wwPDB X-ray Structure Validation Summary Report (i)

May 28, 2020 – 09:29 pm BST

PDB ID	:	2B8K
Title	:	12-subunit RNA Polymerase II
Authors	:	Meyer, P.A.; Ye, P.; Zhang, M.; Suh, M.H.; Fu, J.
Deposited on	:	2005-10-07
Resolution	:	4.15 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
https://www.wwpdb.org/validation/2017/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:

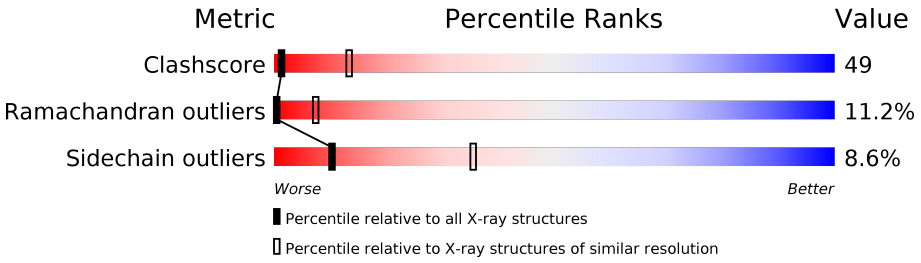
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.15 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))
Clashscore	141614	1028 (4.52-3.80)
Ramachandran outliers	138981	1005 (4.54-3.78)
Sidechain outliers	138945	1024 (4.54-3.76)

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 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 <=5%

Mol	Chain	Length	Quality of chain
1	A	1733	27% 43% 10% • 18%
2	B	1224	29% 48% 12% • 9%
3	C	318	23% 47% 12% • 16%
4	D	221	30% 42% 10% 18%
5	E	215	40% 53% 6%
6	F	155	17% 31% 6% • 46%
7	G	215	30% 42% 7% 20%
8	H	146	32% 49% 10% 9%
9	I	122	40% 43% 13% • •

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Mol	Chain	Length	Quality of chain
10	J	70	19% 51% 23% 7%
11	K	120	41% 47% 8%
12	L	70	13% 34% 19% 34%

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 31040 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 largest subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1416	11140	7021	1946	2111	62	0	0	0

- Molecule 2 is a protein called DNA-directed RNA polymerase II 140 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	1114	8800	5573	1540	1633	54	0	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerase II 45 kDa polypeptide.

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

- Molecule 4 is a protein called DNA-directed RNA polymerase II 32 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	182	1373	851	243	277	2	0	0	0

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III 27 kDa polypeptide.

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

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III 23 kDa polypeptide.

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 DNA-directed RNA polymerase II 19 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	171	Total	C	N	O	S	0	0	0
			1339	861	222	248	8			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	172	SER	-	EXPRESSION TAG	UNP P34087
G	173	HIS	-	EXPRESSION TAG	UNP P34087
G	174	GLU	-	EXPRESSION TAG	UNP P34087
G	175	LYS	-	EXPRESSION TAG	UNP P34087
G	176	ARG	-	EXPRESSION TAG	UNP P34087
G	177	ARG	-	EXPRESSION TAG	UNP P34087
G	178	TRP	-	EXPRESSION TAG	UNP P34087
G	179	LYS	-	EXPRESSION TAG	UNP P34087
G	180	LYS	-	EXPRESSION TAG	UNP P34087
G	181	ASN	-	EXPRESSION TAG	UNP P34087
G	182	PHE	-	EXPRESSION TAG	UNP P34087
G	183	ILE	-	EXPRESSION TAG	UNP P34087
G	184	ALA	-	EXPRESSION TAG	UNP P34087
G	185	VAL	-	EXPRESSION TAG	UNP P34087
G	186	SER	-	EXPRESSION TAG	UNP P34087
G	187	ALA	-	EXPRESSION TAG	UNP P34087
G	188	ALA	-	EXPRESSION TAG	UNP P34087
G	189	ASN	-	EXPRESSION TAG	UNP P34087
G	190	ARG	-	EXPRESSION TAG	UNP P34087
G	191	PHE	-	EXPRESSION TAG	UNP P34087
G	192	LYS	-	EXPRESSION TAG	UNP P34087
G	193	LYS	-	EXPRESSION TAG	UNP P34087
G	194	ILE	-	EXPRESSION TAG	UNP P34087
G	195	SER	-	EXPRESSION TAG	UNP P34087
G	196	SER	-	EXPRESSION TAG	UNP P34087
G	197	SER	-	EXPRESSION TAG	UNP P34087
G	198	GLY	-	EXPRESSION TAG	UNP P34087
G	199	ALA	-	EXPRESSION TAG	UNP P34087
G	200	LEU	-	EXPRESSION TAG	UNP P34087
G	201	ASP	-	EXPRESSION TAG	UNP P34087
G	202	TYR	-	EXPRESSION TAG	UNP P34087

