



wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 08:32 am BST

PDB ID : 5UAG
Title : Escherichia coli RNA polymerase mutant - RpoB D516V
Authors : Molodtsov, V.; Scharf, N.T.; Stefan, M.A.; Garcia, G.A.; Murakami, K.S.
Deposited on : 2016-12-19
Resolution : 3.40 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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

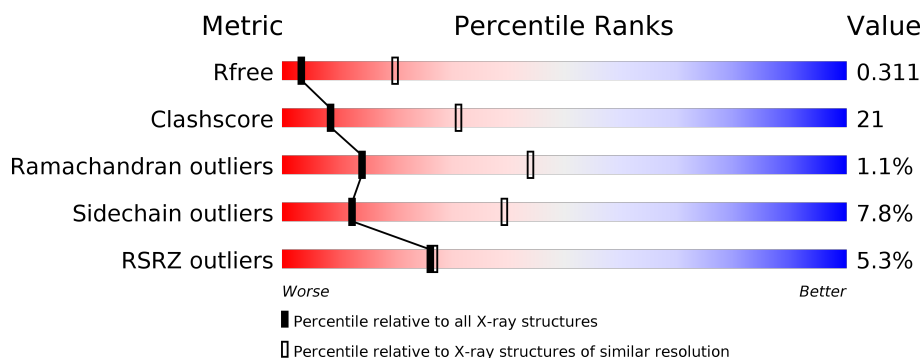
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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 $\leq 5\%$. 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	320	<div> <div>7%</div> <div>39%</div> <div>30%</div> <div>27%</div> </div>
1	B	320	<div> <div>7%</div> <div>32%</div> <div>32%</div> <div>32%</div> </div>
1	G	320	<div> <div>3%</div> <div>36%</div> <div>30%</div> <div>29%</div> </div>
1	H	320	<div> <div>7%</div> <div>33%</div> <div>32%</div> <div>33%</div> </div>
2	C	1342	<div> <div>4%</div> <div>57%</div> <div>39%</div> </div>
2	I	1342	<div> <div>7%</div> <div>58%</div> <div>38%</div> </div>

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Mol	Chain	Length	Quality of chain
3	D	1407	<div><div><div></div><div></div><div></div><div></div></div><div>2%47%31%17%</div></div>
3	J	1407	<div><div><div></div><div></div><div></div><div></div></div><div>4%45%33%18%</div></div>
4	E	90	<div><div><div></div><div></div><div></div><div></div></div><div>3%60%30%9%</div></div>
4	K	90	<div><div><div></div><div></div><div></div><div></div></div><div>22%54%27%7%12%</div></div>
5	F	613	<div><div><div></div><div></div><div></div><div></div></div><div>4%45%28%24%</div></div>
5	L	613	<div><div><div></div><div></div><div></div><div></div></div><div>4%45%28%23%</div></div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 55066 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 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	233	Total	C	N	O	S	0	0	0
			1812	1127	323	356	6			
1	B	217	Total	C	N	O	S	0	0	0
			1677	1047	295	329	6			
1	G	227	Total	C	N	O	S	0	0	0
			1755	1093	311	345	6			
1	H	216	Total	C	N	O	S	0	0	0
			1662	1038	292	326	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1340	Total	C	N	O	S	0	0	0
			10569	6632	1841	2053	43			
2	I	1340	Total	C	N	O	S	0	0	0
			10565	6630	1840	2052	43			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	516	VAL	ASP	engineered mutation	UNP P0A8V2
I	516	VAL	ASP	engineered mutation	UNP P0A8V2

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1167	Total	C	N	O	S	0	0	0
			9065	5700	1622	1697	46			
3	J	1155	Total	C	N	O	S	0	0	0
			9001	5659	1612	1684	46			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	89	Total	C	N	O	S	0	0	0
			691	421	129	140	1			
4	K	79	Total	C	N	O	S	0	0	0
			627	382	118	126	1			

- Molecule 5 is a protein called RNA polymerase sigma factor RpoD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	468	Total	C	N	O	S	0	0	0
			3813	2389	678	723	23			
5	L	469	Total	C	N	O	S	0	0	0
			3821	2393	679	726	23			

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	J	1	Total	Mg	0	0
			1	1		
6	I	1	Total	Mg	0	0
			1	1		
6	D	2	Total	Mg	0	0
			2	2		

- Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

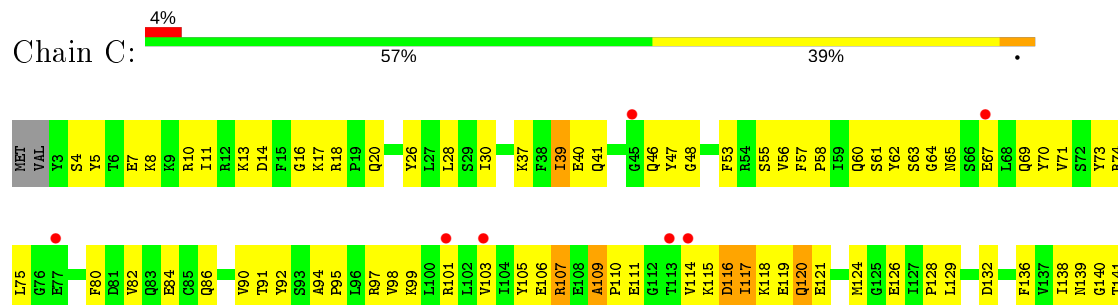
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	J	2	Total	Zn	0	0
			2	2		
7	D	2	Total	Zn	0	0
			2	2		

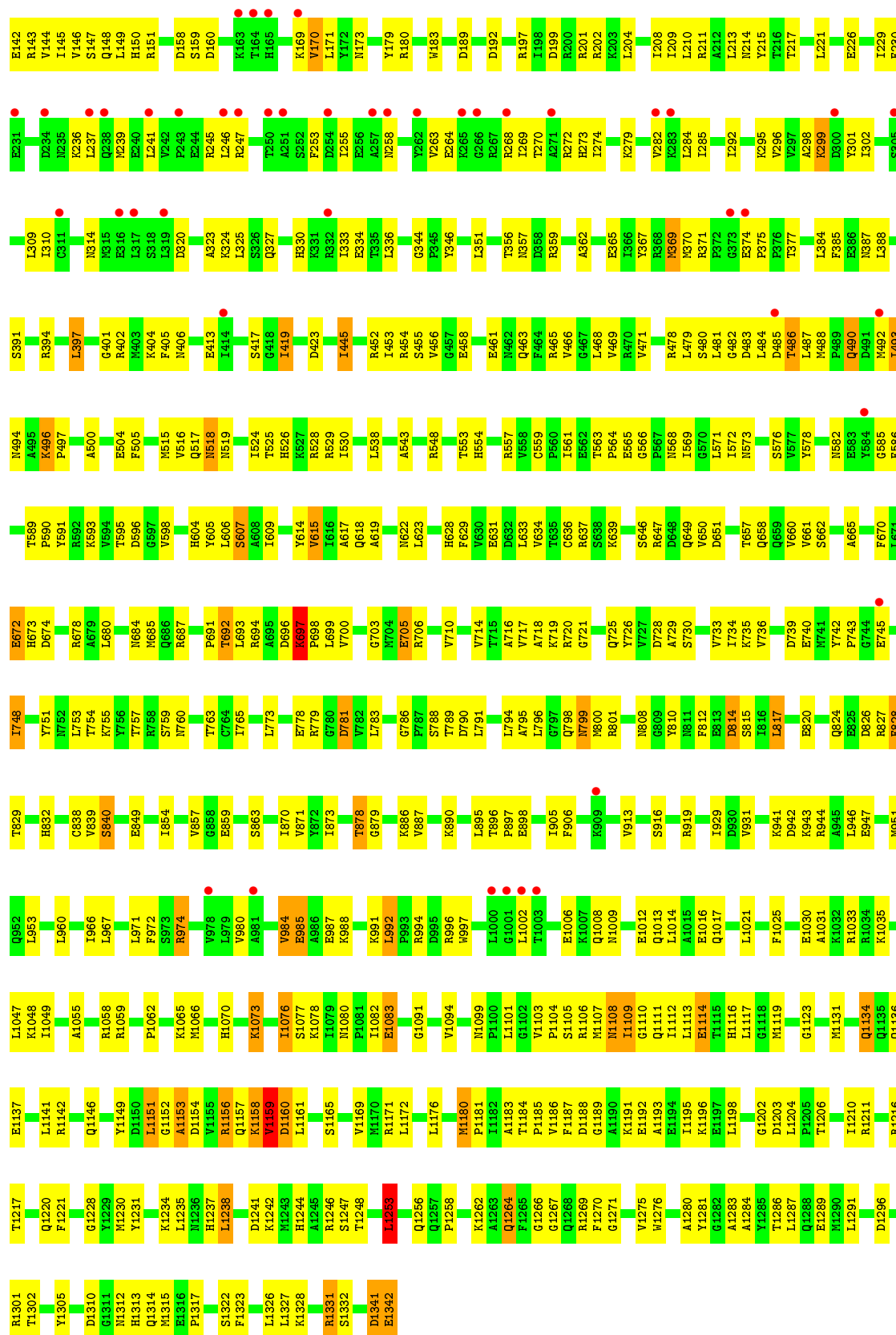
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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 ($\text{RSRZ} > 2$). 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.

