



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 14, 2016 – 07:22 PM EST

PDB ID : 5TMF
Title : Re-refinement of thermus thermophilus RNA polymerase
Authors : Wang, J.
Deposited on : 2016-10-12
Resolution : 3.00 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028320
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) : rb-20028320

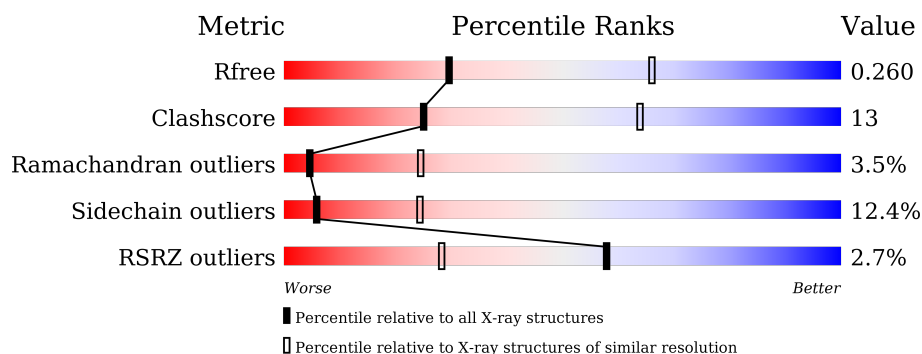
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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 $\leq 5\%$. 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	315	<div> <div>2%</div> <div> <div></div> <div>53%</div> <div>18%</div> <div>•</div> <div>27%</div> </div> </div>
1	B	315	<div> <div>2%</div> <div> <div></div> <div>52%</div> <div>22%</div> <div>•</div> <div>24%</div> </div> </div>
2	C	1119	<div> <div>2%</div> <div> <div></div> <div>63%</div> <div>29%</div> <div>7%</div> <div>•</div> </div> </div>
3	D	1524	<div> <div>4%</div> <div> <div></div> <div>65%</div> <div>29%</div> <div>5%</div> <div>•</div> </div> </div>
4	E	99	<div> <div></div> <div> <div></div> <div>72%</div> <div>18%</div> <div>5%</div> <div>•</div> </div> </div>
5	F	423	<div> <div>2%</div> <div> <div></div> <div>59%</div> <div>21%</div> <div>•</div> <div>17%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	PO4	A	401	-	-	-	X
6	PO4	D	1603	-	-	-	X
7	NE6	C	1201	X	-	-	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 28078 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	231	Total	C	N	O	S	0	0	0
			1816	1159	315	339	3			
1	B	238	Total	C	N	O	S	0	0	0
			1863	1188	322	350	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1119	Total	C	N	O	S	0	0	0
			8829	5581	1577	1647	24			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1504	Total	C	N	O	S	0	0	0
			11864	7518	2091	2219	36			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	95	Total	C	N	O	S	0	0	0
			769	488	133	144	4			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	61	GLU	VAL	conflict	UNP Q72ID6
E	92	ILE	LEU	conflict	UNP Q72ID6
E	95	GLY	VAL	conflict	UNP Q72ID6

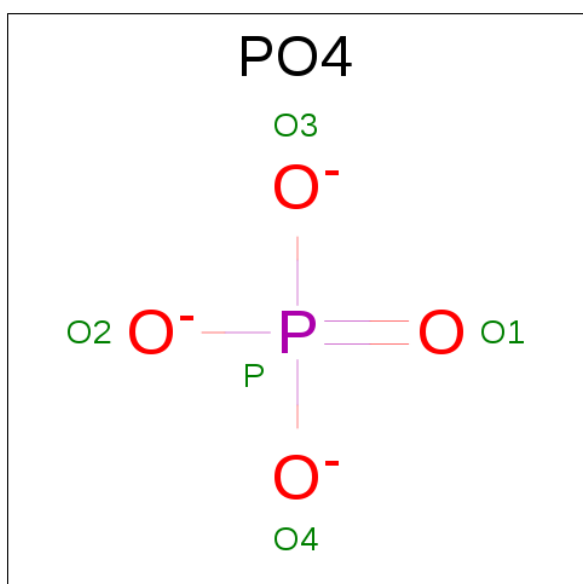
- Molecule 5 is a protein called RNA polymerase sigma factor SigA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	351	Total	C	N	O	S	0	0	0
			2844	1794	515	531	4			

There is a discrepancy between the modelled and reference sequences:

