wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 05:36 AM GMT

PDB ID	:	2R93
Title	:	Elongation complex of RNA polymerase II with a hepatitis delta virus-derived RNA stem loop
Authors	:	Lehmann, E.; Brueckner, F.; Cramer, P.
Deposited on	:	2007-09-12
Resolution	:	4.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

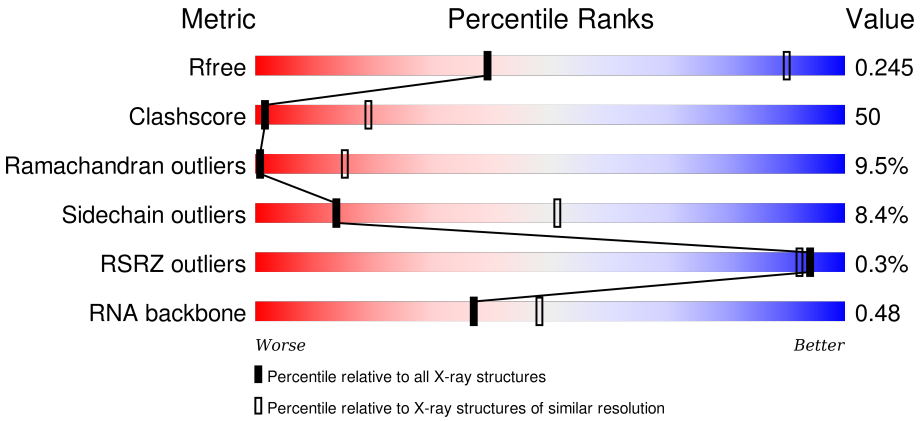
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1010 (4.42-3.56)
Clashscore	102246	1052 (4.40-3.60)
Ramachandran outliers	100387	1005 (4.40-3.60)
Sidechain outliers	100360	1013 (4.42-3.58)
RSRZ outliers	91569	1013 (4.42-3.56)
RNA backbone	2183	1079 (5.04-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	R	18	11% 28% 28% 17% 6% 22%
2	A	1733	29% 44% 8% • 18%
3	B	1224	28% 51% 11% • 9%
4	C	318	26% 48% 8% • 16%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	D	221	33% 38% 9% 19%
6	E	215	35% 57% 7%
7	F	155	19% 32% 6% 43%
8	G	171	30% 61% 8%
9	H	146	2% 27% 51% 14% 8%
10	I	122	37% 46% 12% 5%
11	J	70	20% 53% 19% 7%
12	K	120	38% 47% 9% 7%
13	L	70	% 17% 33% 14% 34%

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 31500 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 RNA chain called RNA (5'-R(*UP*GP*AP*UP*UP*CP*UP*CP*UP*AP*UP*CP*GP*GP*AP*AP*UP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	R	14	289	132	49	96	12	0	0	0

- Molecule 2 is a protein called DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	1422	11194	7054	1959	2119	62	0	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	B	1112	8841	5596	1550	1640	55	0	0	0

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	C	267	2101	1320	349	419	13	0	0	0

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit RPB4.

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

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

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

- Molecule 7 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	F	88	Total	C	N	O	S	0	0	0
			712	455	120	134	3			

- Molecule 8 is a protein called DNA-directed RNA polymerase II subunit RPB7.

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

- Molecule 9 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	H	135	Total	C	N	O	S	0	0	0
			1084	683	183	214	4			

- Molecule 10 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	I	116	Total	C	N	O	S	0	0	0
			944	581	172	181	10			

- Molecule 11 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

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

- Molecule 12 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	K	112	Total	C	N	O	S	0	0	0
			904	580	154	168	2			

- Molecule 13 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	L	46	Total	C	N	O	S	0	0	0
			364	224	72	64	4			

- Molecule 14 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 15 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

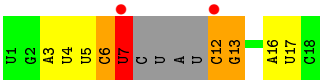
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	A	1	Total	Mg	0	0
			1	1		

3 Residue-property plots (i)

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

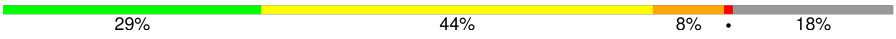
• Molecule 1: RNA (5'-R(*UP*GP*AP*UP*UP*CP*UP*CP*UP*AP*UP*CP*GP*GP*AP*AP *UP*C)-3')