- Chain A:
-

- Chain B:
-
- 7% 32% 32% 32%
- MET GLN GLY SER VAL T6 E7 F8 L9 K10 P11 R12 L13 V14 D15 I16 F17 Q18 V19 S20 S21 T22 H23 A24 K25 V26 T27 L28 E29 P30 L31 E32 R33 G34 F35 G36 H37 T38 L39 G40 N41 R44 R45 I46 L47 L48 S49 S50 G53 C54 A55 V56 T57 E58 V59 E60 I61 R62

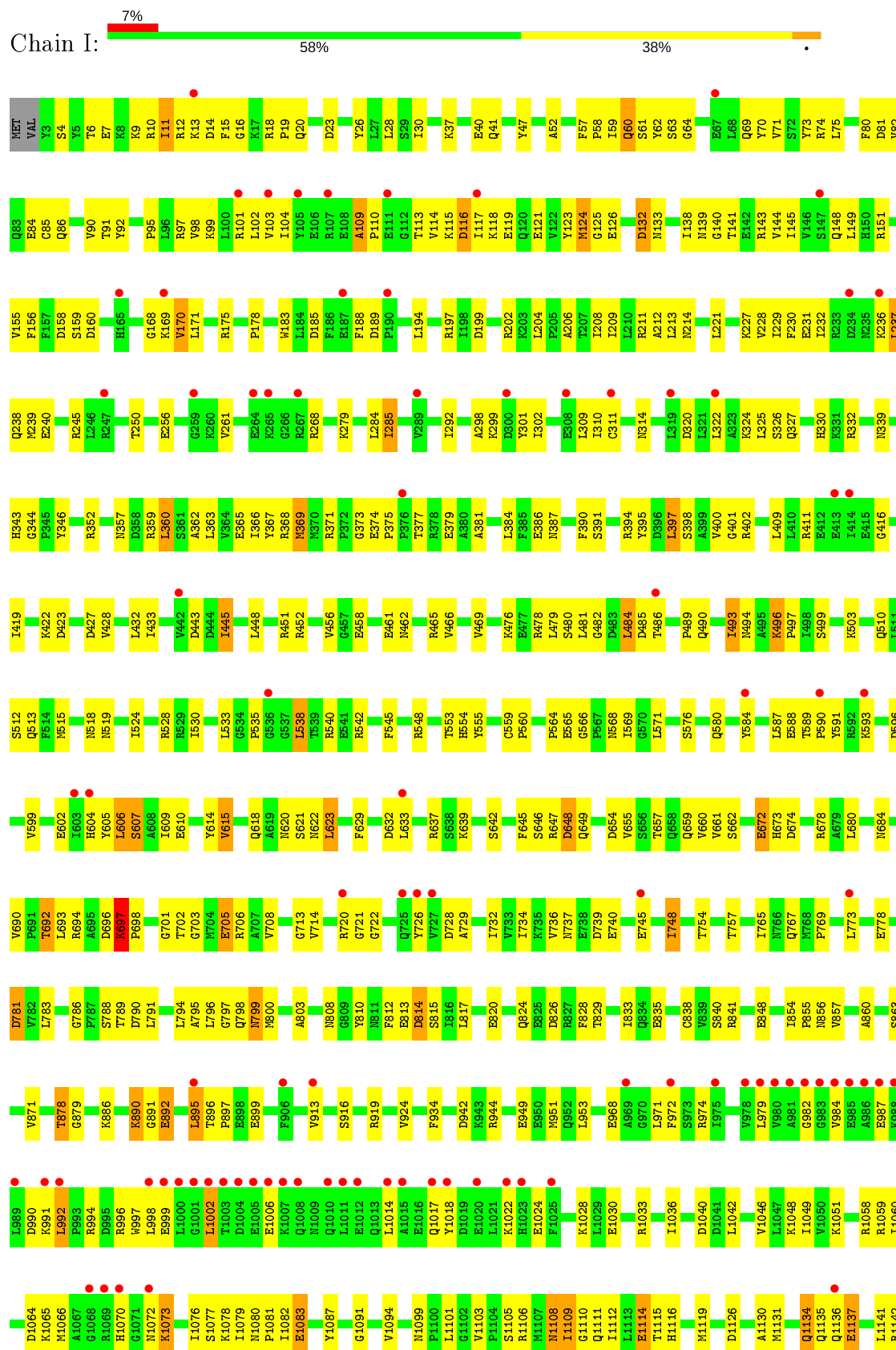
Chain G:

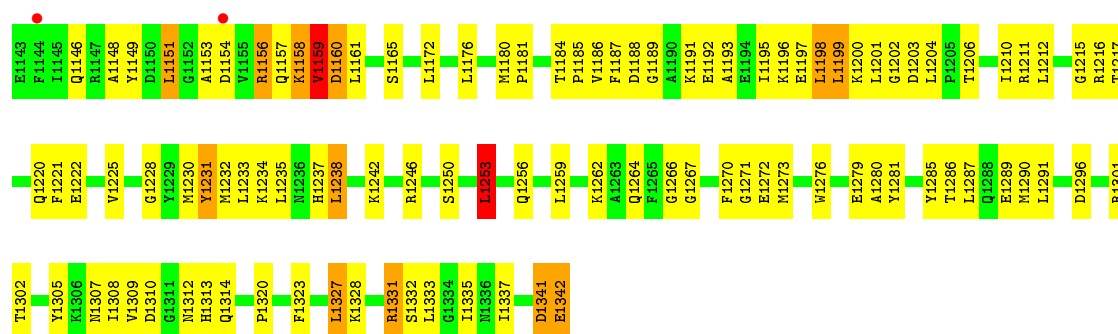




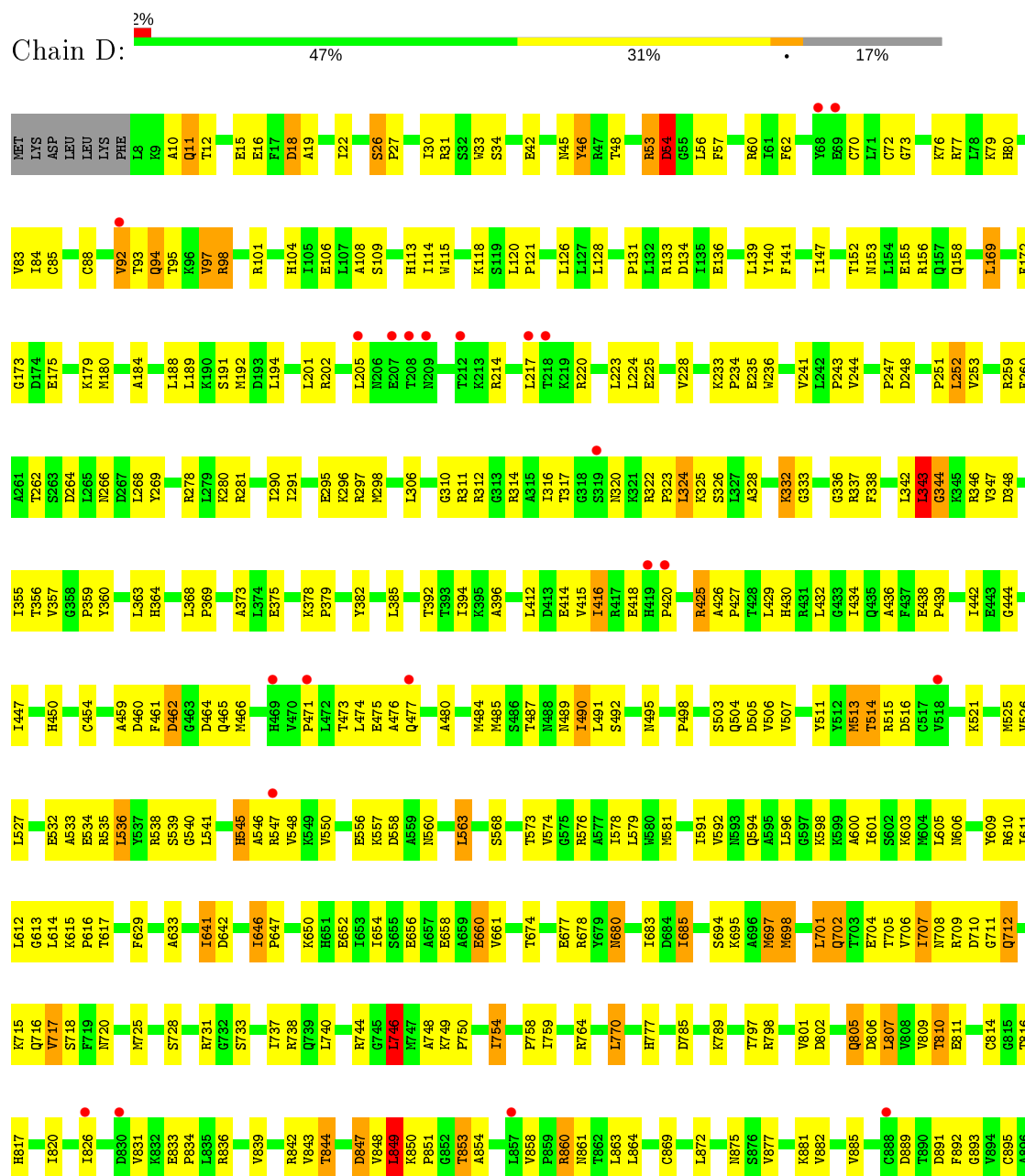
- Molecule 2: DNA-directed RNA polymerase subunit beta