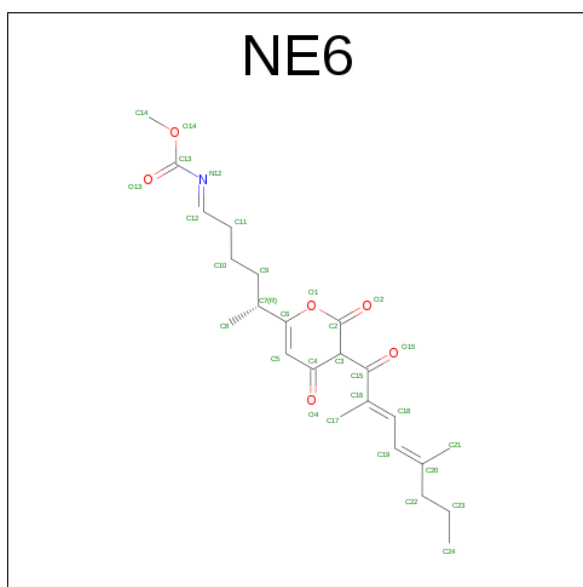
Chain	Residue	Modelled	Actual	Comment	Reference
F	46	THR	ALA	conflict	UNP Q72L95

- Molecule 6 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	P	0	0
			5	4	1		
6	D	1	Total	O	P	0	0
			5	4	1		

- Molecule 7 is methyl [(1E,5R)-5-{(3S)-3-[(2E,4E)-2,5-dimethylocta-2,4-dienoyl]-2,4-dioxo-3,4-dihydro-2H-pyran-6-yl}hexylidene]carbamate (three-letter code: NE6) (formula: C₂₃H₃₁NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	C	1	Total	C	N	O	0	0
			30	23	1	6		

- Molecule 8 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	D	2	Total	Zn	0	0
			2	2		

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	D	2	Total	Mg	0	0
			2	2		

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	2	Total	O	0	0
			2	2		
10	B	3	Total	O	0	0
			3	3		
10	C	23	Total	O	0	0
			23	23		
10	D	20	Total	O	0	0
			20	20		

