwPDB-VP
Wilson B-factor (Å ²)	54.2	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 54.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	28239	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: APC, 3DR, ZN, MG

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	0.26	0/10975	0.70	4/14838 (0.0%)
2	B	0.25	0/8896	0.69	2/11996 (0.0%)
3	C	0.25	0/2133	0.70	0/2891
4	E	0.25	0/1780	0.72	0/2395
5	F	0.25	0/691	0.71	0/933
6	H	0.27	0/1060	0.69	0/1434
7	I	0.24	0/953	0.65	0/1284
8	J	0.24	0/541	0.65	0/727
9	K	0.23	0/937	0.66	0/1265
10	L	0.24	0/353	0.60	0/468
11	T	0.13	0/225	0.28	0/342
12	R	0.05	0/196	0.10	0/304
All	All	0.25	0/28740	0.69	6/38877 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	525	GLN	CB-CA-C	-5.89	109.80	116.63
2	B	570	VAL	CA-C-N	5.55	125.22	119.05
2	B	570	VAL	C-N-CA	5.55	125.22	119.05
1	A	71	GLN	CB-CA-C	-5.49	109.76	117.23
1	A	1098	VAL	CB-CA-C	-5.34	108.69	114.35
1	A	1388	GLY	N-CA-C	5.09	114.84	110.21