Chain I:

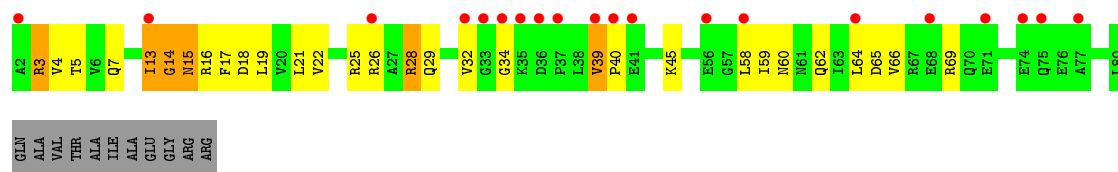




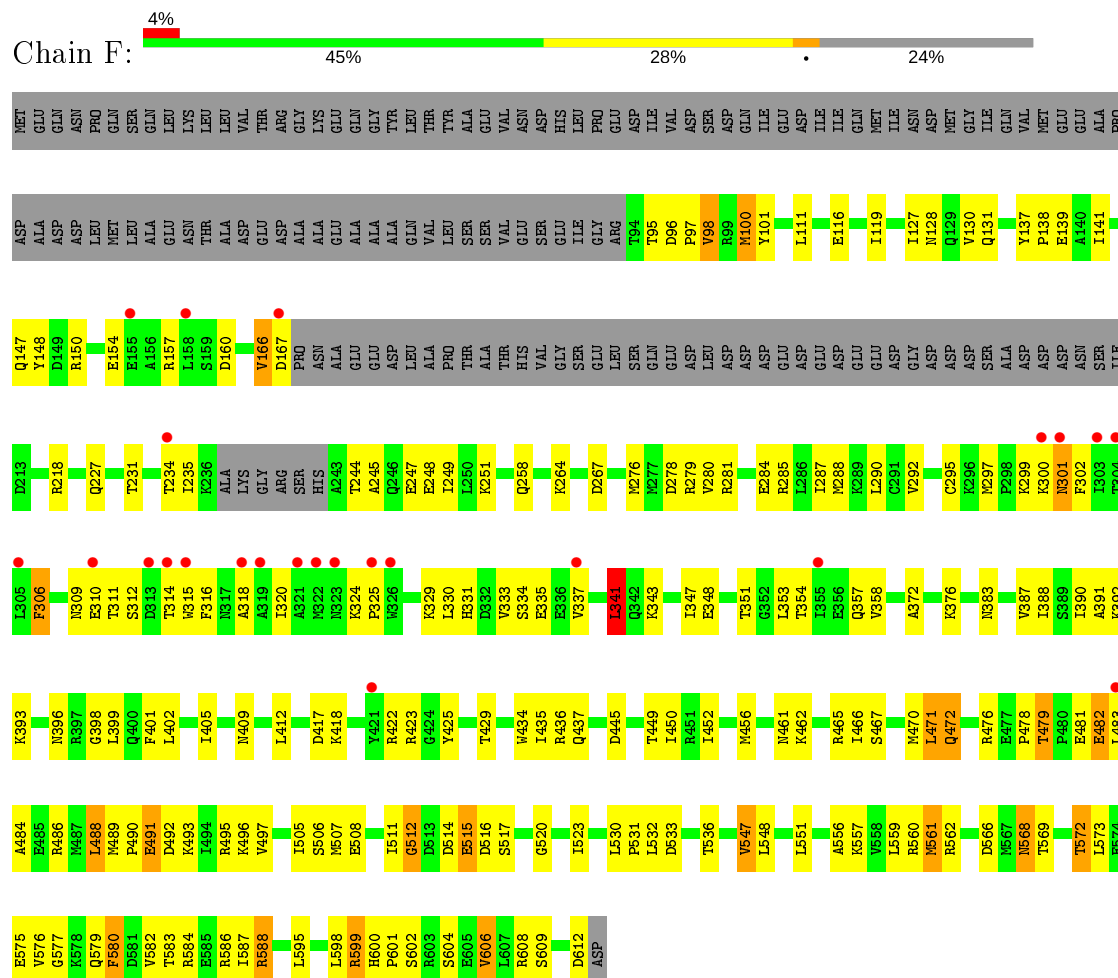
• Molecule 3: DNA-directed RNA polymerase subunit beta'



