wwPDB X-ray Structure Validation Summary Report (i)

May 19, 2020 – 10:54 pm BST

PDB ID	:	3WFP
Title	:	tRNA processing enzyme (apo form 2)
Authors	:	Yamashita, S.; Takeshita, D.; Tomita, K.
Deposited on	:	2013-07-23
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
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:

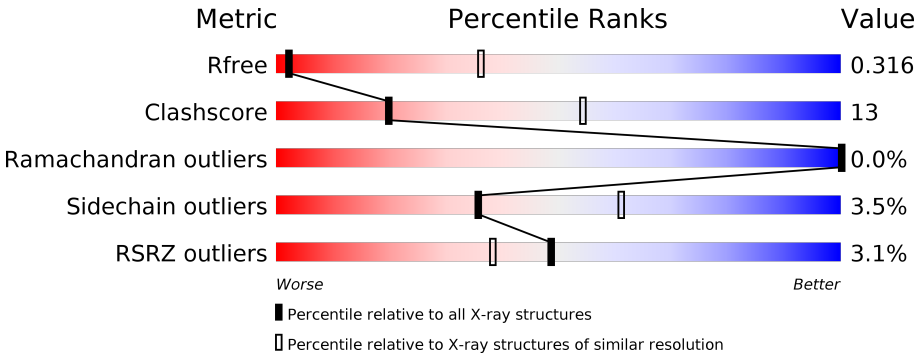
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 4.00 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}	130704	1087 (4.30-3.70)
Clashscore	141614	1148 (4.30-3.70)
Ramachandran outliers	138981	1108 (4.30-3.70)
Sidechain outliers	138945	1099 (4.30-3.70)
RSRZ outliers	127900	1028 (4.34-3.66)

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% 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	497	65% 24% • 8%
1	B	497	67% 22% • 9%
1	C	497	3% 63% 20% • 16%
1	D	497	64% 19% • 16%
1	E	497	61% 21% • 17%
1	F	497	60% 21% • 17%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	497	6% 63% 18% 17%
1	H	497	6% 63% 19% 17%

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
2	SO4	C	1001	-	-	X	X
2	SO4	H	1001	-	-	X	-

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 27564 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.

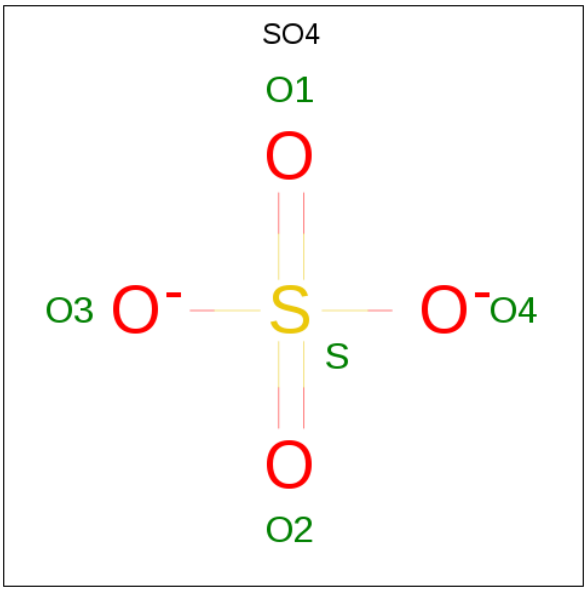
- Molecule 1 is a protein called Poly A polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	455	Total	C	N	O	S	0	0	0
			3624	2334	624	659	7			
1	B	450	Total	C	N	O	S	0	0	0
			3568	2296	611	654	7			
1	C	419	Total	C	N	O	S	0	0	0
			3436	2222	588	619	7			
1	D	419	Total	C	N	O	S	0	0	0
			3436	2222	588	619	7			
1	E	411	Total	C	N	O	S	0	0	0
			3365	2175	572	611	7			
1	F	411	Total	C	N	O	S	0	0	0
			3365	2175	572	611	7			
1	G	411	Total	C	N	O	S	0	0	0
			3365	2175	572	611	7			
1	H	411	Total	C	N	O	S	0	0	0
			3365	2175	572	611	7			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	MET	-	EXPRESSION TAG	UNP O67911
B	16	MET	-	EXPRESSION TAG	UNP O67911
C	16	MET	-	EXPRESSION TAG	UNP O67911
D	16	MET	-	EXPRESSION TAG	UNP O67911
E	16	MET	-	EXPRESSION TAG	UNP O67911
F	16	MET	-	EXPRESSION TAG	UNP O67911
G	16	MET	-	EXPRESSION TAG	UNP O67911
H	16	MET	-	EXPRESSION TAG	UNP O67911