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	10784	0	10872	176	0
2	B	8726	0	8759	159	0
3	C	2095	0	2051	40	0
4	E	1744	0	1772	13	0
5	F	679	0	701	10	0
6	H	1043	0	1015	24	0
7	I	935	0	886	11	0
8	J	532	0	542	13	0
9	K	919	0	929	14	0
10	L	351	0	375	6	0
11	T	214	0	122	4	0
12	R	175	0	87	2	0
13	A	2	0	0	0	0
13	B	1	0	0	0	0
13	C	1	0	0	0	0
13	I	2	0	0	0	0
13	J	1	0	0	0	0
13	L	1	0	0	0	0
14	A	2	0	0	0	0
15	A	31	0	14	1	0
16	B	1	0	0	0	0
All	All	28239	0	28125	414	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (414) 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)
6:H:89:LEU:HD13	6:H:91:ASP:OD1	1.57	1.05
6:H:89:LEU:HD12	6:H:91:ASP:H	1.29	0.98
2:B:29:ASP:HB3	2:B:658:ILE:HG12	1.62	0.82
2:B:25:ILE:HD11	2:B:653:VAL:HB	1.62	0.80
2:B:653:VAL:HG22	2:B:689:LEU:HB3	1.69	0.74
6:H:89:LEU:HD12	6:H:91:ASP:N	2.03	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:5:VAL:HG22	8:J:6:ARG:HG3	1.69	0.73
1:A:35:ILE:HG13	1:A:241:VAL:HG21	1.72	0.71
1:A:875:ALA:HB2	1:A:1366:ARG:HD2	1.73	0.70
1:A:448:PRO:HG3	15:A:1805:APC:H2	1.75	0.69
3:C:6:PRO:HB2	9:K:101:LEU:HD23	1.73	0.69
2:B:287:ARG:NH1	2:B:324:ILE:O	2.26	0.69
2:B:911:ILE:HD11	2:B:941:LEU:HD23	1.74	0.68
2:B:1174:LYS:HB2	2:B:1179:GLN:HB2	1.74	0.68
7:I:92:ARG:HB3	7:I:95:THR:HG23	1.75	0.67
2:B:763:GLN:HG2	2:B:765:PRO:HD2	1.74	0.67
3:C:48:SER:HB3	3:C:158:VAL:HB	1.76	0.67
1:A:704:ALA:HB2	1:A:710:LEU:HD12	1.77	0.66
6:H:89:LEU:CD1	6:H:91:ASP:H	2.06	0.66
4:E:178:ILE:HB	4:E:212:ARG:HD3	1.78	0.66
1:A:338:GLY:HA2	2:B:1129:ARG:HH21	1.60	0.65
2:B:635:ARG:NH1	2:B:742:GLU:OE2	2.27	0.65
3:C:69:LEU:HD12	8:J:6:ARG:HD3	1.79	0.65
2:B:205:ILE:HG13	2:B:461:LEU:HB3	1.79	0.64
1:A:1187:GLN:HG3	1:A:1188:GLN:HG3	1.80	0.64
1:A:469:ARG:NH2	2:B:991:GLY:O	2.29	0.64
2:B:998:ASP:OD1	3:C:35:ARG:NH2	2.31	0.63
2:B:1175:LEU:O	2:B:1176:ASN:ND2	2.30	0.63
3:C:177:GLU:HB2	3:C:231:ASN:HB3	1.81	0.63
1:A:110:CYS:SG	1:A:111:GLY:N	2.72	0.63
1:A:1193:LEU:HB2	1:A:1260:LEU:HD21	1.81	0.63
2:B:165:VAL:HG21	2:B:448:ILE:HD12	1.80	0.63
2:B:1129:ARG:NH1	11:T:22:DT:OP1	2.32	0.63
2:B:287:ARG:HG2	2:B:292:ILE:HA	1.81	0.63
1:A:693:VAL:HG21	1:A:721:PHE:HE2	1.64	0.62
3:C:46:ILE:HD13	3:C:159:ALA:HB2	1.81	0.62
4:E:12:LEU:HD11	4:E:58:MET:HE1	1.82	0.62
1:A:1424:VAL:HG22	1:A:1436:ILE:HD11	1.81	0.62
2:B:642:ASP:HB3	2:B:649:LYS:HG2	1.82	0.62
1:A:899:VAL:HG22	1:A:1029:ARG:HG2	1.82	0.61
1:A:4:GLN:OE1	2:B:1159:ARG:NH1	2.32	0.61
1:A:549:MET:HE1	1:A:656:TRP:HD1	1.66	0.61
1:A:601:LYS:HB2	1:A:603:ASN:HD22	1.66	0.60
1:A:1364:ASN:OD1	1:A:1366:ARG:NH1	2.34	0.60
1:A:1281:ARG:HG2	1:A:1309:ASP:HB2	1.83	0.60
1:A:840:ARG:NH2	1:A:1106:ASN:OD1	2.35	0.60
2:B:800:GLN:HB3	8:J:52:THR:HG22	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:129:TYR:O	6:H:132:LEU:N	2.35	0.60
2:B:916:THR:HG23	2:B:935:ARG:HB2	1.84	0.60
2:B:613:VAL:HG22	2:B:628:THR:HG23	1.84	0.59
1:A:134:ARG:NH1	1:A:220:THR:O	2.35	0.59
2:B:705:MET:HE2	2:B:745:PRO:HB3	1.84	0.59
1:A:1100:ARG:HH21	1:A:1351:GLU:HG2	1.67	0.59
3:C:41:ILE:HB	3:C:172:PRO:HG3	1.84	0.59
1:A:306:ASN:ND2	1:A:321:PRO:O	2.35	0.59
6:H:89:LEU:HD13	6:H:91:ASP:CG	2.27	0.59
1:A:483:ASP:HA	2:B:988:GLY:HA2	1.85	0.58
4:E:4:GLU:OE1	4:E:7:ARG:NH2	2.35	0.58
3:C:46:ILE:HD12	3:C:157:CYS:HB3	1.84	0.58
1:A:40:THR:HG22	1:A:41:MET:HG3	1.83	0.58
2:B:120:ARG:HG2	2:B:955:THR:HG21	1.84	0.58
2:B:63:ILE:O	2:B:67:SER:OG	2.21	0.58
2:B:522:VAL:HG11	2:B:537:LYS:HD2	1.86	0.58
2:B:810:GLU:OE1	2:B:815:ARG:NH2	2.36	0.58
7:I:14:LEU:HD13	7:I:27:PHE:HB3	1.86	0.58
1:A:1348:LEU:HD23	1:A:1372:VAL:HG13	1.86	0.58
2:B:950:ASP:HB2	2:B:969:ARG:HB2	1.86	0.57
3:C:35:ARG:NH1	9:K:41:THR:OG1	2.36	0.57
3:C:145:CYS:SG	3:C:146:LYS:N	2.76	0.57
2:B:837:ASP:OD2	2:B:1020:ARG:NH2	2.38	0.57
2:B:778:MET:HE1	2:B:1094:ARG:HH11	1.69	0.57
6:H:91:ASP:OD1	6:H:92:ASP:N	2.37	0.57
1:A:406:ILE:HB	1:A:431:LYS:HB2	1.86	0.57
2:B:274:PRO:HG2	2:B:359:GLU:HB3	1.86	0.57
2:B:834:ASN:HB3	2:B:840:ILE:HG13	1.87	0.57
1:A:1079:MET:HE3	1:A:1359:ASP:HB2	1.86	0.57
5:F:82:THR:HG22	5:F:84:TYR:H	1.69	0.56
1:A:1325:THR:OG1	4:E:146:HIS:O	2.22	0.56
2:B:273:LEU:HB2	2:B:276:ILE:HD12	1.88	0.56
7:I:101:PHE:HE1	7:I:112:SER:HB3	1.70	0.56
3:C:3:GLU:HG3	3:C:4:GLU:HG3	1.86	0.56
7:I:32:CYS:SG	7:I:33:SER:N	2.77	0.56
3:C:252:GLN:HG3	9:K:95:ILE:HG23	1.87	0.56
1:A:726:ARG:HD3	1:A:766:GLY:HA3	1.87	0.56
1:A:365:GLY:HA3	1:A:469:ARG:HB2	1.87	0.56
2:B:1065:GLN:HG2	2:B:1069:PHE:HB2	1.87	0.56
1:A:34:LYS:H	1:A:34:LYS:HD3	1.70	0.56
2:B:1056:SER:HB3	2:B:1066:SER:HB2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:993:LEU:HD22	1:A:1046:LEU:HG	1.88	0.56
5:F:97:ARG:NH1	5:F:100:GLN:OE1	2.39	0.56
1:A:491:VAL:O	2:B:1150:ARG:NH2	2.39	0.55
2:B:847:ASP:OD2	9:K:6:ARG:NH2	2.39	0.55
1:A:1386:ARG:O	1:A:1391:ARG:NH1	2.39	0.55
2:B:882:THR:HB	2:B:885:MET:HE2	1.89	0.55
1:A:1064:VAL:HG23	1:A:1067:LEU:HD23	1.89	0.55
2:B:839:MET:HE2	2:B:1010:LEU:HD21	1.89	0.55
1:A:477:PRO:HG3	1:A:521:MET:HE2	1.89	0.54
1:A:636:GLU:OE2	1:A:962:ARG:NH1	2.41	0.54
8:J:14:VAL:HB	8:J:50:ILE:HD11	1.88	0.54
2:B:356:LEU:HA	2:B:360:PHE:HB3	1.90	0.54
6:H:8:ASP:OD1	6:H:9:ILE:N	2.39	0.54
1:A:30:ILE:HG23	2:B:1170:THR:HG23	1.90	0.54
1:A:760:GLN:HG2	1:A:765:VAL:HA	1.90	0.54
3:C:54:ASN:ND2	3:C:60:ASP:OD1	2.35	0.54
2:B:995:ARG:NH1	2:B:997:GLU:OE1	2.41	0.54
1:A:902:LEU:HG	1:A:926:GLN:HG3	1.89	0.54
2:B:269:ILE:HD11	2:B:386:LEU:HD21	1.90	0.54
3:C:6:PRO:HB3	3:C:25:VAL:HG13	1.90	0.54
1:A:1138:ILE:HG22	1:A:1279:ILE:HG21	1.90	0.54
1:A:537:ARG:HD2	6:H:121:LEU:HD23	1.90	0.53
2:B:661:LEU:HD11	2:B:684:LEU:HD11	1.91	0.53
5:F:82:THR:O	5:F:136:ARG:NH1	2.37	0.53
2:B:512:ARG:NH1	2:B:533:CYS:O	2.41	0.53
5:F:76:LYS:O	5:F:79:ARG:NH1	2.38	0.53
6:H:85:GLY:HA2	6:H:86:ASP:HB3	1.90	0.53
1:A:1194:ARG:HH21	1:A:1237:ILE:HD13	1.74	0.53
1:A:666:ILE:HG23	2:B:1026:LEU:HB2	1.91	0.53
2:B:487:THR:OG1	2:B:777:ALA:O	2.27	0.53
2:B:1077:THR:HG23	2:B:1079:LYS:H	1.73	0.53
1:A:774:ARG:HG3	1:A:797:LYS:HZ2	1.74	0.53
1:A:873:MET:HE1	1:A:1057:VAL:HG22	1.92	0.53
1:A:1239:ARG:HH22	1:A:1241:ARG:HH21	1.55	0.52
2:B:307:ASP:OD1	2:B:392:ARG:NH1	2.37	0.52
6:H:137:GLN:HG3	6:H:139:ASN:H	1.74	0.52
1:A:1342:GLU:OE2	4:E:212:ARG:NH1	2.42	0.52
1:A:1207:LEU:HD23	1:A:1274:ARG:HD2	1.91	0.52
1:A:879:GLU:OE1	1:A:962:ARG:NH2	2.41	0.52
6:H:89:LEU:HD13	6:H:92:ASP:H	1.73	0.52
1:A:1063:MET:SD	1:A:1436:ILE:HG13	2.50	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:VAL:HB	1:A:1419:ASP:HB3	1.91	0.52
1:A:1148:ILE:HD13	7:I:49:ILE:HD12	1.91	0.52
2:B:521:LEU:HD22	2:B:633:VAL:HG12	1.90	0.52