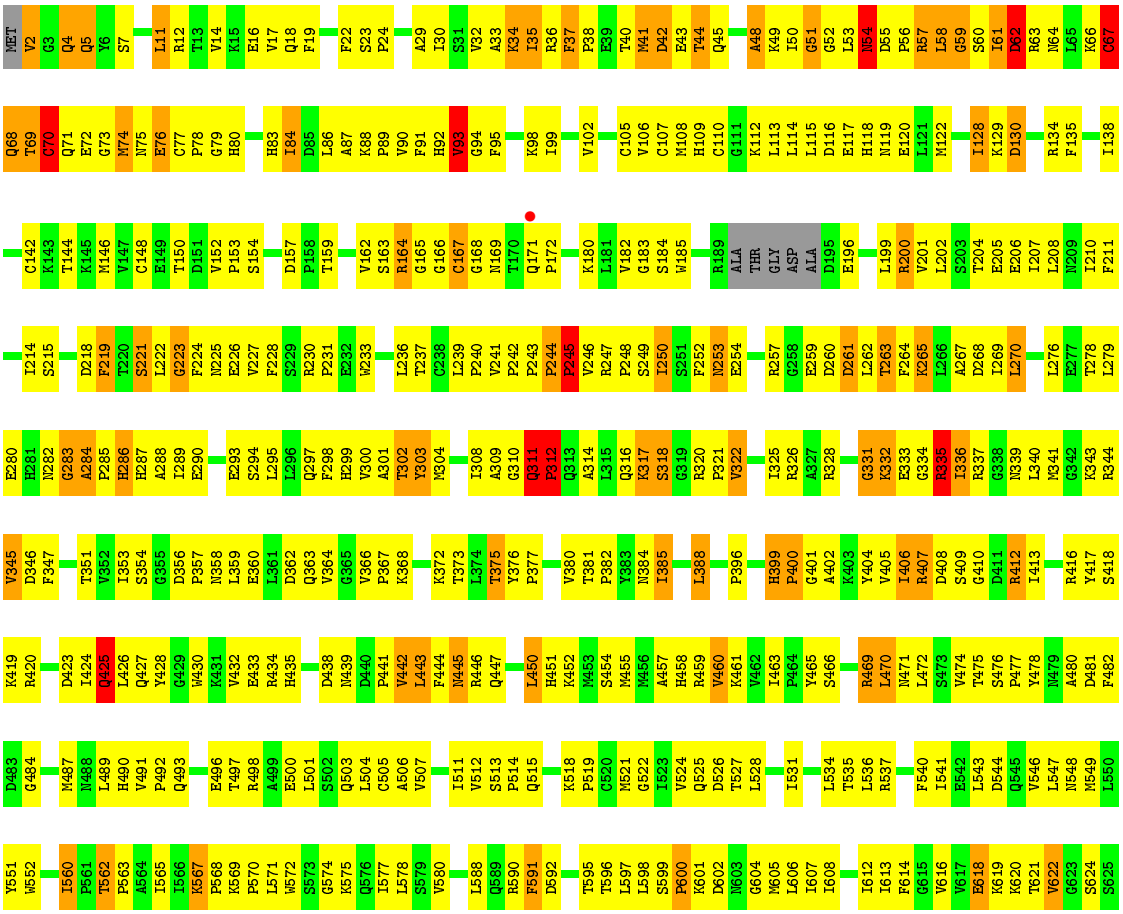
Chain R:

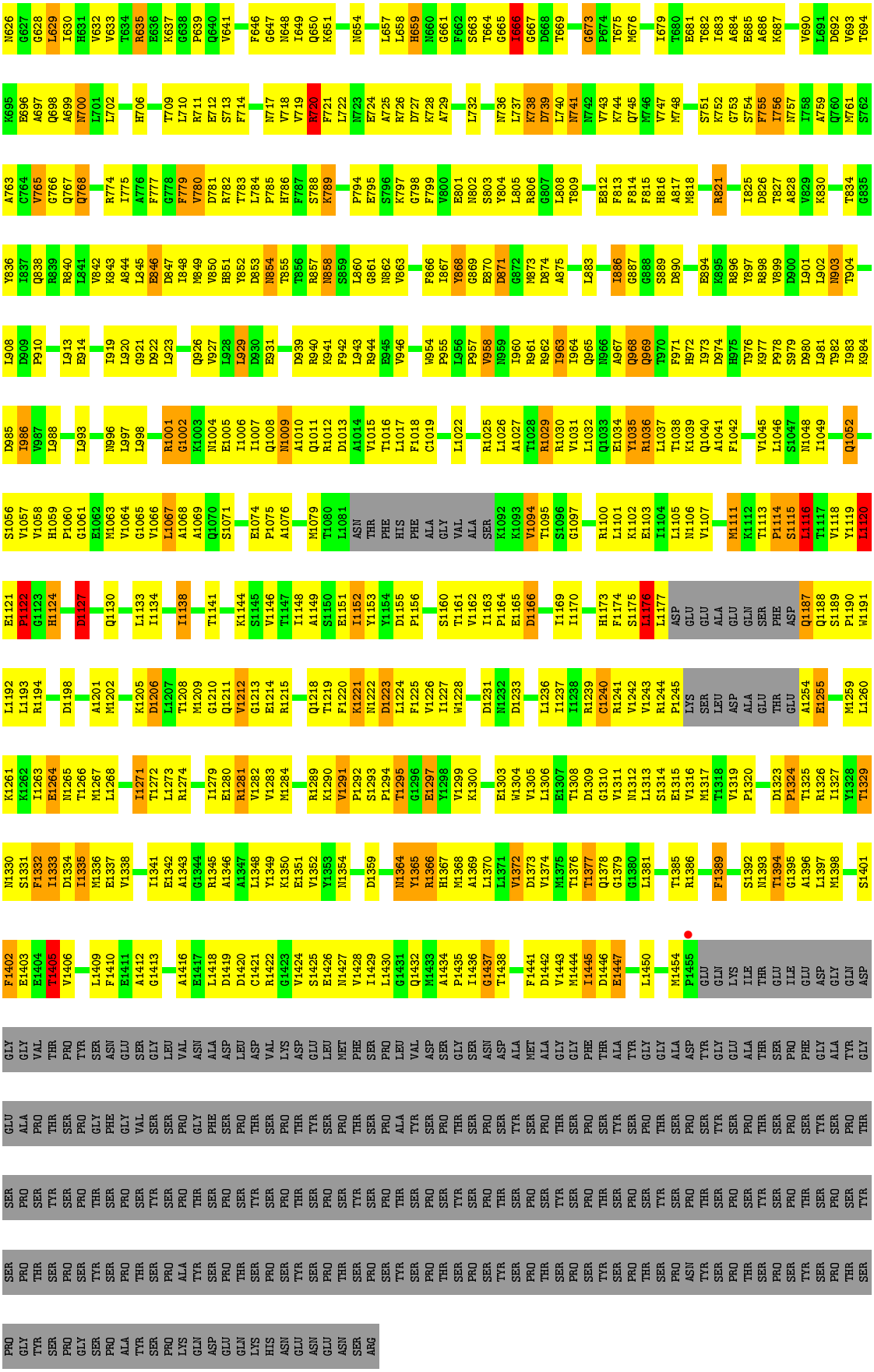


• Molecule 2: DNA-directed RNA polymerase II subunit RPB1

Chain A:

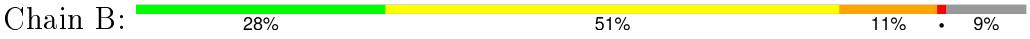


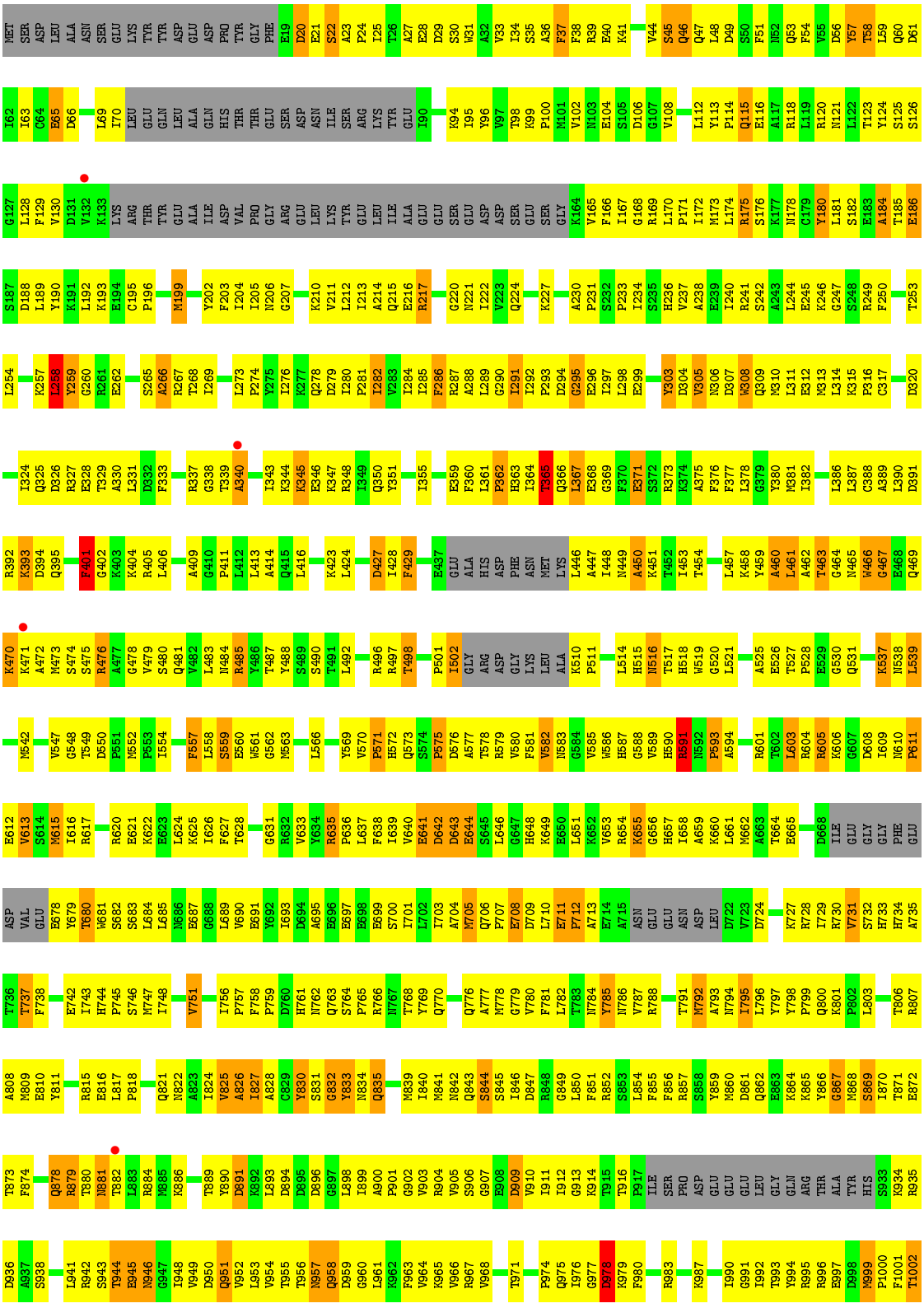


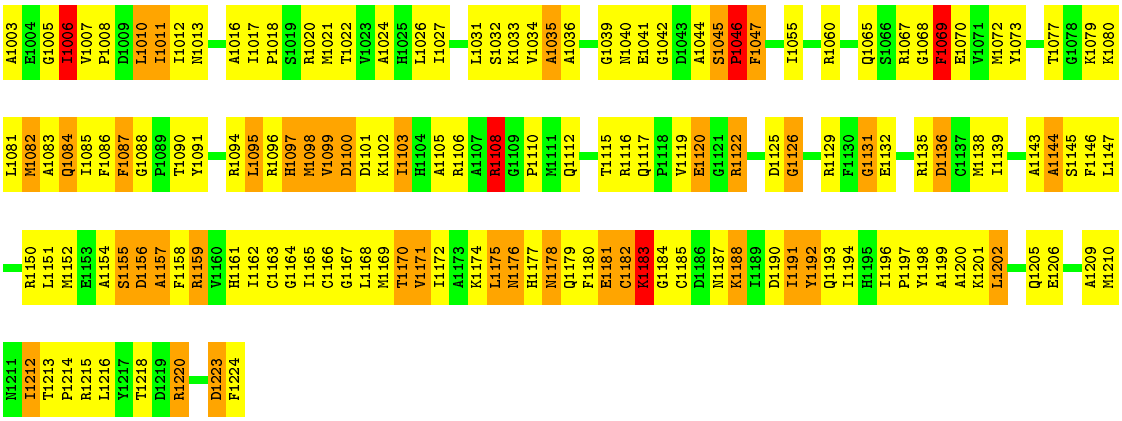


• Molecule 3: DNA-directed RNA polymerase II subunit RPB2

Chain B:

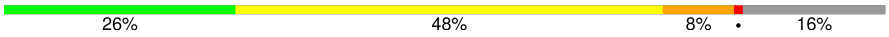


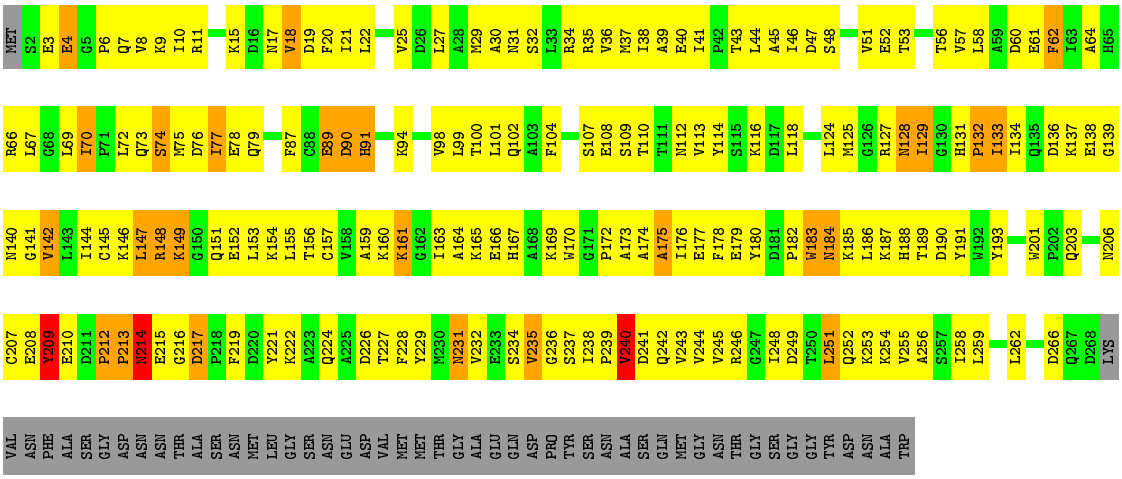




• Molecule 4: DNA-directed RNA polymerase II subunit RPB3

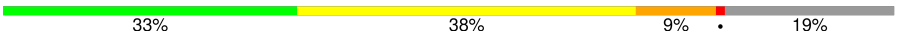
Chain C:

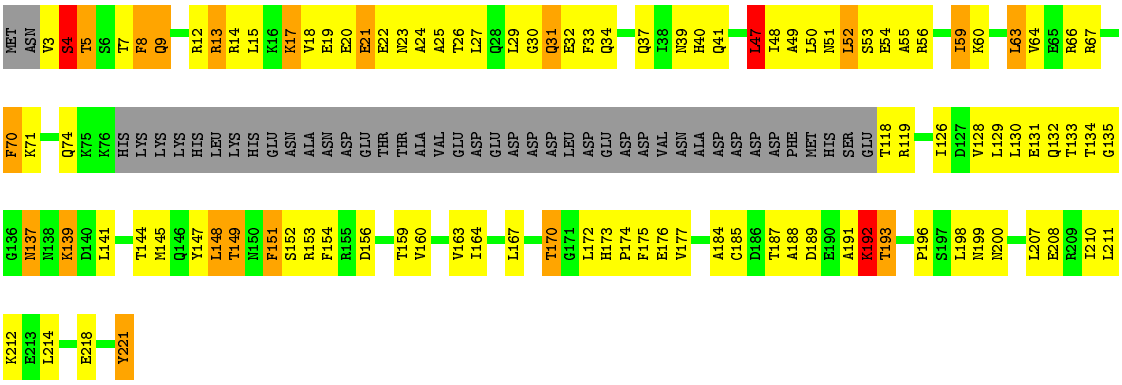




• Molecule 5: DNA-directed RNA polymerase II subunit RPB4

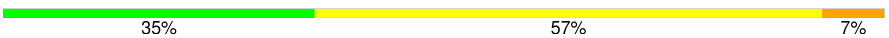
Chain D:

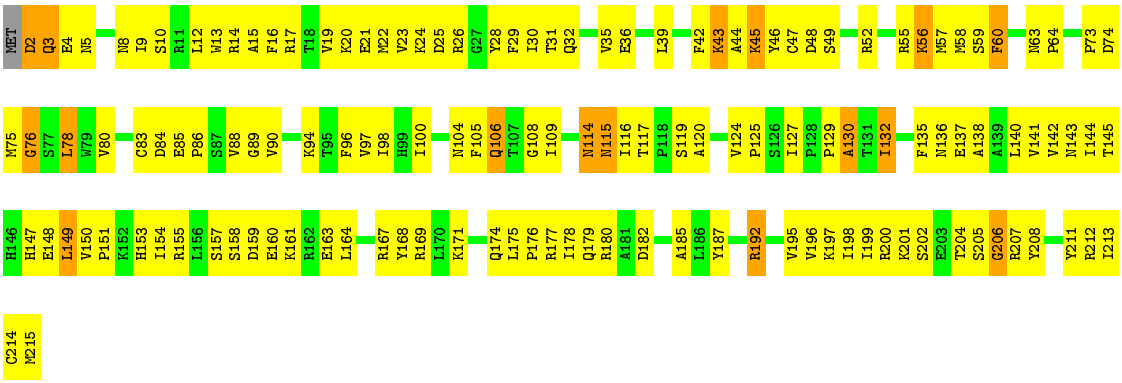




• Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC1

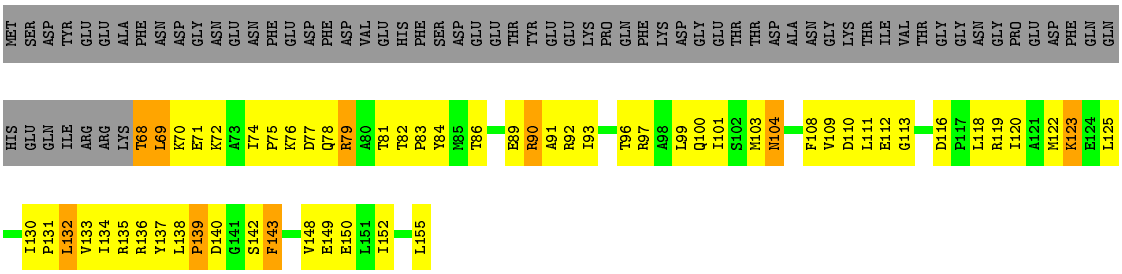
Chain E:





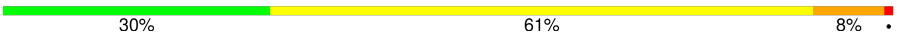
- Molecule 7: DNA-directed RNA polymerases I, II, and III subunit RPABC2