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Chain	Residue	Modelled	Actual	Comment	Reference
G	203	ASP	-	EXPRESSION TAG	UNP P34087
G	204	ILE	-	EXPRESSION TAG	UNP P34087
G	205	PRO	-	EXPRESSION TAG	UNP P34087
G	206	THR	-	EXPRESSION TAG	UNP P34087
G	207	THR	-	EXPRESSION TAG	UNP P34087
G	208	ALA	-	EXPRESSION TAG	UNP P34087
G	209	SER	-	EXPRESSION TAG	UNP P34087
G	210	GLU	-	EXPRESSION TAG	UNP P34087
G	211	ASN	-	EXPRESSION TAG	UNP P34087
G	212	LEU	-	EXPRESSION TAG	UNP P34087
G	213	TYR	-	EXPRESSION TAG	UNP P34087
G	214	PHE	-	EXPRESSION TAG	UNP P34087
G	215	GLN	-	EXPRESSION TAG	UNP P34087

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide.

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 9.

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/III subunit 10.

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 13.6 kDa polypeptide.

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 7.7 kDa polypeptide.

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

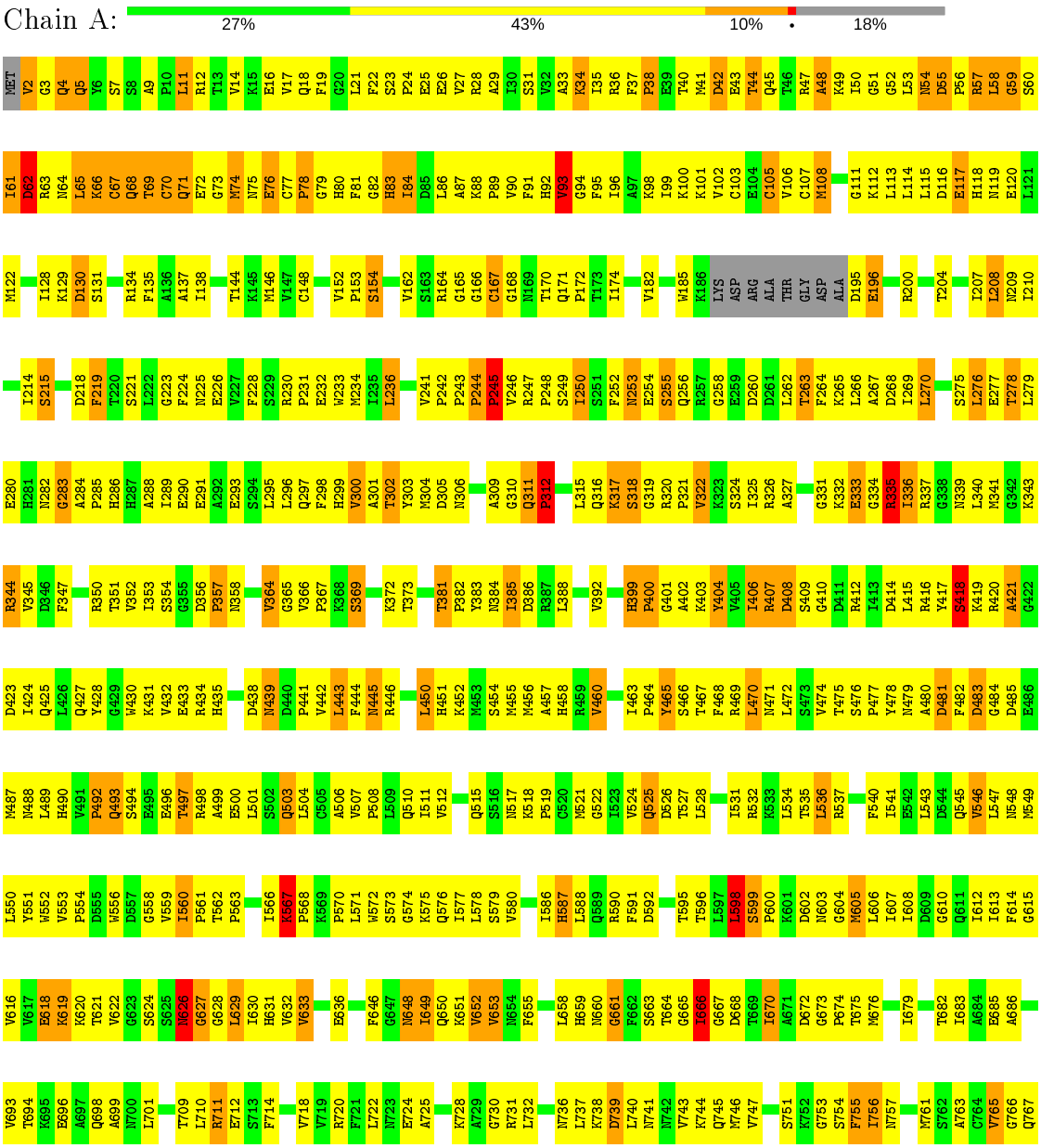
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	J	1	Total	Zn	0	0
			1	1		
13	B	1	Total	Zn	0	0
			1	1		
13	I	2	Total	Zn	0	0
			2	2		
13	C	1	Total	Zn	0	0
			1	1		
13	A	2	Total	Zn	0	0
			2	2		
13	L	1	Total	Zn	0	0
			1	1		