1:A:544:ASP:HB2	9:K:47:ARG:HH21	1.75	0.52
1:A:834:THR:HG21	1:A:1077:THR:HA	1.92	0.51
2:B:1067:ARG:NE	3:C:194:GLU:OE1	2.36	0.51
1:A:37:PHE:HB2	1:A:52:GLY:HA3	1.92	0.51
4:E:20:LYS:NZ	4:E:34:GLU:O	2.42	0.51
8:J:44:TYR:HA	8:J:47:ARG:HB3	1.93	0.51
2:B:639:ILE:HD11	2:B:691:GLU:HG3	1.92	0.51
2:B:28:GLU:OE1	2:B:807:ARG:NH1	2.33	0.51
2:B:579:ARG:HA	2:B:589:VAL:HA	1.92	0.51
10:L:68:GLU:O	10:L:70:ARG:N	2.43	0.51
1:A:562:THR:O	1:A:576:GLN:NE2	2.44	0.50
1:A:528:LEU:HD23	1:A:751:SER:HA	1.94	0.50
1:A:697:ALA:HA	1:A:702:LEU:HB2	1.92	0.50
1:A:1286:LYS:HE2	1:A:1302:PRO:HB2	1.93	0.50
2:B:726:ALA:HB1	2:B:1051:THR:HG21	1.92	0.50
2:B:843:GLN:HB2	2:B:993:THR:HB	1.92	0.50
5:F:81:THR:HB	5:F:136:ARG:HH11	1.77	0.50
1:A:54:ASN:OD1	1:A:247:ARG:NH1	2.41	0.50
2:B:586:TRP:CD1	2:B:588:GLY:H	2.30	0.50
1:A:744:LYS:HE2	1:A:748:MET:HE3	1.94	0.50
2:B:466:TRP:HB2	2:B:479:VAL:HG21	1.93	0.50
1:A:1373:ASP:HA	1:A:1376:THR:HG22	1.93	0.50
2:B:640:VAL:HG22	2:B:651:LEU:HD23	1.94	0.50
2:B:802:PRO:HG2	2:B:805:THR:HG22	1.94	0.49
1:A:95:PHE:HB3	1:A:234:MET:HE2	1.95	0.49
1:A:550:LEU:HD21	1:A:561:PRO:HD2	1.93	0.49
6:H:44:VAL:HG13	6:H:48:PRO:HA	1.94	0.49
10:L:31:CYS:SG	10:L:32:ALA:N	2.85	0.49
2:B:1013:ASN:OD1	2:B:1015:HIS:ND1	2.31	0.49
1:A:4:GLN:HE22	2:B:1159:ARG:H	1.60	0.49
4:E:83:CYS:HB2	4:E:110:PHE:HE1	1.77	0.49
9:K:21:ILE:HD13	9:K:84:LYS:HE2	1.94	0.49
2:B:294:ASP:HB2	7:I:12:ASN:HA	1.94	0.49
9:K:58:PHE:HB3	9:K:76:GLN:HB3	1.94	0.49
1:A:340:LEU:HD13	1:A:1429:ILE:HG23	1.93	0.49
1:A:443:LEU:HD13	1:A:455:MET:HE2	1.95	0.49
5:F:107:VAL:HG12	5:F:109:VAL:H	1.77	0.49
1:A:93:VAL:HG12	1:A:304:MET:HE3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:778:GLY:HA3	2:B:516:ASN:HB2	1.95	0.49
3:C:50:GLU:HG2	10:L:66:GLN:HG2	1.94	0.49
8:J:10:CYS:SG	8:J:11:GLY:N	2.86	0.49
2:B:680:THR:O	2:B:683:SER:OG	2.26	0.49
6:H:89:LEU:CD1	6:H:92:ASP:H	2.25	0.49
2:B:287:ARG:NH1	2:B:321:GLY:O	2.45	0.48
4:E:124:VAL:HG13	4:E:132:ILE:HB	1.95	0.48
8:J:8:PHE:H	8:J:49:MET:HE3	1.78	0.48
8:J:36:LEU:HD11	8:J:51:LEU:HB2	1.94	0.48
9:K:22:ASP:HB2	9:K:32:VAL:HG13	1.95	0.48
10:L:48:CYS:SG	10:L:49:LYS:N	2.86	0.48
1:A:802:ASN:OD1	2:B:729:ILE:N	2.43	0.48
3:C:99:LEU:HD12	3:C:118:LEU:HB3	1.94	0.48
1:A:663:SER:OG	1:A:664:THR:N	2.47	0.48
1:A:839:ARG:HD3	11:T:20:3DR:H5"	1.95	0.48
1:A:1009:ASN:OD1	1:A:1012:ARG:NH2	2.33	0.48
1:A:1324:PRO:HB2	4:E:142:VAL:HG11	1.96	0.48
3:C:162:GLY:HA3	3:C:170:TRP:CE2	2.48	0.48
1:A:1120:LEU:HD21	1:A:1131:ALA:HB2	1.96	0.48
1:A:1142:THR:O	1:A:1145:SER:OG	2.31	0.48
2:B:284:ILE:HG21	2:B:333:PHE:HD2	1.78	0.48
1:A:326:ARG:HG2	1:A:1406:VAL:HG11	1.95	0.48
1:A:344:ARG:HA	2:B:1129:ARG:HA	1.96	0.48
1:A:596:THR:C	1:A:598:LEU:H	2.22	0.47
1:A:848:ILE:HB	1:A:1065:GLY:HA3	1.96	0.47
1:A:868:TYR:CZ	1:A:1064:VAL:HG21	2.49	0.47
1:A:1345:ARG:HG3	1:A:1376:THR:HG21	1.96	0.47
1:A:378:GLU:OE2	1:A:387:ARG:NH2	2.44	0.47
2:B:60:GLN:NE2	2:B:64:CYS:SG	2.87	0.47
3:C:7:GLN:HB2	3:C:23:SER:HB2	1.95	0.47
6:H:84:ALA:HB3	6:H:86:ASP:HB3	1.96	0.47
1:A:243:PRO:HB2	1:A:245:PRO:HD2	1.96	0.47
2:B:313:MET:HE3	2:B:386:LEU:HD22	1.95	0.47
2:B:1002:THR:HG23	2:B:1004:GLU:H	1.78	0.47
5:F:85:MET:HE1	5:F:148:VAL:HG13	1.96	0.47
1:A:68:GLN:O	1:A:70:CYS:N	2.43	0.47
1:A:107:CYS:SG	1:A:108:MET:N	2.88	0.47
1:A:407:ARG:HD2	1:A:413:ILE:HD11	1.96	0.47
1:A:108:MET:O	1:A:110:CYS:N	2.46	0.47
1:A:707:GLY:O	1:A:1281:ARG:NH1	2.45	0.47
2:B:1187:ASN:ND2	2:B:1190:ASP:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:165:LYS:O	9:K:6:ARG:NH1	2.47	0.47
9:K:56:VAL:HG22	9:K:77:THR:HG22	1.97	0.47
3:C:75:MET:O	3:C:246:ARG:NH2	2.45	0.47
1:A:679:ILE:HG23	1:A:729:ALA:HB1	1.97	0.47
1:A:1261:LYS:O	1:A:1264:GLU:HG3	2.15	0.47
2:B:610:ASN:HB3	2:B:613:VAL:HG23	1.96	0.47
6:H:76:THR:OG1	6:H:77:ARG:N	2.48	0.47
1:A:544:ASP:OD1	1:A:545:GLN:N	2.44	0.47
1:A:1116:LEU:HD23	1:A:1311:VAL:HA	1.96	0.47
1:A:471:ASN:O	1:A:474:VAL:HG12	2.14	0.46
1:A:614:PHE:HB3	6:H:122:LEU:HD21	1.97	0.46
2:B:1129:ARG:N	11:T:23:DC:OP1	2.36	0.46
1:A:306:ASN:HB2	1:A:324:SER:HB3	1.97	0.46
1:A:446:ARG:HD2	1:A:480:ALA:HB2	1.97	0.46
1:A:1397:LEU:HB2	1:A:1426:GLU:HG2	1.96	0.46
1:A:1436:ILE:O	1:A:1438:THR:N	2.49	0.46
2:B:1065:GLN:HG3	2:B:1067:ARG:H	1.79	0.46
1:A:115:LEU:HB2	1:A:122:MET:HE3	1.97	0.46
1:A:1163:ILE:HG22	1:A:1165:GLU:H	1.80	0.46
1:A:5:GLN:O	2:B:1159:ARG:NH2	2.48	0.46
2:B:963:PHE:HE2	2:B:965:LYS:HE3	1.81	0.46
7:I:50:THR:HB	7:I:52:ILE:HG22	1.98	0.46
1:A:87:ALA:HB3	1:A:276:LEU:HD23	1.96	0.46
3:C:185:LYS:HG2	3:C:213:PRO:HG3	1.98	0.46
1:A:836:TYR:OH	1:A:1403:GLU:OE2	2.26	0.46
1:A:868:TYR:OH	1:A:1366:ARG:HD3	2.15	0.46
1:A:1111:MET:HG3	1:A:1114:PRO:HG3	1.97	0.46
2:B:37:PHE:O	2:B:39:ARG:N	2.44	0.46
2:B:198:ASP:OD1	2:B:485:ARG:NH2	2.49	0.46
3:C:40:GLU:OE1	3:C:254:LYS:NZ	2.42	0.46
1:A:901:LEU:HB2	1:A:926:GLN:HG2	1.98	0.45
1:A:1224:LEU:HD11	1:A:1240:CYS:HB3	1.98	0.45
2:B:298:LEU:O	2:B:302:CYS:N	2.44	0.45
2:B:736:THR:O	2:B:738:PHE:N	2.48	0.45
3:C:98:VAL:HG22	3:C:158:VAL:HG22	1.98	0.45
1:A:528:LEU:O	1:A:531:ILE:HG22	2.16	0.45
2:B:30:SER:OG	2:B:743:ILE:O	2.25	0.45
2:B:547:VAL:N	2:B:612:GLU:OE2	2.44	0.45
2:B:69:LEU:HB2	2:B:90:ILE:HG12	1.99	0.45
3:C:56:THR:HG21	3:C:63:ILE:HD11	1.97	0.45
3:C:77:ILE:HG12	3:C:129:ILE:HD11	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:706:GLN:OE1	2:B:730:ARG:NH1	2.49	0.45
8:J:36:LEU:HD13	8:J:47:ARG:HG3	1.99	0.45
2:B:1106:ARG:HH11	2:B:1126:GLY:HA2	1.81	0.45
1:A:634:THR:HG1	1:A:642:CYS:HG	1.63	0.45
1:A:962:ARG:HA	1:A:965:GLN:HG2	1.98	0.45
1:A:868:TYR:CE1	1:A:1064:VAL:HG21	2.52	0.45
2:B:34:ILE:HG12	2:B:542:MET:HE1	1.99	0.45
1:A:1011:GLN:O	1:A:1015:VAL:HG23	2.17	0.45
2:B:114:PRO:HG2	2:B:181:LEU:HD11	1.97	0.45
2:B:1104:HIS:CG	2:B:1122:ARG:HG3	2.52	0.45
6:H:133:ASN:OD1	6:H:133:ASN:N	2.37	0.45
1:A:265:LYS:NZ	1:A:302:THR:HG23	2.31	0.45
2:B:120:ARG:HB2	2:B:122:LEU:HG	1.99	0.45
1:A:302:THR:OG1	1:A:306:ASN:OD1	2.35	0.45
1:A:337:ARG:O	2:B:1129:ARG:NH2	2.49	0.45
1:A:883:LEU:HD23	1:A:1021:LEU:HD13	1.99	0.45
2:B:209:GLU:OE1	2:B:788:ARG:NH2	2.49	0.45
1:A:1219:THR:HG21	1:A:1271:ILE:HD11	1.99	0.44
2:B:620:ARG:HD2	7:I:68:LEU:HD11	1.99	0.44
1:A:1333:ILE:HD13	1:A:1381:LEU:HD12	1.99	0.44
2:B:281:PRO:HB2	2:B:284:ILE:HG12	1.99	0.44
2:B:378:LEU:O	2:B:382:ILE:HG12	2.17	0.44
2:B:620:ARG:NH2	7:I:89:GLN:OE1	2.51	0.44
3:C:163:ILE:HG22	3:C:165:LYS:H	1.83	0.44
1:A:206:GLU:O	1:A:210:ILE:HG12	2.18	0.44
1:A:396:PRO:C	1:A:398:GLU:H	2.26	0.44
1:A:523:ILE:HD13	1:A:622:VAL:HG22	2.00	0.44
3:C:33:LEU:HG	3:C:37:MET:HE2	1.98	0.44