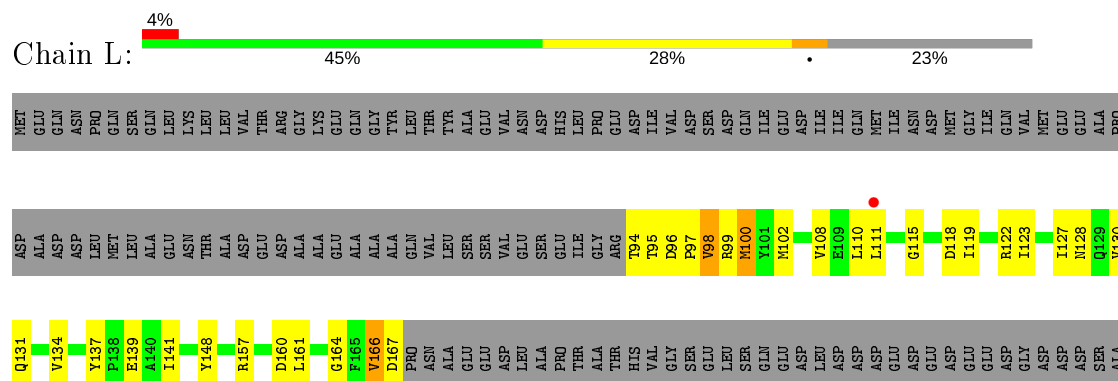




• Molecule 5: RNA polymerase sigma factor RpoD



• Molecule 5: RNA polymerase sigma factor RpoD



M567	M568	T569	D570	Y571	T572	L573	E574	E575	V576	G577	F580	D581	V582	T583	R584	I587	R596	K597	L598	R599	H600	P601	S602	R603	S604	E605	V606	L607	D612	D613																															
P478	T479	P480	E481	E482	L483	A484	E485	R486	M487	L488	M489	P490	E491	D492		R495	K499	I500		I505	S506	N507	E508		T511	G512	D513	D514	E515	D516	S517	G520	E524	D525	L530	P531	L532	D533	T536	T544	V547	L551	K557	V558	L559	R560	M561	R562		D566											
A375	K376		V380	E381		V387	I388	S389	I390	A391	K392	K393	T394	T395	I396		L399	Q400	F401	L402		Q406		I409		V416	D417		F420	Y421	R422	R423	Q424	Y425		T429		I435		D445		T449	I450	R451	I452		N461	K462		R465	I466	S467	R468	Q469	N470	L471		R476	E477		
K289	L290		E293		K299	K300	N301	F302		F306		N309	E310	T311	S312	D313	T314	W315		F316	N317	A318	A319	I320	A321	N322	N323	K324	P325		E328		E335	E336	V337	H338	R339	A340	L341	Q342	K343	L344	Q345		E348		T351		T354		V358		N362		E369	A370	K371	A372	R373	R374	
ASP	ASP	ASP	ASN	SER	ILE	D213		R218		Q227		T231		K236	ALA	LYS	GLY	ARG	SER	HIS		A243	T244		E247	E248	I249	L250	K251	L252	S253	E254		Q258	F259	R260	L261	V262	P263	K264	Q265	F266	D267		V270		M273	R274	V275	M276	M277	D278	R279	V280		R281		R285	L286	I287	M288