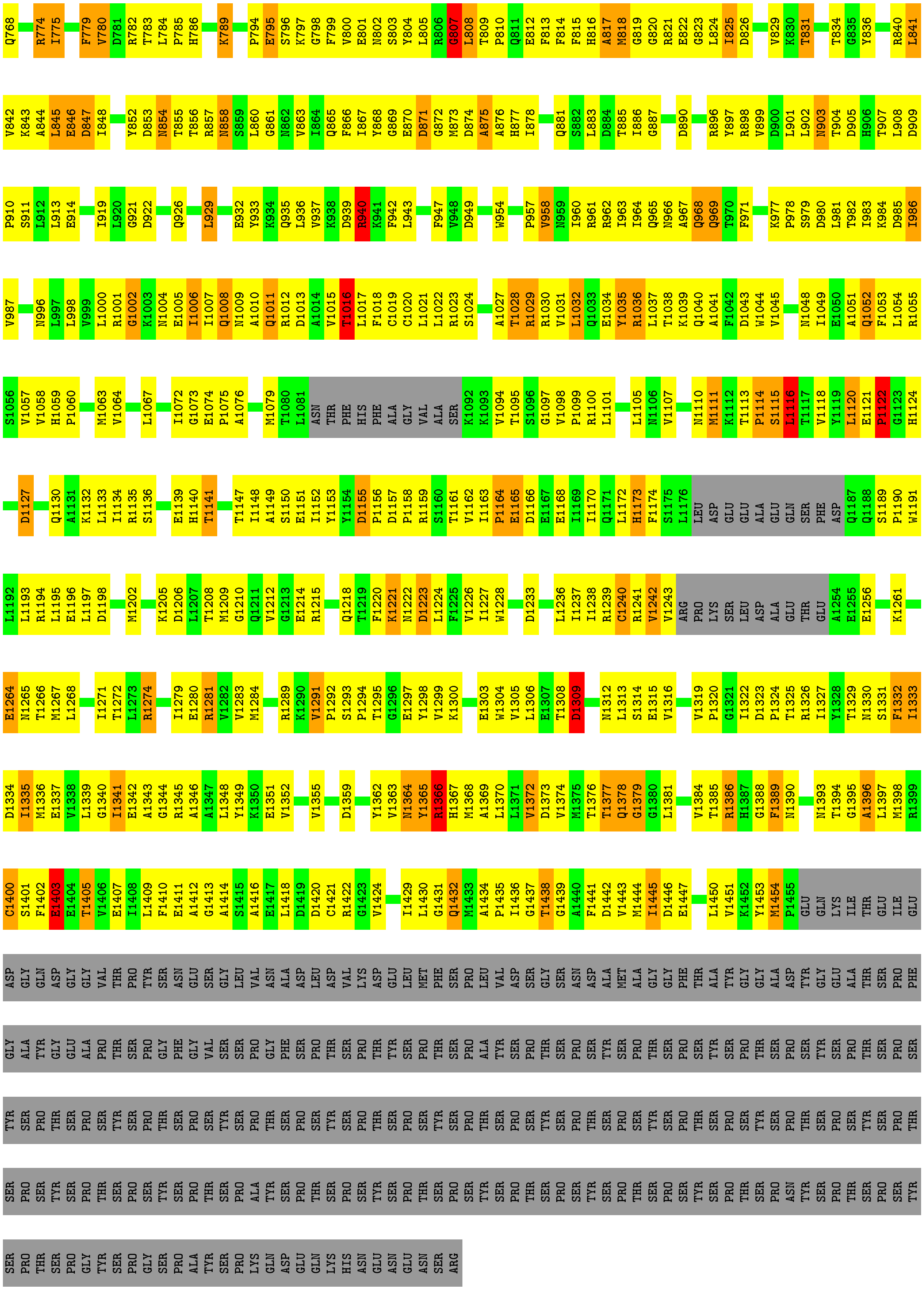
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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 largest subunit