6:H:83:GLN:HA	6:H:84:ALA:HA	1.75	0.44
2:B:118:ARG:HA	2:B:207:GLY:HA2	2.00	0.44
2:B:883:LEU:O	2:B:885:MET:N	2.51	0.44
2:B:1142:GLY:HA3	5:F:88:TYR:HE2	1.82	0.44
3:C:116:LYS:HD3	3:C:140:ASN:HA	2.00	0.44
1:A:541:ILE:HD12	1:A:577:ILE:HG12	2.00	0.44
2:B:1084:GLN:OE1	3:C:192:TRP:N	2.46	0.44
2:B:1175:LEU:C	2:B:1177:HIS:H	2.24	0.44
1:A:12:ARG:HH11	2:B:1192:TYR:HE1	1.65	0.44
1:A:1281:ARG:NE	1:A:1309:ASP:OD2	2.51	0.44
2:B:30:SER:O	2:B:34:ILE:HG13	2.18	0.44
2:B:103:ASN:OD1	2:B:169:ARG:NH2	2.44	0.44
2:B:493:SER:OG	2:B:526:GLU:OE2	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:999:MET:HG3	2:B:1000:PRO:HD2	2.00	0.44
1:A:265:LYS:HZ1	1:A:302:THR:HG23	1.82	0.44
1:A:626:ASN:O	1:A:631:HIS:ND1	2.37	0.44
2:B:604:ARG:HH22	2:B:697:GLU:CD	2.24	0.44
5:F:138:LEU:HD12	5:F:142:SER:HB2	1.99	0.44
2:B:757:PRO:HG2	2:B:984:HIS:NE2	2.32	0.44
2:B:1082:MET:HA	3:C:189:THR:HA	2.00	0.44
9:K:49:GLU:OE2	9:K:97:LYS:NZ	2.33	0.44
1:A:874:ASP:HB2	1:A:1058:VAL:HA	2.00	0.43
1:A:998:LEU:HA	1:A:1011:GLN:HE22	1.82	0.43
1:A:1438:THR:HG23	5:F:92:ARG:HB2	1.99	0.43
2:B:866:TYR:HB2	2:B:870:ILE:HB	1.98	0.43
1:A:331:GLY:HA2	1:A:334:GLY:H	1.83	0.43
2:B:193:LYS:HE2	8:J:65:PRO:HG3	2.00	0.43
2:B:519:TRP:HZ2	2:B:705:MET:HE1	1.83	0.43
1:A:402:ALA:HA	1:A:434:ARG:HA	2.00	0.43
2:B:846:ILE:HG23	2:B:974:PRO:HG2	1.99	0.43
2:B:983:ARG:NH1	2:B:1091:TYR:HB3	2.33	0.43
2:B:1001:PHE:HE2	3:C:178:PHE:HB3	1.83	0.43
6:H:81:PRO:O	6:H:83:GLN:N	2.52	0.43
1:A:357:PRO:HD2	2:B:833:TYR:CZ	2.52	0.43
1:A:1094:VAL:HA	1:A:1113:THR:HG21	2.00	0.43
2:B:939:THR:HA	2:B:940:PRO:HD3	1.85	0.43
2:B:942:ARG:HB2	2:B:945:GLU:HB2	2.00	0.43
4:E:202:SER:HB3	4:E:206:GLY:H	1.83	0.43
2:B:496:ARG:NH2	2:B:540:SER:O	2.45	0.43
3:C:39:ALA:HA	3:C:164:ALA:HB3	2.00	0.43
2:B:95:ILE:HD11	2:B:128:LEU:HB3	2.01	0.43
2:B:121:ASN:HA	2:B:207:GLY:HA3	2.00	0.43
1:A:765:VAL:HG22	1:A:800:VAL:HB	2.00	0.43
4:E:24:LYS:HB3	4:E:30:ILE:HB	2.01	0.43
2:B:600:LEU:HB3	2:B:615:MET:SD	2.59	0.43
10:L:38:LEU:HD21	10:L:48:CYS:HA	2.01	0.43
1:A:444:PHE:HD1	1:A:444:PHE:HA	1.71	0.42
1:A:1132:LYS:HG3	1:A:1135:ARG:HH12	1.84	0.42
2:B:428:ILE:HD11	2:B:448:ILE:HG23	2.01	0.42
2:B:789:MET:HE1	2:B:967:ARG:HB2	2.00	0.42
1:A:378:GLU:OE2	1:A:384:ASN:ND2	2.52	0.42
1:A:399:HIS:CE1	1:A:462:VAL:HG21	2.54	0.42
2:B:779:GLY:HA2	2:B:796:LEU:HB2	2.01	0.42
2:B:916:THR:HA	2:B:917:PRO:HD3	1.80	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:952:VAL:HG13	2:B:966:VAL:HG22	2.01	0.42
2:B:280:ILE:HD11	2:B:337:ARG:HG3	2.01	0.42
2:B:984:HIS:CE1	2:B:1025:HIS:HA	2.54	0.42
3:C:77:ILE:O	3:C:161:LYS:NZ	2.41	0.42
1:A:1239:ARG:HH22	1:A:1241:ARG:NH2	2.18	0.42
1:A:1353:TYR:HD2	1:A:1368:MET:HE1	1.85	0.42
2:B:63:ILE:HD12	2:B:95:ILE:HB	2.01	0.42
2:B:227:LYS:HG2	2:B:236:HIS:CD2	2.53	0.42
2:B:840:ILE:HB	2:B:1011:ILE:HB	2.01	0.42
1:A:215:SER:OG	1:A:216:VAL:N	2.50	0.42
2:B:199:MET:SD	2:B:199:MET:N	2.85	0.42
3:C:69:LEU:O	8:J:6:ARG:HD2	2.20	0.42
1:A:695:LYS:HE3	1:A:695:LYS:HB2	1.86	0.42
1:A:1261:LYS:HE3	1:A:1261:LYS:HB2	1.88	0.42
10:L:47:ARG:HG2	10:L:54:ARG:HG2	2.02	0.42
1:A:1318:THR:O	4:E:14:ARG:NH2	2.53	0.42
2:B:120:ARG:HA	2:B:963:PHE:HZ	1.85	0.42
2:B:861:ASP:OD1	2:B:914:LYS:NZ	2.52	0.42
2:B:1060:ARG:HA	2:B:1060:ARG:HD2	1.90	0.42
1:A:231:PRO:HA	1:A:234:MET:HG3	2.02	0.42
1:A:1198:ASP:O	1:A:1202:MET:HG2	2.20	0.42
1:A:1410:PHE:CD2	2:B:1212:ILE:HD11	2.55	0.42
2:B:941:LEU:HD22	2:B:942:ARG:H	1.85	0.42
8:J:18:TRP:O	8:J:21:TYR:HB3	2.20	0.42
1:A:443:LEU:HD12	2:B:1146:PHE:CZ	2.55	0.42
2:B:326:ASP:OD1	2:B:329:THR:OG1	2.24	0.42
2:B:1138:MET:HE2	2:B:1146:PHE:CD1	2.55	0.42
4:E:63:ASN:HA	4:E:64:PRO:HD3	1.88	0.41
1:A:76:GLU:OE2	2:B:1159:ARG:NH1	2.52	0.41
1:A:545:GLN:HG2	1:A:549:MET:HE3	2.02	0.41
1:A:1193:LEU:HB3	1:A:1240:CYS:HB2	2.02	0.41
1:A:1290:LYS:HE2	1:A:1298:TYR:HB3	2.01	0.41
7:I:85:PHE:HB3	7:I:101:PHE:CD2	2.55	0.41
8:J:64:ASN:N	8:J:65:PRO:HD2	2.34	0.41
12:R:3:C:H2'	12:R:4:G:C8	2.55	0.41
1:A:532:ARG:HH12	1:A:745:GLN:HA	1.85	0.41
1:A:901:LEU:HD22	1:A:919:ILE:HG23	2.02	0.41
1:A:1410:PHE:HD2	2:B:1212:ILE:HD11	1.85	0.41
2:B:256:VAL:HG11	2:B:382:ILE:HD13	2.02	0.41
2:B:364:ILE:HG13	2:B:365:THR:OG1	2.20	0.41
2:B:408:LEU:HB3	2:B:409:ALA:H	1.65	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:18:VAL:HG23	3:C:232:VAL:HB	2.03	0.41
3:C:212:PRO:HA	3:C:213:PRO:HD3	1.85	0.41
6:H:89:LEU:HD12	6:H:90:ALA:N	2.35	0.41
1:A:268:ASP:HB3	1:A:299:HIS:CE1	2.56	0.41
1:A:449:SER:HB3	2:B:1137:CYS:SG	2.61	0.41
1:A:607:ILE:HG12	1:A:612:ILE:HA	2.02	0.41
1:A:821:ARG:O	1:A:825:ILE:HG12	2.20	0.41
1:A:1260:LEU:HD12	1:A:1263:ILE:HD12	2.03	0.41
2:B:471:LYS:HA	2:B:473:MET:HE2	2.01	0.41
2:B:899:ILE:HG21	2:B:949:VAL:HG21	2.02	0.41
3:C:54:ASN:OD1	3:C:56:THR:HG22	2.21	0.41
6:H:6:PHE:HB3	6:H:59:ILE:HB	2.02	0.41
1:A:464:PRO:HB2	9:K:4:PRO:HD3	2.02	0.41
3:C:99:LEU:HB3	3:C:120:ILE:HD13	2.02	0.41
1:A:311:GLN:N	1:A:312:PRO:HD2	2.36	0.41
1:A:436:ILE:HD11	1:A:491:VAL:HG11	2.03	0.41
1:A:642:CYS:O	1:A:645:LEU:HB3	2.20	0.41
2:B:258:LEU:HB2	2:B:385:LEU:HD21	2.01	0.41
1:A:575:LYS:HB3	1:A:612:ILE:HD13	2.03	0.41
2:B:857:ARG:NH2	11:T:26:DG:OP1	2.54	0.41
1:A:1064:VAL:HA	1:A:1067:LEU:HB3	2.02	0.41
1:A:91:PHE:HZ	1:A:207:ILE:HD12	1.87	0.40
1:A:560:ILE:HB	6:H:79:TRP:H	1.86	0.40
1:A:1207:LEU:HD22	1:A:1273:LEU:HD23	2.03	0.40
2:B:226:PHE:HA	2:B:395:GLN:HG3	2.03	0.40
2:B:394:ASP:H	7:I:91:ARG:HG3	1.86	0.40
2:B:681:TRP:CH2	2:B:690:VAL:HG11	2.55	0.40
2:B:992:ILE:HG13	9:K:67:PHE:HE1	1.86	0.40
1:A:598:LEU:O	6:H:122:LEU:HD12	2.21	0.40
1:A:1002:GLY:O	1:A:1008:GLN:NE2	2.54	0.40
2:B:102:VAL:HG23	2:B:112:LEU:HB2	2.04	0.40
12:R:3:C:H2'	12:R:4:G:H8	1.86	0.40
1:A:68:GLN:C	1:A:70:CYS:H	2.27	0.40
1:A:320:ARG:HA	1:A:321:PRO:HD3	1.97	0.40
1:A:500:GLU:O	1:A:504:LEU:HB2	2.21	0.40
2:B:855:PHE:HZ	2:B:857:ARG:HH11	1.69	0.40
3:C:84:ARG:HD2	9:K:11:LEU:HD21	2.03	0.40
1:A:1195:LEU:HB2	1:A:1238:ILE:HB	2.03	0.40
2:B:31:TRP:CE3	2:B:34:ILE:HD12	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1358/1733 (78%)	1239 (91%)	110 (8%)	9 (1%)	18	52
2	B	1077/1224 (88%)	991 (92%)	77 (7%)	9 (1%)	16	50
3	C	264/318 (83%)	245 (93%)	17 (6%)	2 (1%)	16	50
4	E	211/215 (98%)	200 (95%)	10 (5%)	1 (0%)	24	59
5	F	82/155 (53%)	77 (94%)	5 (6%)	0	100	100
6	H	124/146 (85%)	107 (86%)	15 (12%)	2 (2%)	7	36
7	I	113/122 (93%)	100 (88%)	13 (12%)	0	100	100
8	J	63/70 (90%)	57 (90%)	6 (10%)	0	100	100
9	K	112/120 (93%)	108 (96%)	3 (3%)	1 (1%)	14	47
10	L	42/70 (60%)	33 (79%)	7 (17%)	2 (5%)	2	14
All	All	3446/4173 (83%)	3157 (92%)	263 (8%)	26 (1%)	16	50