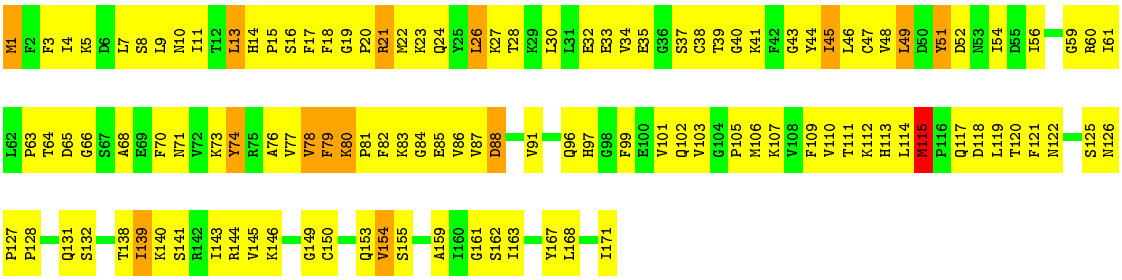
Chain F:



- Molecule 8: DNA-directed RNA polymerase II subunit RPB7

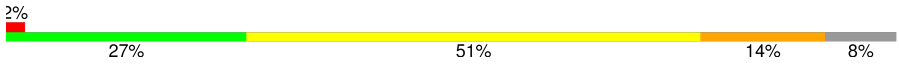
Chain G:

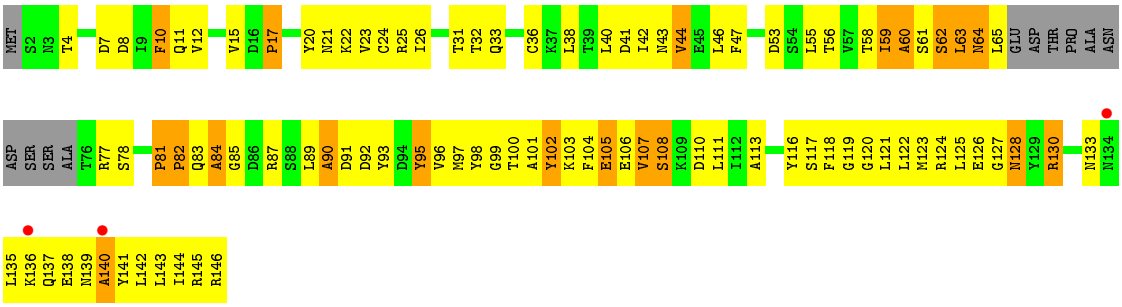




- Molecule 9: DNA-directed RNA polymerases I, II, and III subunit RPABC3

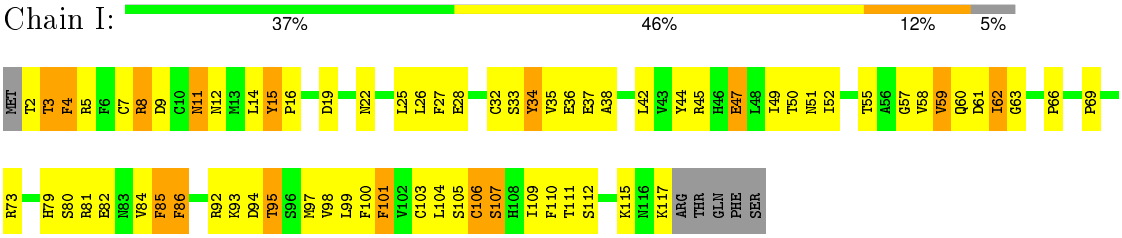
Chain H:





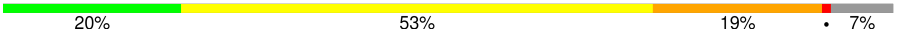
• Molecule 10: DNA-directed RNA polymerase II subunit RPB9

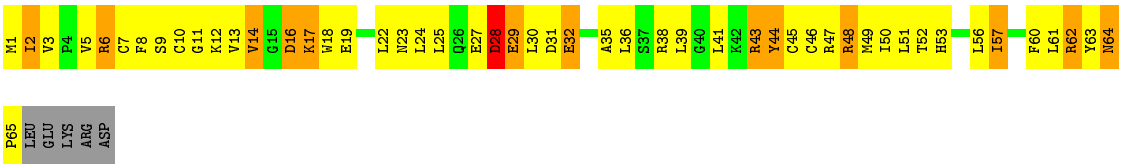
Chain I:



• Molecule 11: DNA-directed RNA polymerases I, II, and III subunit RPABC5

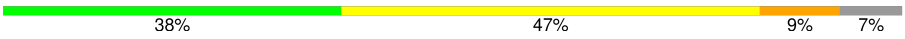
Chain J:

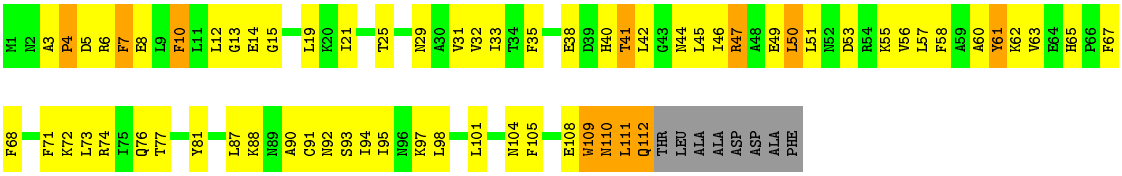




• Molecule 12: DNA-directed RNA polymerase II subunit RPB11

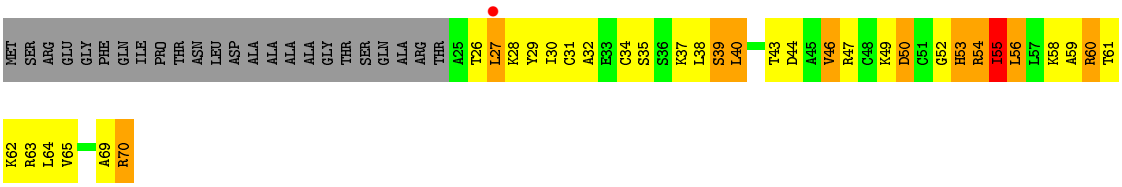
Chain K:





• Molecule 13: DNA-directed RNA polymerases I, II, and III subunit RPABC4

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	223.34Å 394.88Å 284.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 4.00 48.28 – 4.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-4.00) 97.2 (48.28-4.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$< I/\sigma(I) >$ [1]	4.00 (at 4.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.216 , 0.241 0.224 , 0.245	Depositor DCC
R_{free} test set	2068 reflections (2.01%)	DCC
Wilson B-factor (Å^2)	103.2	Xtriage
Anisotropy	0.674	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.25 , 46.8	EDS
Estimated twinning fraction	0.011 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.010 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	0 of 105627 reflections	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	31500	wwPDB-VP
Average B, all atoms (Å^2)	126.0	wwPDB-VP

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

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	R	0.87	0/321	1.11	3/496 (0.6%)
2	A	0.42	0/11394	0.71	6/15407 (0.0%)
3	B	0.41	0/9013	0.68	0/12152
4	C	0.42	0/2139	0.72	1/2899 (0.0%)
5	D	0.40	0/1444	0.66	0/1935
6	E	0.38	0/1788	0.64	0/2406
7	F	0.53	0/723	0.92	2/974 (0.2%)
8	G	0.44	0/1368	0.72	0/1844
9	H	0.38	0/1102	0.64	0/1492
10	I	0.36	0/962	0.64	0/1295
11	J	0.47	0/541	0.72	0/727
12	K	0.44	0/922	0.65	0/1244
13	L	0.48	0/366	0.72	0/485
All	All	0.42	0/32083	0.70	12/43356 (0.0%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	F	70	LYS	N-CA-C	-10.69	82.14	111.00
7	F	69	LEU	CA-CB-CG	9.42	136.97	115.30
1	R	7	U	O4'-C1'-N1	7.69	114.35	108.20
2	A	1176	LEU	N-CA-C	7.45	131.12	111.00
2	A	1176	LEU	CA-CB-CG	7.44	132.41	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	R	289	0	153	11	0
2	A	11194	0	11279	1192	0
3	B	8841	0	8875	1024	0
4	C	2101	0	2056	260	0
5	D	1434	0	1460	119	0
6	E	1752	0	1776	150	0
7	F	712	0	737	108	0
8	G	1340	0	1357	159	0
9	H	1084	0	1057	128	0
10	I	944	0	901	98	0
11	J	532	0	543	90	0
12	K	904	0	911	106	0
13	L	364	0	387	49	0
14	A	2	0	0	0	0
14	B	1	0	0	0	0
14	C	1	0	0	0	0
14	I	2	0	0	0	0
14	J	1	0	0	0	0
14	L	1	0	0	0	0
15	A	1	0	0	0	0
All	All	31500	0	31492	3165	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 50.

The worst 5 of 3165 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)
7:F:68:THR:HG21	7:F:69:LEU:N	1.59	1.16
7:F:69:LEU:HD23	7:F:71:GLU:CB	1.77	1.14
7:F:69:LEU:HD23	7:F:71:GLU:HB2	1.17	1.12
2:A:58:LEU:HD12	2:A:59:GLY:N	1.65	1.11
2:A:34:LYS:NZ	2:A:57:ARG:HH12	1.50	1.09