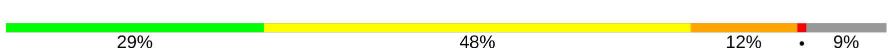
Chain A:

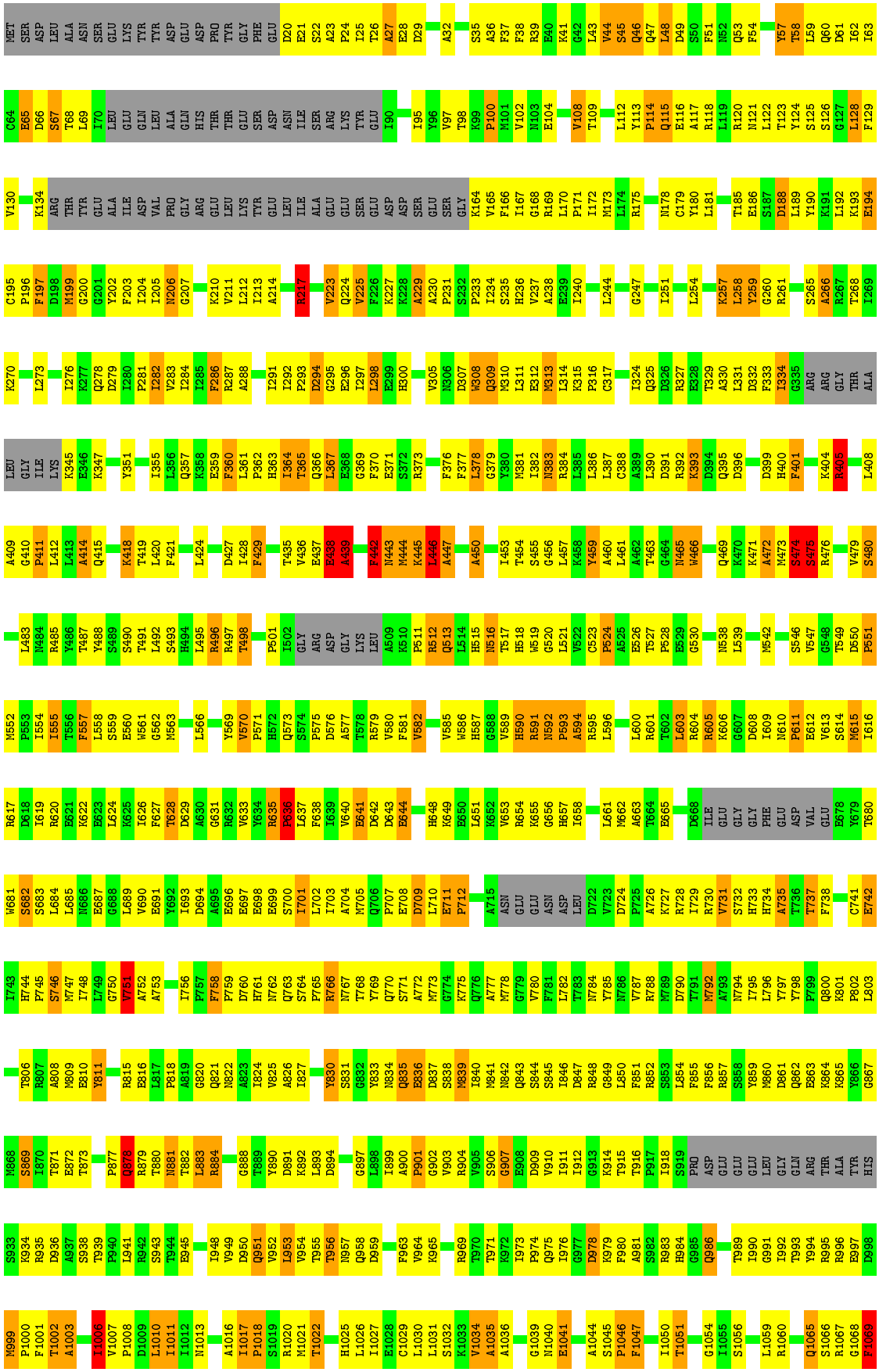


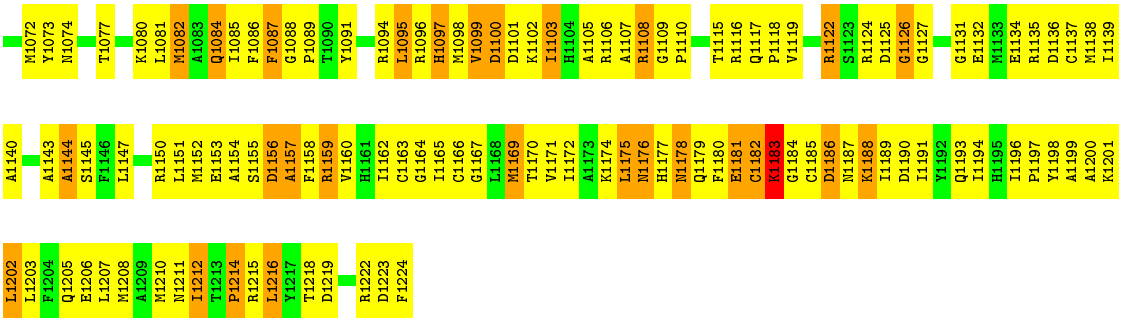


• Molecule 2: DNA-directed RNA polymerase II 140 kDa polypeptide

Chain B:

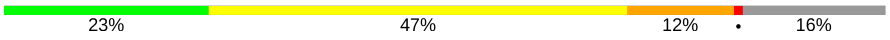


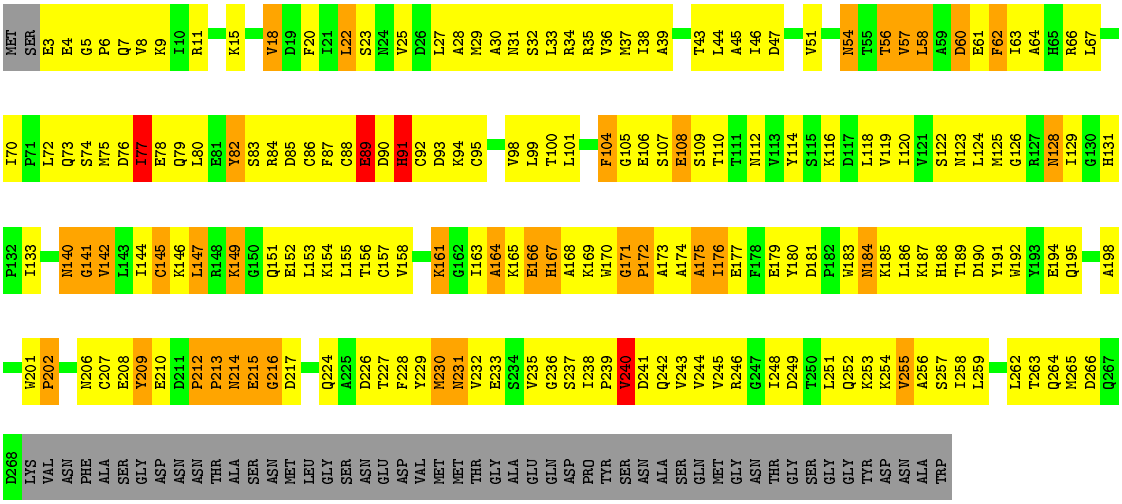




• Molecule 3: DNA-directed RNA polymerase II 45 kDa polypeptide

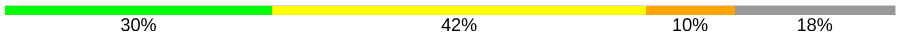
Chain C:

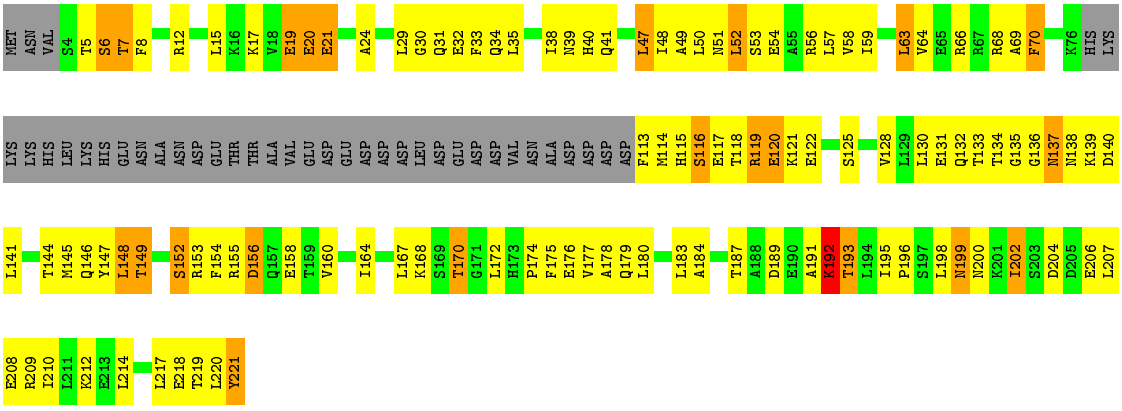




• Molecule 4: DNA-directed RNA polymerase II 32 kDa polypeptide

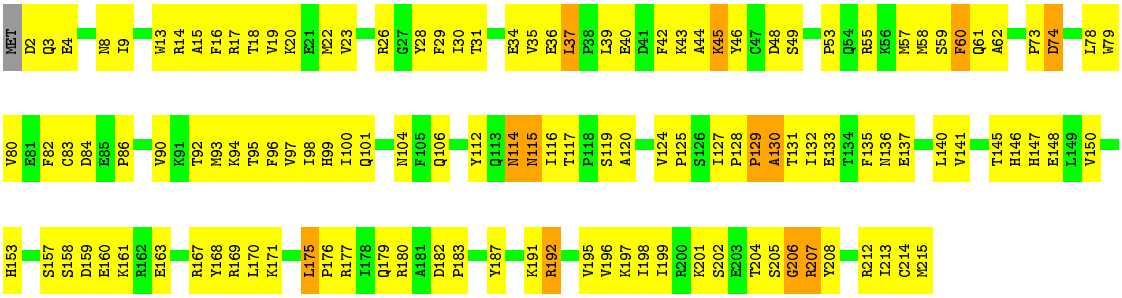
Chain D:





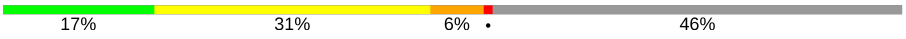
• Molecule 5: DNA-directed RNA polymerases I, II, and III 27 kDa polypeptide

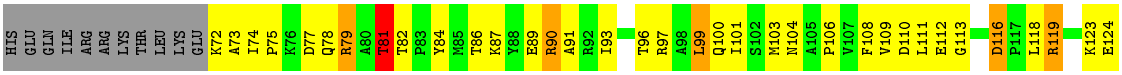
Chain E:

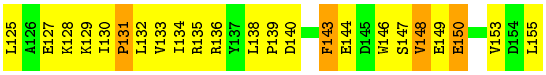


• Molecule 6: DNA-directed RNA polymerases I, II, and III 23 kDa polypeptide

Chain F:

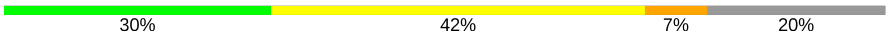






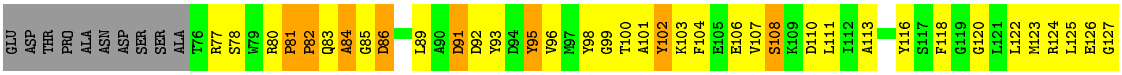
• Molecule 7: DNA-directed RNA polymerase II 19 kDa polypeptide

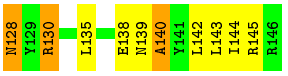
Chain G:



• Molecule 8: DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide

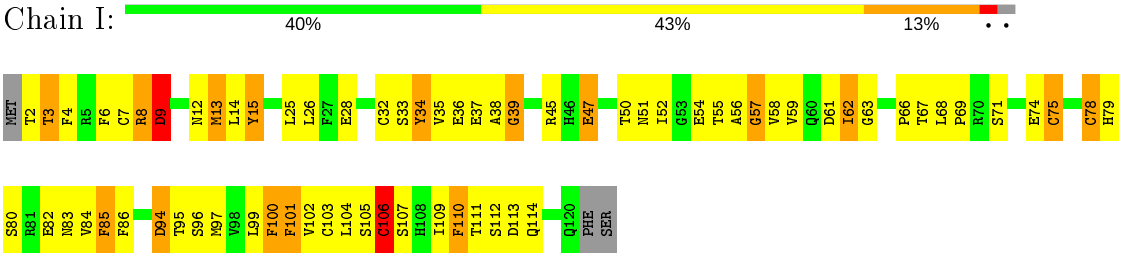
Chain H:





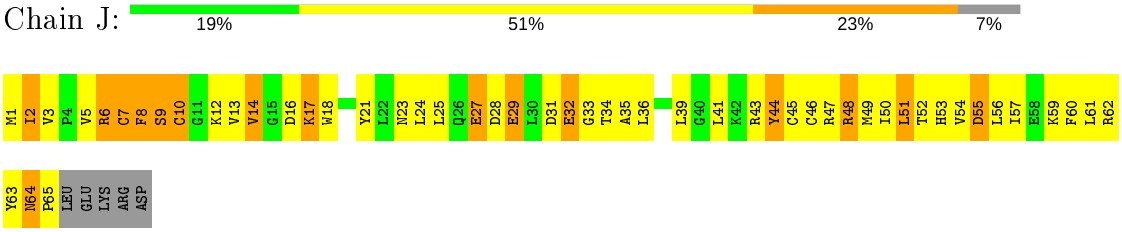
• Molecule 9: DNA-directed RNA polymerase II subunit 9

Chain I:



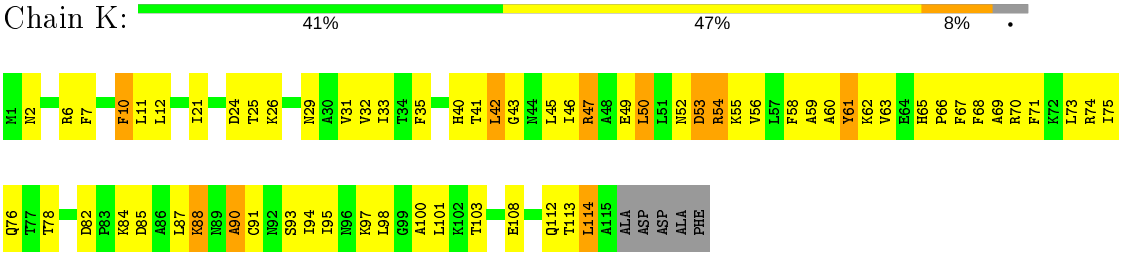
• Molecule 10: DNA-directed RNA polymerases I/II/III subunit 10

Chain J:



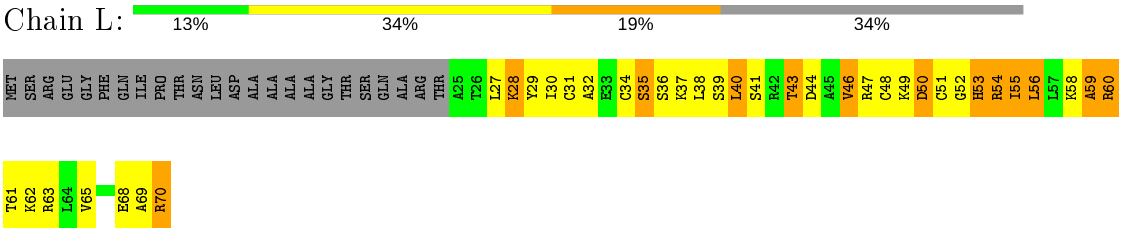
• Molecule 11: DNA-directed RNA polymerase II 13.6 kDa polypeptide

Chain K:



• Molecule 12: DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide

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	220.69Å 394.33Å 281.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	158.11 – 4.15 161.46 – 4.15	Depositor EDS
% Data completeness (in resolution range)	(Not available) (158.11-4.15) 83.4 (161.46-4.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.20 (at 4.15Å)	Xtriage
Refinement program		Depositor
R, R_{free}	0.387 , (Not available) 0.306 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	118.6	Xtriage
Anisotropy	0.584	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 156.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.023 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.023 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o,F_c correlation	0.82	EDS
Total number of atoms	31040	wwPDB-VP
Average B, all atoms (Å^2)	169.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.01% 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, 0.333 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: ZN

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	0.49	3/11339 (0.0%)	0.75	9/15334 (0.1%)
2	B	0.53	6/8971 (0.1%)	0.97	25/12103 (0.2%)
3	C	0.52	0/2133	0.76	0/2891
4	D	0.49	0/1382	0.81	3/1862 (0.2%)
5	E	0.44	0/1788	0.64	0/2406
6	F	0.53	0/691	0.78	0/933
7	G	0.53	0/1367	0.74	0/1844
8	H	0.40	0/1086	0.66	0/1470
9	I	0.83	1/989 (0.1%)	0.94	3/1331 (0.2%)
10	J	0.54	0/541	0.90	1/727 (0.1%)
11	K	0.50	0/938	0.68	0/1267
12	L	0.55	0/365	0.79	0/485
All	All	0.52	10/31590 (0.0%)	0.82	41/42653 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
2	B	1	10
3	C	0	1
9	I	0	1
All	All	1	14