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	322	VAL
1	A	1437	GLY
1	A	78	PRO
1	A	110	CYS
1	A	1279	ILE
2	B	468	GLU
2	B	1046	PRO
4	E	86	PRO
10	L	69	ALA
1	A	40	THR
2	B	337	ARG
2	B	884	ARG
3	C	148	ARG
9	K	26	LYS

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Mol	Chain	Res	Type
2	B	737	THR
3	C	90	ASP
10	L	41	SER
1	A	958	VAL
1	A	1063	MET
2	B	367	LEU
2	B	1017	ILE
2	B	1108	ARG
6	H	82	PRO
6	H	18	GLY
1	A	1107	VAL
2	B	260	GLY

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1196/1520 (79%)	1136 (95%)	60 (5%)	22	55
2	B	952/1061 (90%)	912 (96%)	40 (4%)	26	60
3	C	234/274 (85%)	228 (97%)	6 (3%)	40	69
4	E	195/197 (99%)	189 (97%)	6 (3%)	35	66
5	F	74/137 (54%)	72 (97%)	2 (3%)	39	68
6	H	114/128 (89%)	109 (96%)	5 (4%)	25	59
7	I	109/116 (94%)	106 (97%)	3 (3%)	38	68
8	J	60/65 (92%)	57 (95%)	3 (5%)	22	55
9	K	99/102 (97%)	92 (93%)	7 (7%)	13	44
10	L	39/57 (68%)	39 (100%)	0	100	100
All	All	3072/3657 (84%)	2940 (96%)	132 (4%)	26	59