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	184.83Å 205.04Å 307.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.99 – 3.40 29.99 – 3.40	Depositor EDS
% Data completeness (in resolution range)	89.0 (29.99-3.40) 89.0 (29.99-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 3.39Å)	Xtriage
Refinement program	PHENIX (1.10.1 _2155: ???)	Depositor
R, R_{free}	0.277 , 0.311 0.277 , 0.311	Depositor DCC
R_{free} test set	1977 reflections (1.38%)	wwPDB-VP
Wilson B-factor (Å ²)	135.9	Xtriage
Anisotropy	0.254	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 85.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	55066	wwPDB-VP
Average B, all atoms (Å ²)	163.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.84% 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: 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	0.46	1/1834 (0.1%)	0.85	0/2485
1	B	0.45	0/1697	1.00	3/2300 (0.1%)
1	G	0.52	1/1777 (0.1%)	0.93	5/2408 (0.2%)
1	H	0.44	0/1681	0.98	3/2278 (0.1%)
2	C	0.44	0/10738	0.83	7/14488 (0.0%)
2	I	0.42	1/10734 (0.0%)	0.81	12/14483 (0.1%)
3	D	0.45	0/9205	0.84	12/12430 (0.1%)
3	J	0.45	0/9140	0.88	22/12341 (0.2%)
4	E	0.43	0/693	0.76	1/935 (0.1%)
4	K	0.43	0/629	0.81	2/847 (0.2%)
5	F	0.42	0/3864	0.83	5/5194 (0.1%)
5	L	0.43	0/3872	0.83	3/5205 (0.1%)
All	All	0.44	3/55864 (0.0%)	0.85	75/75394 (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	G	0	1
2	C	0	4
2	I	0	2
3	D	0	2
3	J	0	3
4	E	0	1
5	L	0	1
All	All	0	14

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	29	GLU	C-N	9.36	1.52	1.34
2	I	373	GLY	C-N	7.20	1.50	1.34
1	A	29	GLU	C-N	6.31	1.46	1.34

The worst 5 of 75 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	425	ARG	NE-CZ-NH2	14.52	127.56	120.30
3	J	425	ARG	NE-CZ-NH1	-13.50	113.55	120.30
3	J	343	LEU	CB-CG-CD1	-11.67	91.16	111.00
1	G	12	ARG	NE-CZ-NH1	-10.66	114.97	120.30
3	D	343	LEU	CB-CG-CD2	-10.37	93.37	111.00

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	109	ALA	Peptide
2	C	236	LYS	Peptide
2	C	658	GLN	Sidechain
2	C	985	GLU	Mainchain
3	D	1184	ASP	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	1812	0	1839	111	0
1	B	1677	0	1703	127	0
1	G	1755	0	1773	105	0
1	H	1662	0	1687	111	0
2	C	10569	0	10587	439	0
2	I	10565	0	10581	437	0
3	D	9065	0	9210	430	0
3	J	9001	0	9165	461	0
4	E	691	0	695	26	0
4	K	627	0	634	26	0
5	F	3813	0	3880	150	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	L	3821	0	3884	149	0
6	D	2	0	0	0	0
6	I	1	0	0	0	0
6	J	1	0	0	0	0
7	D	2	0	0	0	0
7	J	2	0	0	0	0
All	All	55066	0	55638	2292	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 21.

The worst 5 of 2292 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:I:1271:GLY:HA2	3:J:343:LEU:HD11	1.25	1.18
2:C:1269:ARG:HG2	3:D:343:LEU:HD12	1.24	1.11
2:C:696:ASP:HB2	2:C:798:GLN:HG2	1.35	1.08
3:D:1167:LYS:HZ3	3:D:1170:LYS:HB2	1.18	1.06
3:J:54:ASP:OD2	3:J:60:ARG:NH1	1.89	1.03

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	231/320 (72%)	201 (87%)	25 (11%)	5 (2%)	6	29
1	B	213/320 (67%)	186 (87%)	24 (11%)	3 (1%)	11	37
1	G	225/320 (70%)	193 (86%)	26 (12%)	6 (3%)	5	26
1	H	212/320 (66%)	189 (89%)	19 (9%)	4 (2%)	8	31
2	C	1338/1342 (100%)	1229 (92%)	99 (7%)	10 (1%)	22	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	I	1338/1342 (100%)	1227 (92%)	100 (8%)	11 (1%)	19	51
3	D	1163/1407 (83%)	1067 (92%)	86 (7%)	10 (1%)	17	49
3	J	1151/1407 (82%)	1054 (92%)	81 (7%)	16 (1%)	11	37
4	E	87/90 (97%)	82 (94%)	5 (6%)	0	100	100
4	K	77/90 (86%)	72 (94%)	3 (4%)	2 (3%)	5	26
5	F	462/613 (75%)	421 (91%)	36 (8%)	5 (1%)	14	44
5	L	463/613 (76%)	422 (91%)	39 (8%)	2 (0%)	34	67
All	All	6960/8184 (85%)	6343 (91%)	543 (8%)	74 (1%)	14	44