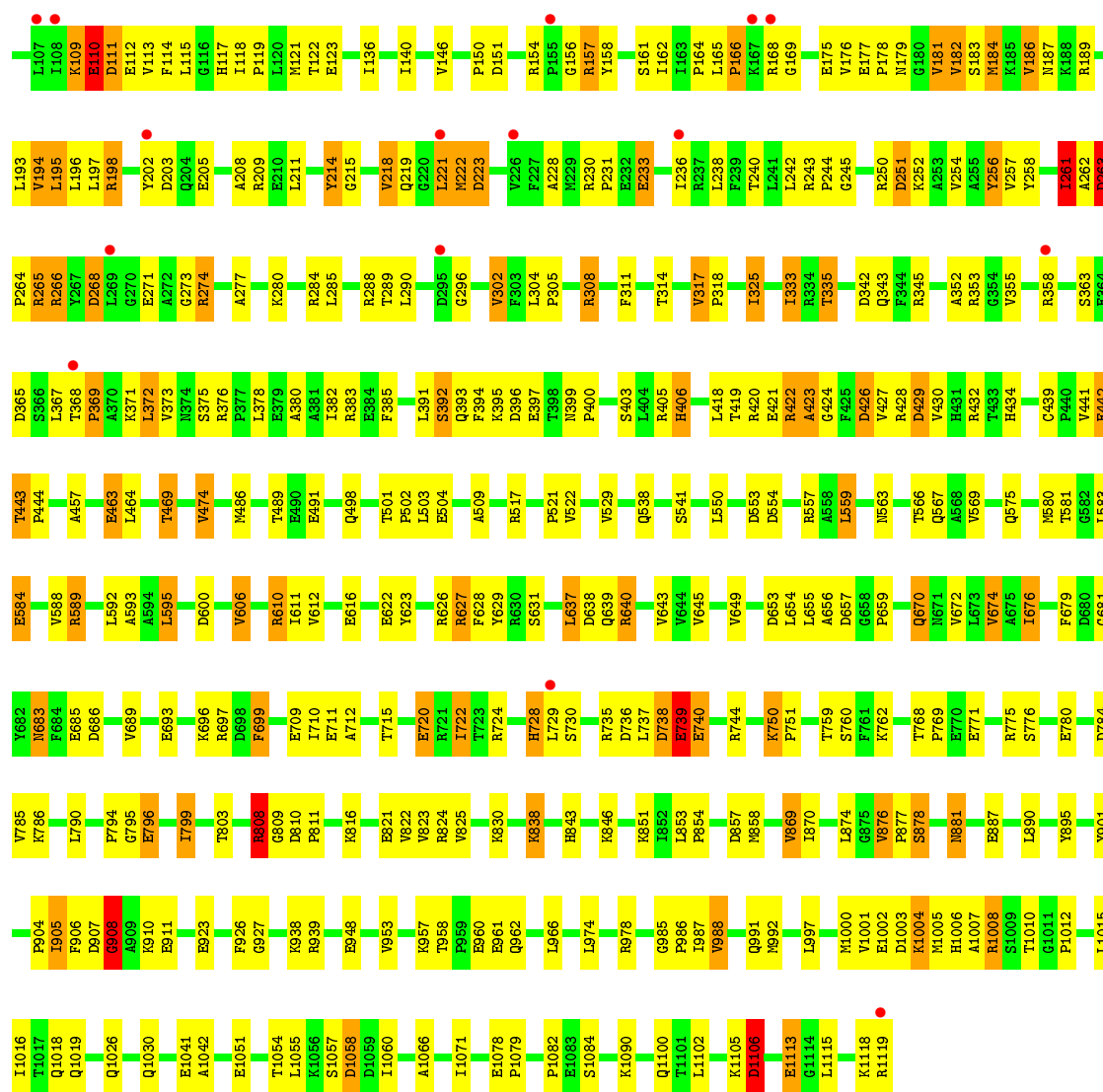
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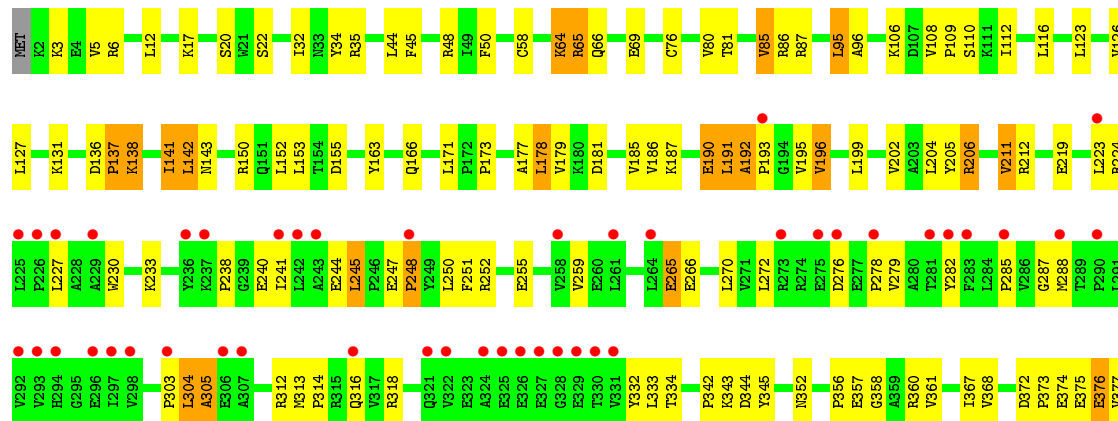
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	F	1	Total	O	0	0
			1	1		