All (132) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	PHE

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Mol	Chain	Res	Type
1	A	61	ILE
1	A	93	VAL
1	A	126	LEU
1	A	132	LYS
1	A	179	LEU
1	A	208	LEU
1	A	222	LEU
1	A	235	ILE
1	A	270	LEU
1	A	271	LYS
1	A	287	HIS
1	A	308	ILE
1	A	322	VAL
1	A	351	THR
1	A	443	LEU
1	A	444	PHE
1	A	451	HIS
1	A	452	LYS
1	A	463	ILE
1	A	475	THR
1	A	481	ASP
1	A	512	VAL
1	A	532	ARG
1	A	605	MET
1	A	612	ILE
1	A	618	GLU
1	A	629	LEU
1	A	666	ILE
1	A	688	LYS
1	A	702	LEU
1	A	710	LEU
1	A	740	LEU
1	A	765	VAL
1	A	780	VAL
1	A	797	LYS
1	A	826	ASP
1	A	896	ARG
1	A	899	VAL
1	A	919	ILE
1	A	926	GLN
1	A	934	LYS
1	A	977	LYS

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Mol	Chain	Res	Type
1	A	1015	VAL
1	A	1017	LEU
1	A	1034	GLU
1	A	1116	LEU
1	A	1207	LEU
1	A	1262	LYS
1	A	1269	GLU
1	A	1297	GLU
1	A	1322	ILE
1	A	1329	THR
1	A	1350	LYS
1	A	1354	ASN
1	A	1374	VAL
1	A	1377	THR
1	A	1400	CYS
1	A	1406	VAL
1	A	1407	GLU
2	B	28	GLU
2	B	46	GLN
2	B	70	ILE
2	B	90	ILE
2	B	109	THR
2	B	134	LYS
2	B	319	GLU
2	B	331	LEU
2	B	364	ILE
2	B	365	THR
2	B	483	LEU
2	B	547	VAL
2	B	549	THR
2	B	567	GLU
2	B	570	VAL
2	B	606	LYS
2	B	628	THR
2	B	737	THR
2	B	751	VAL
2	B	797	TYR
2	B	825	VAL
2	B	916	THR
2	B	931	TYR
2	B	983	ARG
2	B	987	LYS

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Mol	Chain	Res	Type
2	B	997	GLU
2	B	1007	VAL
2	B	1028	GLU
2	B	1051	THR
2	B	1057	LYS
2	B	1065	GLN
2	B	1099	VAL
2	B	1147	LEU
2	B	1159	ARG
2	B	1160	VAL
2	B	1176	ASN
2	B	1188	LYS
2	B	1189	ILE
2	B	1194	ILE
2	B	1202	LEU
3	C	18	VAL
3	C	25	VAL
3	C	77	ILE
3	C	137	LYS
3	C	240	VAL
3	C	253	LYS
4	E	3	GLN
4	E	98	ILE
4	E	127	ILE
4	E	156	LEU
4	E	169	ARG
4	E	201	LYS
5	F	93	ILE
5	F	97	ARG
6	H	15	VAL
6	H	26	ILE
6	H	103	LYS
6	H	124	ARG
6	H	133	ASN
7	I	14	LEU
7	I	59	VAL
7	I	111	THR
8	J	3	VAL
8	J	5	VAL
8	J	46	CYS
9	K	1	MET
9	K	11	LEU

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Mol	Chain	Res	Type
9	K	18	LYS
9	K	20	LYS
9	K	32	VAL
9	K	101	LEU
9	K	113	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	316	GLN
1	A	611	GLN
1	A	935	GLN
1	A	965	GLN
2	B	115	GLN
2	B	215	GLN
2	B	255	GLN
2	B	449	ASN
2	B	762	ASN
2	B	770	GLN
2	B	843	GLN
2	B	862	GLN
2	B	951	GLN
2	B	984	HIS
2	B	1040	ASN
2	B	1093	GLN
2	B	1176	ASN
2	B	1177	HIS
5	F	104	ASN
6	H	35	GLN
6	H	128	ASN
7	I	22	ASN
9	K	112	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	R	7/8 (87%)	1 (14%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	R	8	G

There are no RNA pucker outliers to report.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	3DR	T	20	11	8,11,12	1.35	1 (12%)	7,14,17	1.27	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	3DR	T	20	11	-	2/3/15/16	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	T	20	3DR	O4'-C4'	-2.40	1.40	1.44

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	T	20	3DR	O4'-C4'-C3'	2.33	107.15	103.73

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	T	20	3DR	O4'-C4'-C5'-O5'
11	T	20	3DR	C3'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	T	20	3DR	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
15	APC	A	1805	14	29,33,33	1.67	8 (27%)	44,52,52	1.90	13 (29%)

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	APC	A	1805	14	-	5/19/38/38	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	A	1805	APC	PB-O3B	4.03	1.62	1.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	A	1805	APC	C5-C4	3.60	1.45	1.39
15	A	1805	APC	C4-N9	-3.02	1.31	1.37
15	A	1805	APC	PA-O2A	-2.65	1.49	1.56
15	A	1805	APC	C5-C6	2.60	1.48	1.41
15	A	1805	APC	C5-N7	-2.57	1.34	1.39
15	A	1805	APC	PB-O2B	-2.55	1.50	1.56
15	A	1805	APC	C8-N9	-2.08	1.34	1.37

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	A	1805	APC	C5-C4-N3	-5.72	118.84	126.72
15	A	1805	APC	C4-C5-N7	-4.03	105.98	110.58
15	A	1805	APC	N3-C4-N9	3.93	133.85	127.17
15	A	1805	APC	C2-N3-C4	3.78	121.06	111.83
15	A	1805	APC	N3-C2-N1	-2.94	124.14	128.58
15	A	1805	APC	C6-C5-N7	2.78	137.45	132.09
15	A	1805	APC	C4-N9-C8	2.67	108.54	105.74
15	A	1805	APC	O2A-PA-O1A	2.62	118.47	109.95
15	A	1805	APC	C3'-C2'-C1'	2.59	106.37	101.46
15	A	1805	APC	C5-N7-C8	2.58	107.50	103.45
15	A	1805	APC	C2'-C1'-N9	-2.53	107.02	113.30
15	A	1805	APC	N9-C8-N7	-2.29	110.69	113.94
15	A	1805	APC	O3B-PG-O1G	-2.08	100.08	111.04

There are no chirality outliers.