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



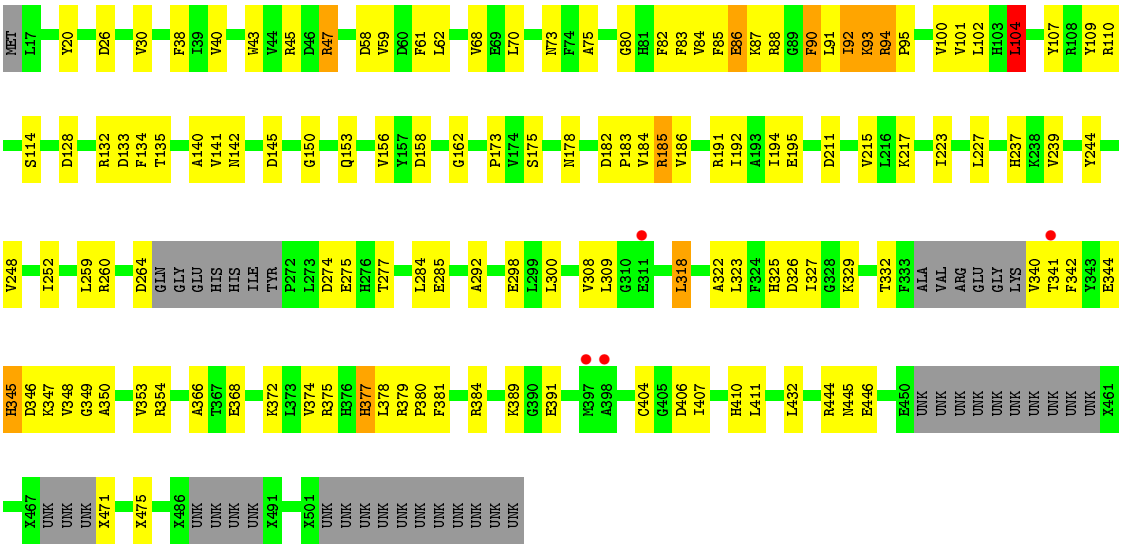
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0
2	F	1	Total O S 5 4 1	0	0
2	G	1	Total O S 5 4 1	0	0
2	H	1	Total O S 5 4 1	0	0

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 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.