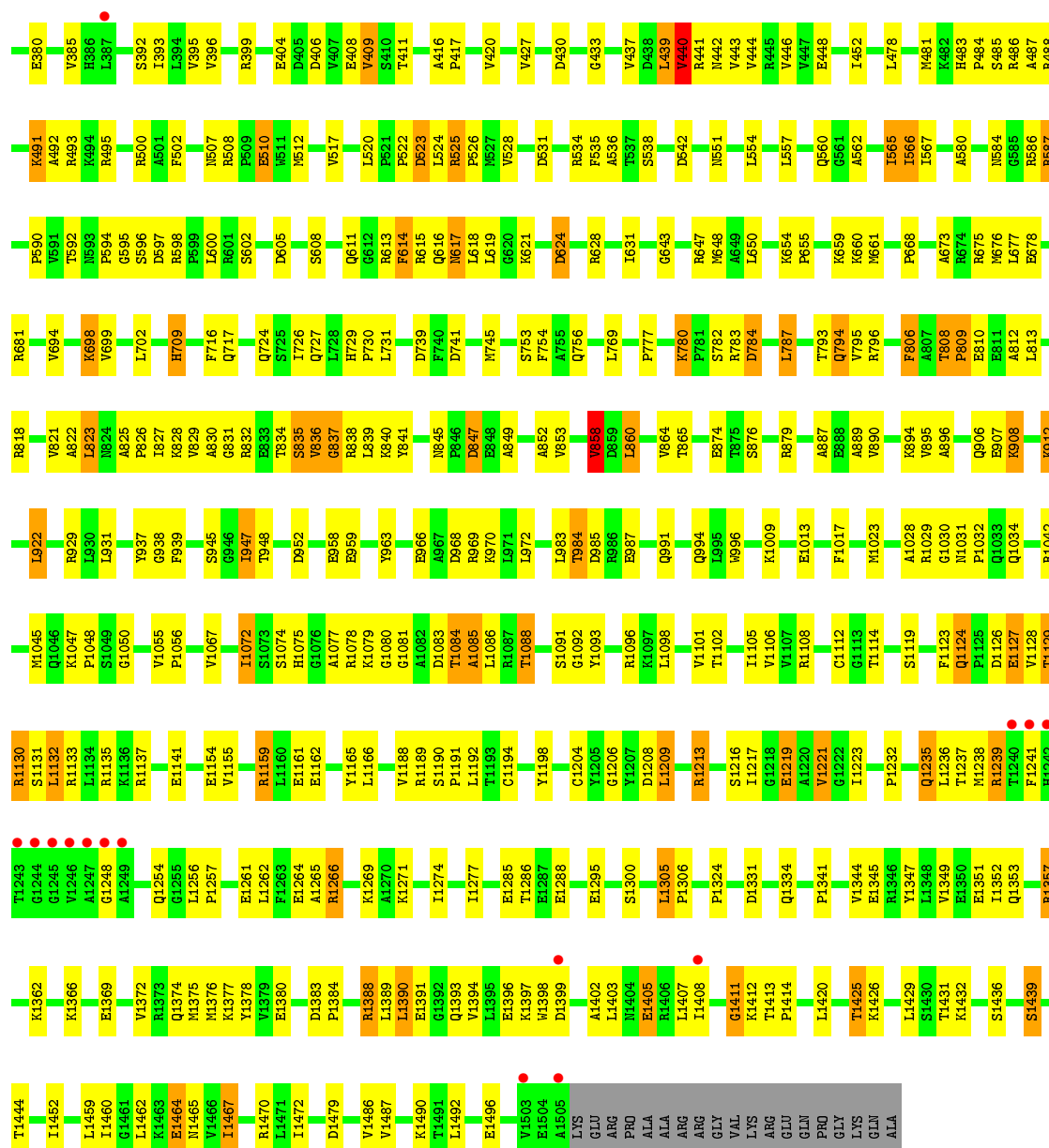
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

- Chain C:
-
- | Amino Acid | Category |
|------------|----------|
| M1 | Red |
| E2 | Red |
| I3 | Red |
| K4 | Red |
| R5 | Red |
| F6 | Red |
| G7 | Red |
| G8 | Red |
| L15 | Green |
| P16 | Green |
| P17 | Green |
| E20 | Green |
| I21 | Green |
| I21 | Green |
| Q22 | Green |
| V23 | Green |
| E24 | Green |
| S25 | Green |
| Y26 | Green |
| D83 | Orange |
| E37 | Orange |
| K38 | Orange |
| R39 | Orange |
| V42 | Orange |
| G43 | Orange |
| I54 | Yellow |
| E55 | Yellow |
| K59 | Yellow |
| G60 | Yellow |
| I66 | Yellow |
| L69 | Yellow |
| E70 | Yellow |
| Y71 | Yellow |
| W72 | Yellow |
| L73 | Yellow |
| G74 | Yellow |
| P79 | Yellow |
| Q91 | Orange |
| A92 | Orange |
| P93 | Orange |
| L94 | Orange |
| Y95 | Orange |
| L98 | Orange |
| Q99 | Orange |
| L100 | Orange |
| H101 | Orange |
| H102 | Orange |
| K103 | Orange |
| Y104 | Orange |



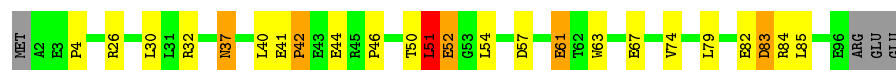
• Molecule 3: DNA-directed RNA polymerase subunit beta'