All (5) torsion outliers are listed below:

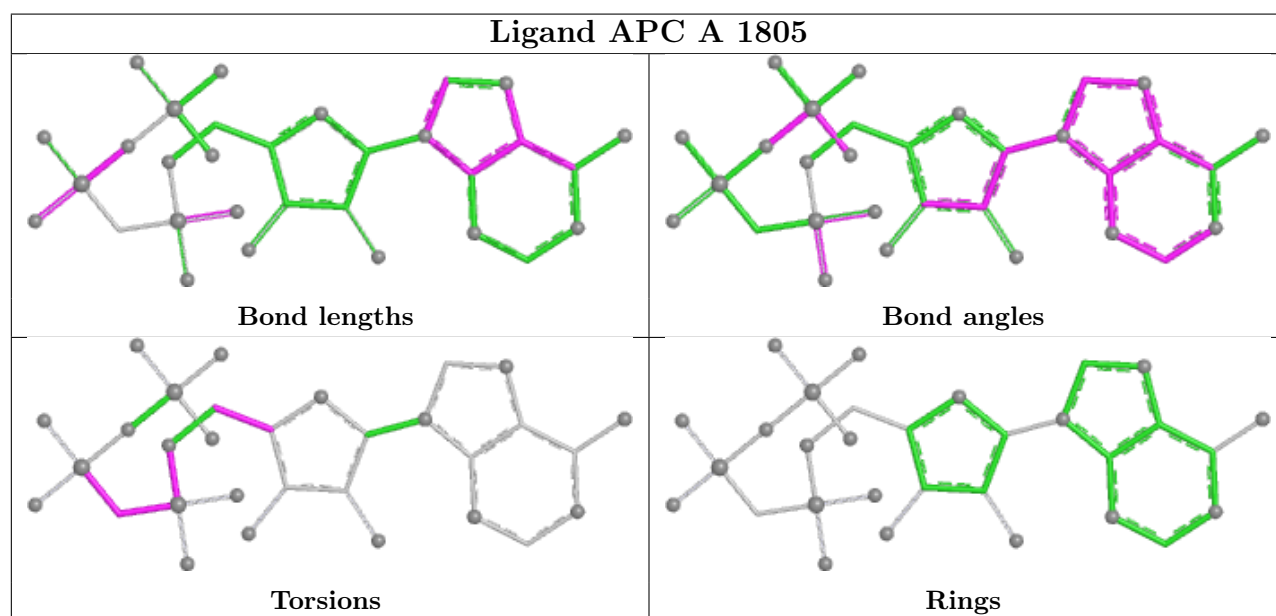
Mol	Chain	Res	Type	Atoms
15	A	1805	APC	PA-C3A-PB-O1B
15	A	1805	APC	O4'-C4'-C5'-O5'
15	A	1805	APC	C3'-C4'-C5'-O5'
15	A	1805	APC	PB-C3A-PA-O1A
15	A	1805	APC	C5'-O5'-PA-O1A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	A	1805	APC	1	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1372/1733 (79%)	0.46	95 (6%) 23 14	12, 61, 151, 315	0
2	B	1097/1224 (89%)	0.32	71 (6%) 25 16	14, 50, 122, 258	0
3	C	266/318 (83%)	0.16	5 (1%) 66 46	15, 50, 100, 176	0
4	E	213/215 (99%)	0.71	20 (9%) 14 9	23, 90, 172, 289	0
5	F	84/155 (54%)	0.21	3 (3%) 46 28	31, 61, 113, 145	0
6	H	130/146 (89%)	1.02	19 (14%) 6 4	43, 88, 147, 188	0
7	I	115/122 (94%)	0.47	6 (5%) 33 21	29, 66, 105, 149	0
8	J	65/70 (92%)	0.02	2 (3%) 51 32	22, 39, 92, 168	0
9	K	114/120 (95%)	0.08	0 100 100	22, 57, 98, 133	0
10	L	44/70 (62%)	1.59	16 (36%) 1 1	30, 93, 180, 216	0
11	T	10/29 (34%)	0.99	2 (20%) 3 2	50, 60, 162, 166	0
12	R	8/8 (100%)	-0.21	0 100 100	42, 54, 134, 171	0
All	All	3518/4210 (83%)	0.42	239 (6%) 23 15	12, 59, 142, 315	0

All (239) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
8	J	65	PRO	6.7
1	A	250	ILE	6.3
2	B	474	SER	6.3
10	L	45	ALA	6.0
1	A	65	LEU	5.8
1	A	179	LEU	5.6
2	B	530	GLY	5.4
2	B	477	ALA	4.9
6	H	139	ASN	4.8
1	A	147	VAL	4.7
6	H	76	THR	4.6

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Mol	Chain	Res	Type	RSRZ
6	H	136	LYS	4.5
1	A	49	LYS	4.4
2	B	643	ASP	4.4
6	H	84	ALA	4.3
2	B	918	ILE	4.3
1	A	98	LYS	4.2
10	L	27	LEU	4.1
1	A	59	GLY	4.1
2	B	1183	LYS	4.0
2	B	502	ILE	4.0
1	A	69	THR	4.0
7	I	57	GLY	3.9
2	B	266	ALA	3.9
1	A	1080	THR	3.9
6	H	83	GLN	3.8
1	A	1257	ASP	3.8
1	A	73	GLY	3.7
10	L	41	SER	3.7
2	B	261	ARG	3.7
2	B	929	THR	3.6
1	A	1446	ASP	3.6
2	B	648	HIS	3.6
10	L	53	HIS	3.6
4	E	125	PRO	3.5
1	A	1403	GLU	3.5
4	E	9	ILE	3.5
1	A	323	LYS	3.5
11	T	29	DG	3.4
1	A	826	ASP	3.4
2	B	275	TYR	3.4
1	A	397	ASN	3.4
2	B	575	PRO	3.4
5	F	72	LYS	3.3
2	B	867	GLY	3.3
1	A	1174	PHE	3.3
2	B	446	LEU	3.3
1	A	1359	ASP	3.3
1	A	221	SER	3.3
6	H	129	TYR	3.3
2	B	733	HIS	3.3
1	A	1330	ASN	3.3
10	L	40	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	973	ILE	3.2
2	B	868	MET	3.2
2	B	646	LEU	3.2
2	B	447	ALA	3.2
2	B	509	ALA	3.2
1	A	975	HIS	3.2
1	A	1387	HIS	3.2
5	F	73	ALA	3.2
2	B	881	ASN	3.1
2	B	472	ALA	3.1
2	B	106	ASP	3.1
2	B	467	GLY	3.1
1	A	56	PRO	3.1
2	B	471	LYS	3.1
1	A	1187	GLN	3.1
6	H	86	ASP	3.1
1	A	312	PRO	3.1
1	A	1109	LYS	3.1
1	A	107	CYS	3.0
4	E	127	ILE	3.0
10	L	35	SER	3.0
2	B	576	ASP	3.0
1	A	899	VAL	3.0
1	A	44	THR	3.0
2	B	1189	ILE	3.0
2	B	20	ASP	3.0
1	A	1108	ALA	2.9
11	T	19	DA	2.9
10	L	66	GLN	2.9
1	A	74	MET	2.9
1	A	1110	ASN	2.9
2	B	68	THR	2.9
6	H	62	SER	2.9
1	A	310	GLY	2.9
2	B	647	GLY	2.9
4	E	110	PHE	2.9
1	A	1078	GLN	2.9
6	H	63	LEU	2.9
10	L	42	ARG	2.9
4	E	95	THR	2.9
1	A	1243	VAL	2.9
2	B	895	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	215	SER	2.9
6	H	135	LEU	2.9
1	A	4	GLN	2.9
1	A	1256	GLU	2.8
1	A	79	GLY	2.8
1	A	174	ILE	2.8
1	A	1161	THR	2.8
4	E	93	MET	2.8
1	A	45	GLN	2.8
4	E	90	VAL	2.8
1	A	801	GLU	2.8
4	E	179	GLN	2.7
10	L	64	LEU	2.7
7	I	116	ASN	2.7
6	H	92	ASP	2.7
1	A	223	GLY	2.7
5	F	104	ASN	2.7
2	B	957	ASN	2.7
4	E	86	PRO	2.6
1	A	108	MET	2.6
1	A	141	LEU	2.6
1	A	61	ILE	2.6
3	C	267	GLN	2.6
3	C	4	GLU	2.6
4	E	97	VAL	2.6
1	A	1425	SER	2.6
2	B	1184	GLY	2.6
1	A	315	LEU	2.6
4	E	123	LEU	2.6
4	E	115	ASN	2.6
2	B	27	ALA	2.6
1	A	249	SER	2.6
2	B	629	ASP	2.6
1	A	72	GLU	2.6
2	B	262	GLU	2.5
2	B	345	LYS	2.5
3	C	78	GLU	2.5
4	E	98	ILE	2.5
1	A	1388	GLY	2.5
7	I	60	GLN	2.5
2	B	1176	ASN	2.5
2	B	476	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	1167	GLY	2.5
2	B	1170	THR	2.5
10	L	46	VAL	2.5
1	A	1125	ALA	2.5
1	A	1411	GLU	2.5
2	B	468	GLU	2.5
1	A	54	ASN	2.5
10	L	43	THR	2.4
10	L	36	SER	2.4
1	A	66	LYS	2.4
1	A	596	THR	2.4
1	A	227	VAL	2.4
1	A	1126	ALA	2.4
2	B	230	ALA	2.4
2	B	870	ILE	2.4
7	I	52	ILE	2.4
1	A	247	ARG	2.4
2	B	810	GLU	2.4
1	A	317	LYS	2.4
1	A	1211	GLN	2.4
6	H	137	GLN	2.4
10	L	28	LYS	2.4
6	H	138	GLU	2.4
2	B	372	SER	2.4
1	A	1124	HIS	2.4
1	A	1173	HIS	2.4
1	A	1258	HIS	2.4
2	B	668	ASP	2.4
6	H	140	ALA	2.4
2	B	370	PHE	2.4
1	A	60	SER	2.4
1	A	76	GLU	2.3
1	A	1393	ASN	2.3
7	I	4	PHE	2.3
1	A	42	ASP	2.3
6	H	82	PRO	2.3
2	B	734	HIS	2.3
1	A	177	ASP	2.3
4	E	3	GLN	2.3
1	A	129	LYS	2.3
1	A	1064	VAL	2.3
2	B	1162	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
10	L	52	GLY	2.3
4	E	100	ILE	2.2
1	A	48	ALA	2.2
1	A	91	PHE	2.2
4	E	85	GLU	2.2
1	A	109	HIS	2.2
2	B	267	ARG	2.2
2	B	1192	TYR	2.2
2	B	869	SER	2.2
1	A	64	ASN	2.2
1	A	120	GLU	2.2
4	E	105	PHE	2.2
2	B	365	THR	2.2
7	I	3	THR	2.2
2	B	574	SER	2.2
1	A	71	GLN	2.2
2	B	357	GLN	2.2
3	C	226	ASP	2.2
6	H	77	ARG	2.2
2	B	319	GLU	2.2
1	A	1419	ASP	2.2
2	B	115	GLN	2.1
6	H	108	SER	2.1
1	A	1307	GLU	2.1
2	B	711	GLU	2.1
2	B	369	GLY	2.1
4	E	55	ARG	2.1
4	E	129	PRO	2.1
2	B	887	HIS	2.1
2	B	889	THR	2.1
1	A	1188	GLN	2.1
2	B	65	GLU	2.1
6	H	106	GLU	2.1
10	L	39	SER	2.1
2	B	29	ASP	2.1
2	B	66	ASP	2.1
2	B	470	LYS	2.1
1	A	1422	ARG	2.1
1	A	1378	GLN	2.1
1	A	1302	PRO	2.1
1	A	211	PHE	2.1
1	A	237	THR	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	884	ARG	2.1
2	B	1217	TYR	2.1
4	E	121	MET	2.1
2	B	1157	ALA	2.1
1	A	411	ASP	2.1
1	A	3	GLY	2.1
1	A	1123	GLY	2.1
1	A	180	LYS	2.0
10	L	37	LYS	2.0
1	A	115	LEU	2.0
6	H	87	ARG	2.0
1	A	968	GLN	2.0
8	J	26	GLN	2.0
1	A	593	GLU	2.0
2	B	475	SER	2.0
2	B	724	ASP	2.0
3	C	205	LYS	2.0
1	A	1315	GLU	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
11	3DR	T	20	11/12	0.82	0.18	82,98,111,121	0