5 of 74 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	136	GLU
1	A	232	VAL
2	C	170	VAL
2	C	484	LEU
2	C	1137	GLU

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	201/279 (72%)	192 (96%)	9 (4%)	27	58
1	B	186/279 (67%)	173 (93%)	13 (7%)	15	44
1	G	193/279 (69%)	182 (94%)	11 (6%)	20	50
1	H	183/279 (66%)	172 (94%)	11 (6%)	19	49
2	C	1155/1157 (100%)	1066 (92%)	89 (8%)	13	40
2	I	1154/1157 (100%)	1063 (92%)	91 (8%)	12	39
3	D	962/1168 (82%)	885 (92%)	77 (8%)	12	38
3	J	960/1168 (82%)	881 (92%)	79 (8%)	11	37
4	E	72/74 (97%)	64 (89%)	8 (11%)	6	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	K	67/74 (90%)	63 (94%)	4 (6%)	19	49
5	F	417/540 (77%)	381 (91%)	36 (9%)	10	35
5	L	418/540 (77%)	382 (91%)	36 (9%)	10	35
All	All	5968/6994 (85%)	5504 (92%)	464 (8%)	12	39

5 of 464 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	F	429	THR
2	I	116	ASP
5	L	98	VAL
5	F	476	ARG
1	G	50	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 89 such sidechains are listed below:

Mol	Chain	Res	Type
5	F	147	GLN
1	H	128	HIS
5	L	301	ASN
5	F	227	GLN
5	F	455	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 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

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, 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	233/320 (72%)	-0.03	4 (1%) 70 68	105, 144, 198, 236	0
1	B	217/320 (67%)	0.49	23 (10%) 6 7	121, 192, 243, 265	0
1	G	227/320 (70%)	0.25	10 (4%) 34 34	162, 195, 234, 271	0
1	H	216/320 (67%)	0.61	23 (10%) 6 7	175, 215, 240, 264	0
2	C	1340/1342 (99%)	0.07	52 (3%) 39 38	78, 133, 242, 297	0
2	I	1340/1342 (99%)	0.33	93 (6%) 16 18	104, 171, 269, 334	0
3	D	1167/1407 (82%)	0.09	32 (2%) 54 53	83, 120, 204, 261	0
3	J	1155/1407 (82%)	0.24	60 (5%) 27 27	99, 146, 228, 277	0
4	E	89/90 (98%)	-0.03	3 (3%) 45 44	118, 156, 179, 198	0
4	K	79/90 (87%)	1.24	20 (25%) 0 0	211, 251, 298, 305	0
5	F	468/613 (76%)	0.17	24 (5%) 28 28	115, 167, 295, 326	0
5	L	469/613 (76%)	0.20	25 (5%) 26 27	130, 181, 301, 320	0
All	All	7000/8184 (85%)	0.21	369 (5%) 26 27	78, 156, 252, 334	0

The worst 5 of 369 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	I	982	GLY	7.7
2	C	319	LEU	7.0
2	I	1005	GLU	6.7
2	I	1000	LEU	6.6
2	I	999	GLU	6.5

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. 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(\AA^2)	Q<0.9
7	ZN	D	2003	1/1	0.70	0.20	189,189,189,189	0
6	MG	D	2001	1/1	0.71	0.27	189,189,189,189	0
7	ZN	D	2004	1/1	0.74	0.29	189,189,189,189	0
6	MG	D	2002	1/1	0.78	0.29	189,189,189,189	0
6	MG	J	2001	1/1	0.85	0.29	189,189,189,189	0
6	MG	I	1401	1/1	0.85	0.30	189,189,189,189	0
7	ZN	J	2003	1/1	0.88	0.22	189,189,189,189	0
7	ZN	J	2002	1/1	0.94	0.13	310,310,310,310	0

6.5 Other polymers [i](#)

There are no such residues in this entry.