• Molecule 4: DNA-directed RNA polymerase subunit omega

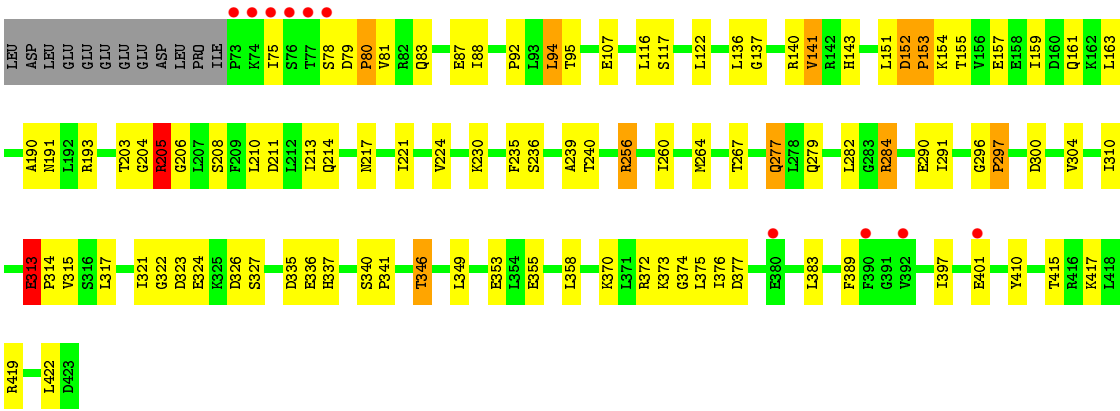
Chain E: 72% 18% 5%



• Molecule 5: RNA polymerase sigma factor SigA

Chain F: 59% 21% 17%





4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	235.09 Å 235.09 Å 250.88 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.80 – 3.00 46.80 – 3.00	Depositor EDS
% Data completeness (in resolution range)	95.8 (46.80-3.00) 96.0 (46.80-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 3.01 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.203 , 0.234 0.207 , 0.260	Depositor DCC
R_{free} test set	1177 reflections (0.79%)	DCC
Wilson B-factor (Å ²)	83.9	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 63.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.048 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.956 for H, K, L 0.044 for -H-K, K, -L	Depositor
Outliers	0 of 150767 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	28078	wwPDB-VP
Average B, all atoms (Å ²)	129.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.60% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NE6, PO4, MG, 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	0.44	0/1848	0.62	0/2512
1	B	0.42	0/1896	0.59	0/2579
2	C	0.47	0/8997	0.66	1/12164 (0.0%)
3	D	0.48	0/12073	0.66	3/16324 (0.0%)
4	E	0.46	0/783	0.63	1/1054 (0.1%)
5	F	0.42	0/2890	0.62	1/3888 (0.0%)
All	All	0.46	0/28487	0.65	6/38521 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	51	LEU	CA-CB-CG	5.89	128.85	115.30
3	D	837	GLY	N-CA-C	-5.79	98.63	113.10
3	D	95	LEU	CA-CB-CG	5.68	128.36	115.30
3	D	618	LEU	CA-CB-CG	5.51	127.98	115.30
5	F	313	GLU	C-N-CD	-5.11	109.37	120.60

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	A	1816	0	1871	41	0
1	B	1863	0	1914	41	0
2	C	8829	0	8933	275	0
3	D	11864	0	12094	339	0
4	E	769	0	775	15	0
5	F	2844	0	2926	56	0
6	A	5	0	0	0	0
6	D	5	0	0	0	0
7	C	30	0	30	5	0
8	D	2	0	0	0	0
9	D	2	0	0	0	0
10	A	2	0	0	0	0
10	B	3	0	0	0	0
10	C	23	0	0	3	0
10	D	20	0	0	4	0
10	F	1	0	0	1	0
All	All	28078	0	28543	717	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 13.

The worst 5 of 717 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)
3:D:1265:ALA:HA	3:D:1266:ARG:CB	1.72	1.19
3:D:613:ARG:HB3	3:D:614:PHE:HA	1.21	1.18
2:C:93:PRO:HA	2:C:117:HIS:HB2	1.31	1.06
2:C:93:PRO:HA	2:C:117:HIS:CB	1.85	1.06
3:D:1085:ALA:HA	3:D:1088:THR:HG22	1.39	1.04