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	I	39	GLY	C-N	-21.36	0.84	1.34
2	B	442	PHE	C-N	-8.69	1.14	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	446	LEU	N-CA	-8.12	1.30	1.46
2	B	439	ALA	C-N	7.40	1.51	1.34
1	A	1274	ARG	C-N	-6.45	1.21	1.33

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	475	SER	CB-CA-C	-51.20	12.82	110.10
9	I	39	GLY	O-C-N	-18.15	93.66	122.70
2	B	439	ALA	N-CA-CB	-16.49	87.01	110.10
2	B	442	PHE	C-N-CA	15.77	161.13	121.70
2	B	476	ARG	C-N-CA	-15.07	84.02	121.70

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	475	SER	CA

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	303	TYR	Sidechain
1	A	807	GLY	Mainchain
2	B	217	ARG	Mainchain
2	B	405	ARG	Mainchain
2	B	438	GLU	Peptide

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	A	11140	0	11218	1169	0
2	B	8800	0	8777	947	0
3	C	2095	0	2053	241	0
4	D	1373	0	1312	144	0
5	E	1752	0	1776	149	0
6	F	679	0	701	94	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	G	1339	0	1357	145	0
8	H	1068	0	1040	107	0
9	I	971	0	929	91	0
10	J	532	0	542	93	0
11	K	920	0	929	83	0
12	L	363	0	387	47	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
All	All	31040	0	31021	3039	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 49.

The worst 5 of 3039 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)
2:B:469:GLN:CA	2:B:474:SER:CB	1.80	1.51
4:D:119:ARG:N	4:D:121:LYS:HB2	1.46	1.30
4:D:113:PHE:CB	4:D:156:ASP:OD1	1.78	1.30
4:D:118:THR:HA	4:D:121:LYS:CB	1.64	1.27
2:B:435:THR:CG2	2:B:439:ALA:HB2	1.63	1.26

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
1	A	1406/1733 (81%)	949 (68%)	293 (21%)	164 (12%)	0 6
2	B	1096/1224 (90%)	744 (68%)	226 (21%)	126 (12%)	0 6
3	C	264/318 (83%)	159 (60%)	66 (25%)	39 (15%)	0 3
4	D	178/221 (80%)	124 (70%)	35 (20%)	19 (11%)	0 8
5	E	212/215 (99%)	147 (69%)	50 (24%)	15 (7%)	1 17
6	F	82/155 (53%)	64 (78%)	14 (17%)	4 (5%)	2 23
7	G	169/215 (79%)	131 (78%)	26 (15%)	12 (7%)	1 17
8	H	129/146 (88%)	84 (65%)	29 (22%)	16 (12%)	0 5
9	I	117/122 (96%)	79 (68%)	31 (26%)	7 (6%)	1 20
10	J	63/70 (90%)	37 (59%)	10 (16%)	16 (25%)	0 1
11	K	113/120 (94%)	89 (79%)	18 (16%)	6 (5%)	2 22
12	L	44/70 (63%)	19 (43%)	14 (32%)	11 (25%)	0 1
All	All	3873/4609 (84%)	2626 (68%)	812 (21%)	435 (11%)	0 7

5 of 435 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	48	ALA
1	A	54	ASN
1	A	55	ASP
1	A	57	ARG

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
1	A	1239/1520 (82%)	1135 (92%)	104 (8%)	11 36
2	B	952/1061 (90%)	865 (91%)	87 (9%)	9 32
3	C	234/274 (85%)	212 (91%)	22 (9%)	8 30
4	D	138/200 (69%)	122 (88%)	16 (12%)	5 24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
5	E	196/197 (100%)	187 (95%)	9 (5%)	27 53
6	F	74/137 (54%)	65 (88%)	9 (12%)	5 22
7	G	152/190 (80%)	142 (93%)	10 (7%)	16 43
8	H	117/128 (91%)	111 (95%)	6 (5%)	24 51
9	I	113/116 (97%)	99 (88%)	14 (12%)	4 22
10	J	60/65 (92%)	54 (90%)	6 (10%)	7 28
11	K	99/102 (97%)	92 (93%)	7 (7%)	14 41
12	L	40/57 (70%)	37 (92%)	3 (8%)	13 40
All	All	3414/4047 (84%)	3121 (91%)	293 (9%)	10 35

5 of 293 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	466	TRP
2	B	956	THR
9	I	85	PHE
2	B	516	ASN
2	B	682	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 77 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	60	GLN
2	B	518	HIS
9	I	12	ASN
2	B	121	ASN
2	B	366	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 8 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	1
1	A	1
9	I	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	807:GLY	C	808:LEU	N	1.20
1	B	442:PHE	C	443:ASN	N	1.14
1	I	39:GLY	C	40:SER	N	0.84

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.