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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
2	A	1412/1733 (82%)	1032 (73%)	252 (18%)	128 (9%)	1 16
3	B	1096/1224 (90%)	781 (71%)	206 (19%)	109 (10%)	1 13
4	C	265/318 (83%)	169 (64%)	66 (25%)	30 (11%)	0 10
5	D	174/221 (79%)	133 (76%)	27 (16%)	14 (8%)	1 19
6	E	212/215 (99%)	166 (78%)	32 (15%)	14 (7%)	1 25
7	F	85/155 (55%)	70 (82%)	11 (13%)	4 (5%)	3 33
8	G	169/171 (99%)	128 (76%)	32 (19%)	9 (5%)	2 31
9	H	131/146 (90%)	78 (60%)	33 (25%)	20 (15%)	0 5
10	I	114/122 (93%)	76 (67%)	26 (23%)	12 (10%)	1 11
11	J	63/70 (90%)	37 (59%)	16 (25%)	10 (16%)	0 5
12	K	110/120 (92%)	88 (80%)	15 (14%)	7 (6%)	2 26
13	L	44/70 (63%)	20 (46%)	12 (27%)	12 (27%)	0 0
All	All	3875/4565 (85%)	2778 (72%)	728 (19%)	369 (10%)	1 15

5 of 369 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	42	ASP
2	A	48	ALA
2	A	54	ASN
2	A	57	ARG
2	A	62	ASP

5.3.2 Protein sidechains (i)

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
2	A	1245/1520 (82%)	1136 (91%)	109 (9%)	12 48
3	B	964/1061 (91%)	882 (92%)	82 (8%)	13 51
4	C	235/274 (86%)	219 (93%)	16 (7%)	20 59
5	D	160/200 (80%)	138 (86%)	22 (14%)	4 29
6	E	196/197 (100%)	187 (95%)	9 (5%)	33 70
7	F	78/137 (57%)	72 (92%)	6 (8%)	16 55
8	G	152/152 (100%)	133 (88%)	19 (12%)	6 32
9	H	119/128 (93%)	115 (97%)	4 (3%)	44 77
10	I	110/116 (95%)	104 (94%)	6 (6%)	27 66
11	J	60/65 (92%)	53 (88%)	7 (12%)	7 35
12	K	97/102 (95%)	89 (92%)	8 (8%)	14 51
13	L	40/57 (70%)	37 (92%)	3 (8%)	17 56
All	All	3456/4009 (86%)	3165 (92%)	291 (8%)	14 51

5 of 291 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	473	MET
3	B	957	ASN
10	I	15	TYR
3	B	502	ILE
3	B	724	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 97 such sidechains are listed below:

Mol	Chain	Res	Type
3	B	518	HIS
3	B	1065	GLN
10	I	90	GLN
3	B	706	GLN
3	B	842	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	R	12/18 (66%)	4 (33%)	0

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	R	6	C
1	R	7	U
1	R	13	G
1	R	17	U

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	R	14/18 (77%)	0.81	2 (14%) 4 4	128, 147, 176, 188	0
2	A	1422/1733 (82%)	-0.37	2 (0%) 95 95	57, 116, 171, 200	0
3	B	1112/1224 (90%)	-0.33	4 (0%) 93 90	61, 126, 184, 200	0
4	C	267/318 (83%)	-0.39	0 100 100	73, 111, 159, 176	0
5	D	178/221 (80%)	-0.32	0 100 100	88, 133, 179, 192	0
6	E	214/215 (99%)	-0.34	0 100 100	93, 154, 191, 199	0
7	F	88/155 (56%)	-0.52	0 100 100	61, 93, 130, 153	0
8	G	171/171 (100%)	-0.38	0 100 100	88, 116, 155, 163	0
9	H	135/146 (92%)	0.18	3 (2%) 65 54	131, 161, 187, 196	0
10	I	116/122 (95%)	-0.16	0 100 100	110, 161, 191, 196	0
11	J	65/70 (92%)	-0.50	0 100 100	79, 109, 145, 149	0
12	K	112/120 (93%)	-0.42	0 100 100	76, 115, 140, 158	0
13	L	46/70 (65%)	0.07	1 (2%) 65 54	107, 170, 191, 193	0
All	All	3940/4583 (85%)	-0.33	12 (0%) 94 92	57, 122, 182, 200	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	B	471	LYS	3.5
2	A	1455	PRO	3.0
2	A	171	GLN	2.4
9	H	140	ALA	2.3
9	H	136	LYS	2.2

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

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
14	ZN	I	203	1/1	0.99	0.18	0.49	113,113,113,113	0
14	ZN	B	1307	1/1	0.99	0.20	-0.31	78,78,78,78	0
14	ZN	J	101	1/1	0.99	0.24	-0.50	86,86,86,86	0
14	ZN	C	302	1/1	0.99	0.13	-0.80	71,71,71,71	0
14	ZN	A	1508	1/1	0.99	0.14	-1.22	79,79,79,79	0
14	ZN	I	204	1/1	0.89	0.04	-1.84	190,190,190,190	0
14	ZN	A	1506	1/1	0.97	0.07	-4.52	119,119,119,119	0
15	MG	A	1	1/1	0.97	0.14	-	68,68,68,68	0
14	ZN	L	105	1/1	0.96	0.06	-	156,156,156,156	0

6.5 Other polymers (i)

There are no such residues in this entry.