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	229/315 (73%)	211 (92%)	17 (7%)	1 (0%)	39	80
1	B	236/315 (75%)	218 (92%)	16 (7%)	2 (1%)	24	66
2	C	1117/1119 (100%)	928 (83%)	151 (14%)	38 (3%)	5	25
3	D	1502/1524 (99%)	1228 (82%)	208 (14%)	66 (4%)	3	18
4	E	93/99 (94%)	71 (76%)	16 (17%)	6 (6%)	1	8
5	F	349/423 (82%)	302 (86%)	36 (10%)	11 (3%)	5	27
All	All	3526/3795 (93%)	2958 (84%)	444 (13%)	124 (4%)	4	24

5 of 124 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	42	VAL
2	C	194	VAL
2	C	195	LEU
2	C	223	ASP
2	C	261	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	202/273 (74%)	183 (91%)	19 (9%)	11	39
1	B	206/273 (76%)	192 (93%)	14 (7%)	20	56
2	C	941/941 (100%)	802 (85%)	139 (15%)	4	17
3	D	1264/1279 (99%)	1106 (88%)	158 (12%)	6	24
4	E	83/87 (95%)	76 (92%)	7 (8%)	14	45
5	F	306/371 (82%)	272 (89%)	34 (11%)	8	29
All	All	3002/3224 (93%)	2631 (88%)	371 (12%)	6	24

5 of 371 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	1006	HIS

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Mol	Chain	Res	Type
3	D	344	ASP
5	F	95	THR
3	D	3	LYS
3	D	143	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	1100	GLN
3	D	680	GLN
5	F	175	HIS
3	D	352	ASN
3	D	442	ASN

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 7 ligands modelled in this entry, 4 are monoatomic - leaving 3 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
6	PO4	A	401	-	4,4,4	0.61	0	6,6,6	0.24	0
7	NE6	C	1201	-	26,30,30	2.42	4 (15%)	20,39,39	3.93	4 (20%)
6	PO4	D	1603	-	4,4,4	0.53	0	6,6,6	0.22	0

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
6	PO4	A	401	-	-	0/0/0/0	0/0/0/0
7	NE6	C	1201	-	1/1/9/13	0/26/46/46	0/0/1/1
6	PO4	D	1603	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	C	1201	NE6	C5-C4	-3.39	1.39	1.45
7	C	1201	NE6	O2-C2	2.12	1.26	1.21
7	C	1201	NE6	O14-C13	4.55	1.44	1.33
7	C	1201	NE6	O4-C4	9.58	1.36	1.22

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	1201	NE6	O4-C4-C3	-2.04	120.82	125.65
7	C	1201	NE6	C21-C20-C22	2.81	119.65	115.37
7	C	1201	NE6	O1-C2-O2	7.17	123.11	116.86
7	C	1201	NE6	O14-C13-N12	15.09	119.82	108.53

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	C	1201	NE6	C3

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	1201	NE6	5	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	231/315 (73%)	-0.53	4 (1%) 73 45	67, 96, 155, 259	0
1	B	238/315 (75%)	-0.39	3 (1%) 79 53	82, 145, 226, 248	0
2	C	1119/1119 (100%)	-0.36	20 (1%) 71 43	56, 104, 253, 323	0
3	D	1504/1524 (98%)	-0.26	60 (3%) 42 17	56, 107, 251, 301	0
4	E	95/99 (95%)	-0.44	0 100 100	82, 129, 203, 210	0
5	F	351/423 (82%)	-0.29	10 (2%) 56 27	78, 129, 236, 277	0
All	All	3538/3795 (93%)	-0.32	97 (2%) 58 28	56, 111, 246, 323	0

The worst 5 of 97 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	328	GLY	9.1
3	D	1248	GLY	7.6
3	D	243	ALA	6.2
3	D	297	ILE	6.1
3	D	329	GLU	5.7

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

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, 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	LLDF	B-factors(Å ²)	Q<0.9
6	PO4	D	1603	5/5	0.80	0.23	4.55	143,144,156,163	0
6	PO4	A	401	5/5	0.98	0.23	2.75	122,124,129,130	0
9	MG	D	1604	1/1	0.91	0.28	1.00	101,101,101,101	0
8	ZN	D	1602	1/1	1.00	0.15	0.05	84,84,84,84	0
7	NE6	C	1201	30/30	0.96	0.21	-0.04	76,92,105,115	0
8	ZN	D	1601	1/1	0.99	0.13	-0.26	104,104,104,104	0
9	MG	D	1605	1/1	0.98	0.27	-	98,98,98,98	0

6.5 Other polymers [i](#)

There are no such residues in this entry.