6.3 Carbohydrates [i](#)

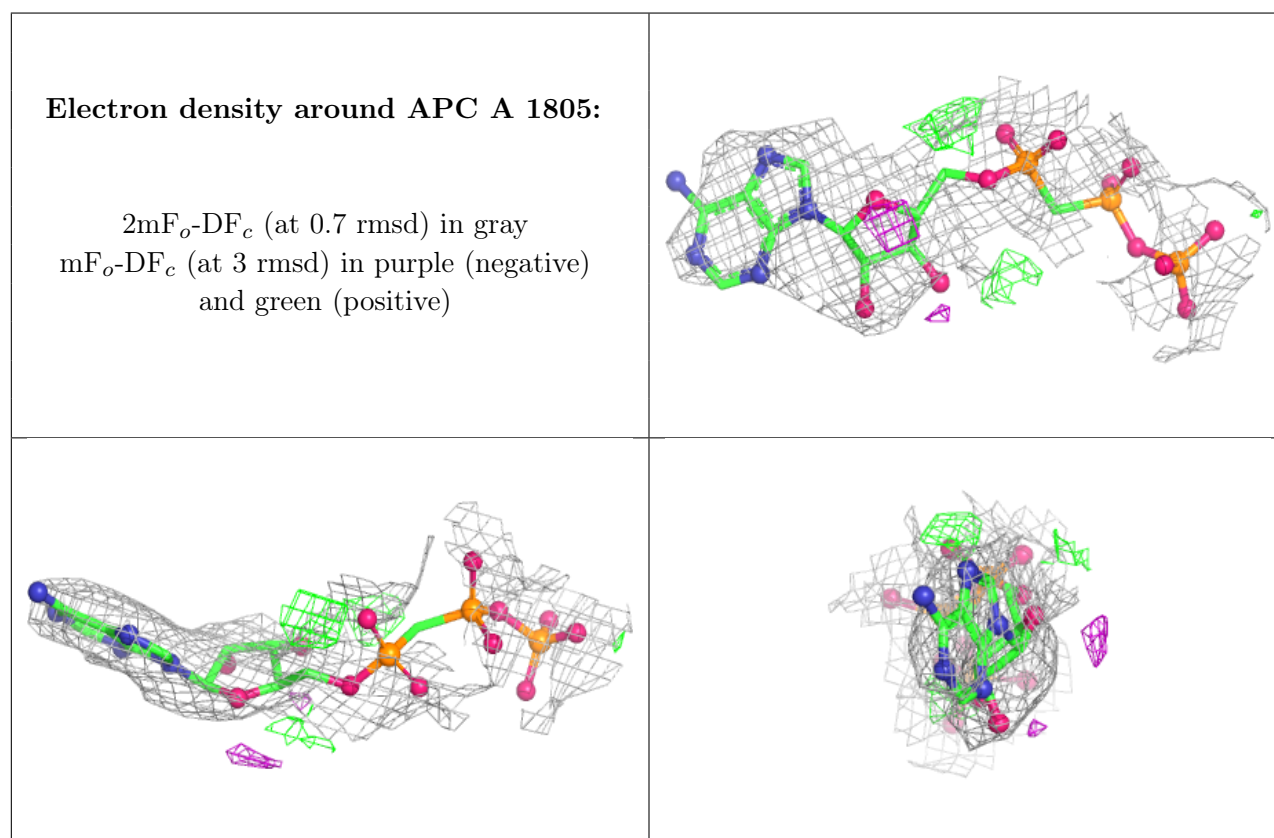
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
15	APC	A	1805	31/31	0.77	0.21	117,127,182,195	0
13	ZN	A	1801	1/1	0.91	0.08	173,173,173,173	0
14	MG	A	1804	1/1	0.94	0.07	68,68,68,68	0
13	ZN	A	1802	1/1	0.97	0.05	91,91,91,91	0
13	ZN	I	202	1/1	0.99	0.04	45,45,45,45	0
13	ZN	L	101	1/1	0.99	0.03	101,101,101,101	0
13	ZN	B	1301	1/1	0.99	0.04	82,82,82,82	0
13	ZN	C	401	1/1	0.99	0.03	47,47,47,47	0
14	MG	A	1803	1/1	1.00	0.04	6,6,6,6	0
13	ZN	J	101	1/1	1.00	0.04	38,38,38,38	0
13	ZN	I	201	1/1	1.00	0.05	53,53,53,53	0

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



6.5 Other polymers ⓘ

There are no such residues in this entry.