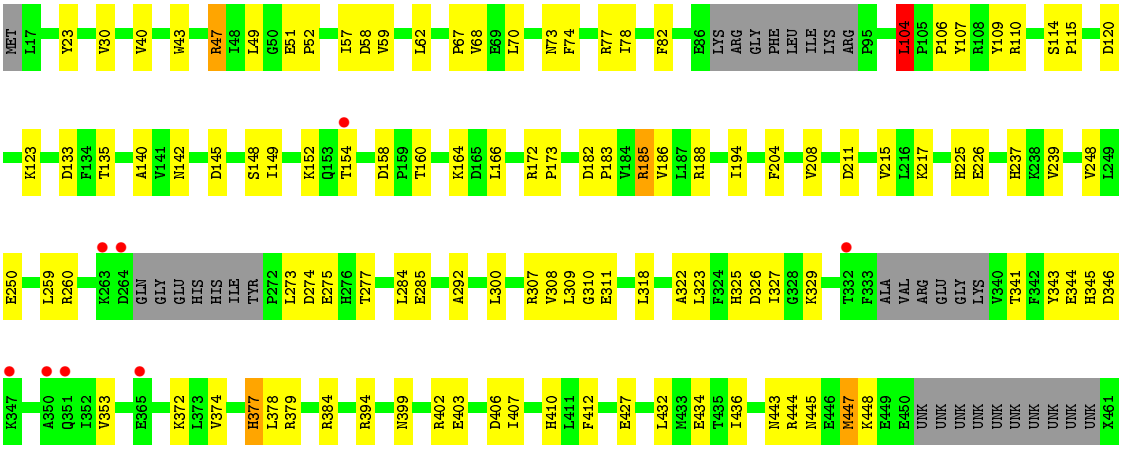
- Molecule 1: Poly A polymerase

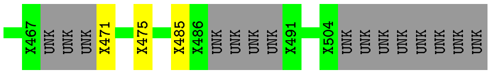
Chain A:



- Molecule 1: Poly A polymerase

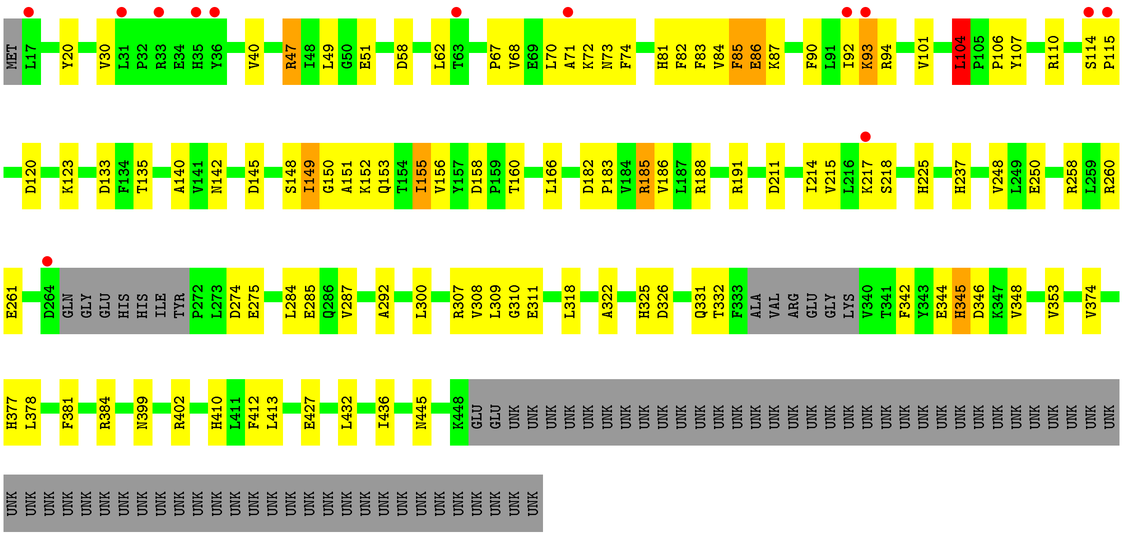
Chain B:





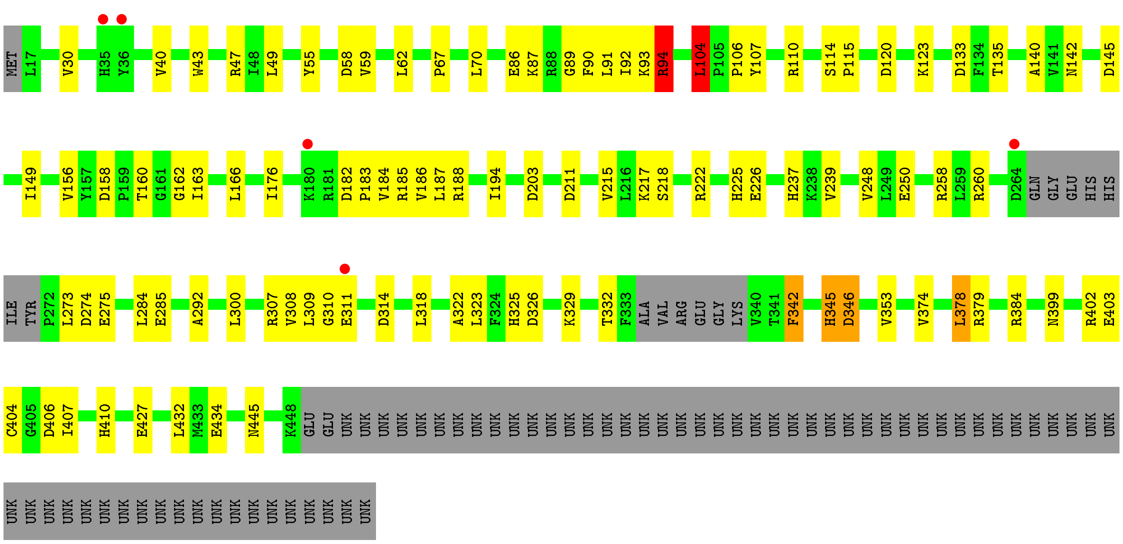
- Molecule 1: Poly A polymerase

Chain C:



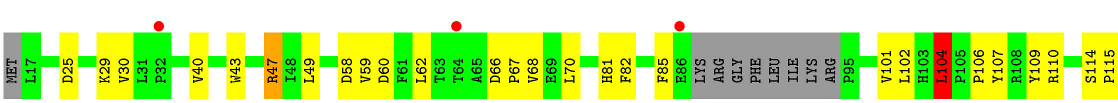
- Molecule 1: Poly A polymerase

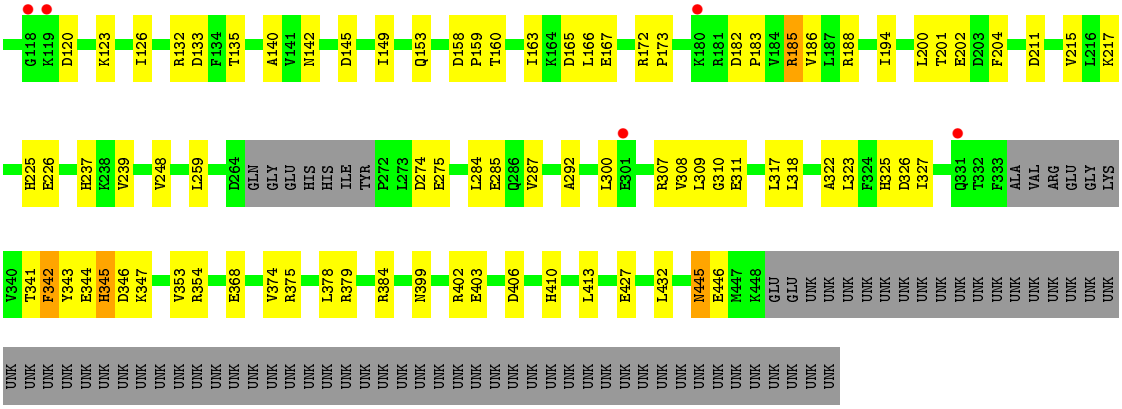
Chain D:



- Molecule 1: Poly A polymerase

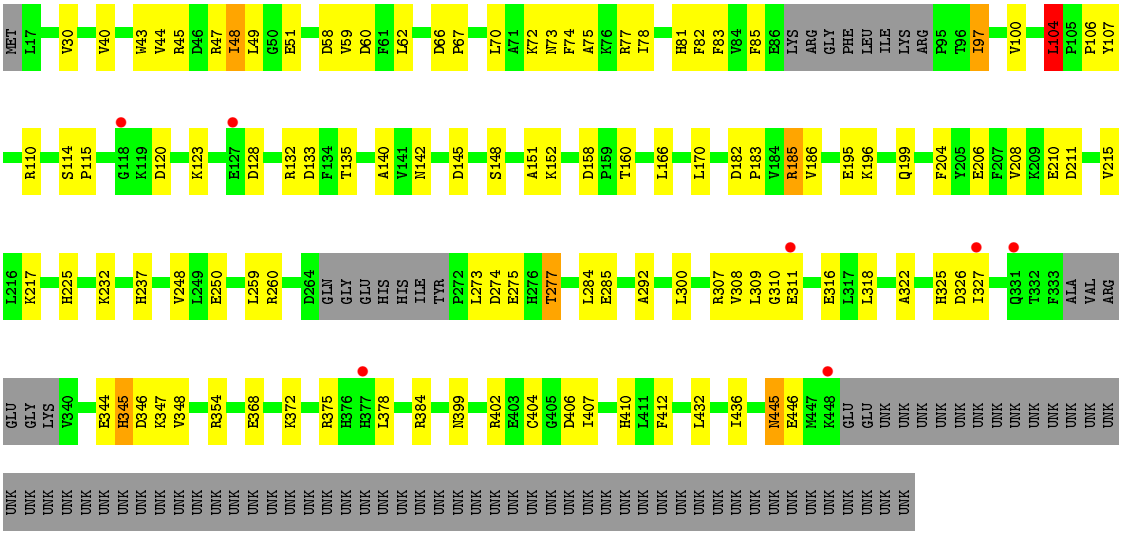
Chain E:





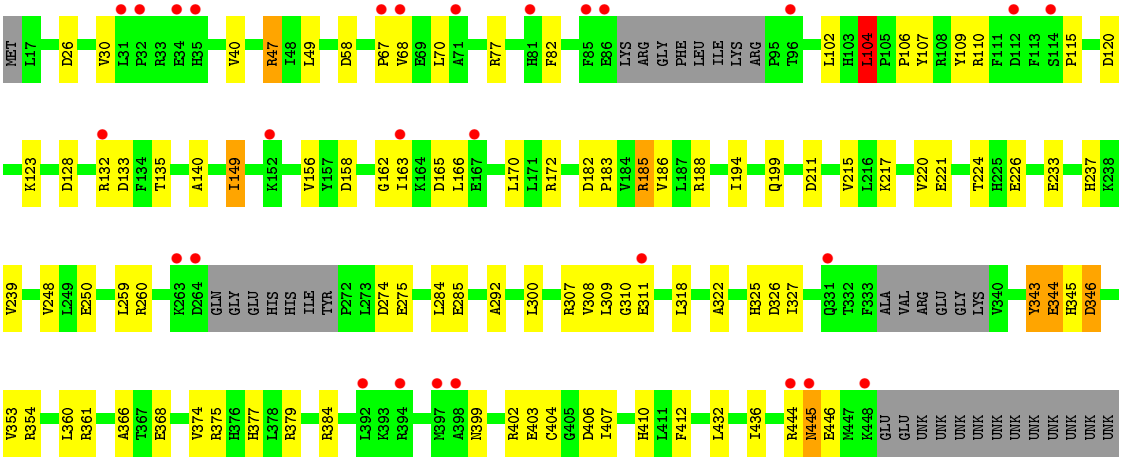
• Molecule 1: Poly A polymerase

Chain F:



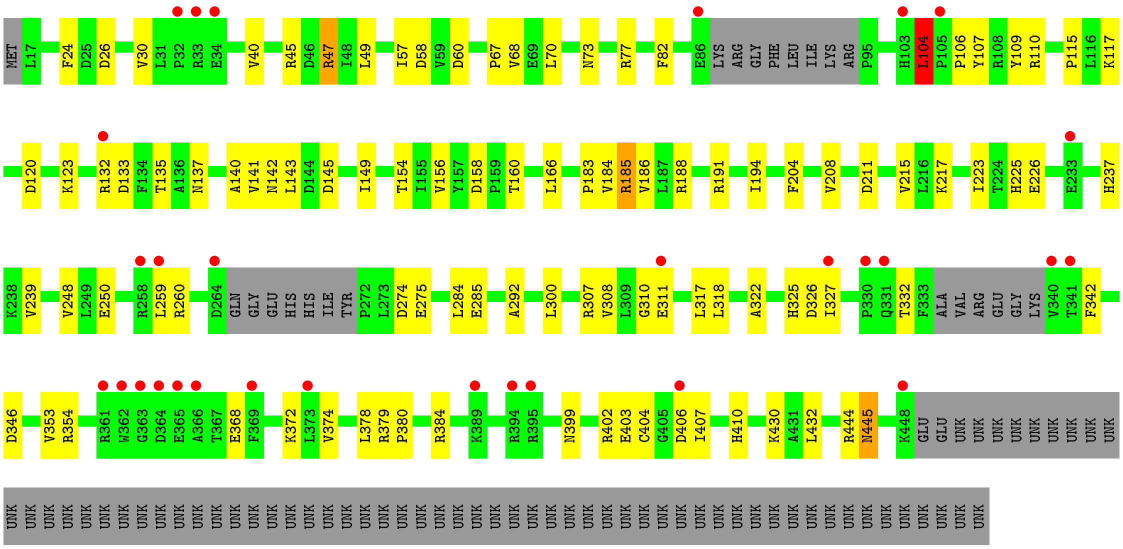
• Molecule 1: Poly A polymerase

Chain G:



- Molecule 1: Poly A polymerase

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	126.91Å 138.36Å 147.62Å 90.00° 111.04° 90.00°	Depositor
Resolution (Å)	19.97 – 4.00 48.81 – 4.01	Depositor EDS
% Data completeness (in resolution range)	86.8 (19.97-4.00) 76.7 (48.81-4.01)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.68 (at 4.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.258 , 0.314 0.262 , 0.316	Depositor DCC
R_{free} test set	1756 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	68.6	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 107.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.38$, $< L^2 > = 0.21$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.76	EDS
Total number of atoms	27564	wwPDB-VP
Average B, all atoms (Å^2)	142.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.68% 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: SO4

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	0.24	0/3527	0.42	1/4750 (0.0%)
1	B	0.23	0/3454	0.42	1/4653 (0.0%)
1	C	0.23	0/3509	0.42	1/4726 (0.0%)
1	D	0.26	0/3509	0.45	2/4726 (0.0%)
1	E	0.22	0/3436	0.40	2/4629 (0.0%)
1	F	0.27	0/3436	0.46	2/4629 (0.0%)
1	G	0.23	0/3436	0.42	2/4629 (0.0%)
1	H	0.22	0/3436	0.40	1/4629 (0.0%)
All	All	0.24	0/27743	0.42	12/37371 (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})
1	D	94	ARG	C-N-CD	5.83	140.64	128.40
1	B	104	LEU	CA-CB-CG	5.72	128.45	115.30
1	G	104	LEU	CA-CB-CG	5.71	128.43	115.30
1	F	104	LEU	CA-CB-CG	5.70	128.41	115.30
1	H	104	LEU	CA-CB-CG	5.70	128.41	115.30

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	3624	0	3522	107	0
1	B	3568	0	3439	80	0
1	C	3436	0	3470	104	0
1	D	3436	0	3470	107	0
1	E	3365	0	3384	76	0
1	F	3365	0	3384	96	0
1	G	3365	0	3384	84	0
1	H	3365	0	3384	59	0
2	A	5	0	0	0	0
2	B	5	0	0	1	0
2	C	5	0	0	2	0
2	D	5	0	0	0	0
2	E	5	0	0	1	0
2	F	5	0	0	1	0
2	G	5	0	0	0	0
2	H	5	0	0	2	0
All	All	27564	0	27437	690	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 690 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)
1:A:92:ILE:HD12	1:A:93:LYS:N	1.27	1.41
1:C:345:HIS:HD2	1:C:346:ASP:N	1.30	1.28
1:C:345:HIS:CD2	1:C:346:ASP:H	1.57	1.20
1:A:92:ILE:CD1	1:A:93:LYS:H	1.55	1.19
1:C:345:HIS:CD2	1:C:346:ASP:N	2.10	1.16

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	415/497 (84%)	409 (99%)	6 (1%)	0	100	100
1	B	405/497 (82%)	402 (99%)	2 (0%)	1 (0%)	47	79
1	C	413/497 (83%)	407 (98%)	6 (2%)	0	100	100
1	D	413/497 (83%)	407 (98%)	6 (2%)	0	100	100
1	E	403/497 (81%)	402 (100%)	1 (0%)	0	100	100
1	F	403/497 (81%)	400 (99%)	3 (1%)	0	100	100
1	G	403/497 (81%)	400 (99%)	3 (1%)	0	100	100
1	H	403/497 (81%)	399 (99%)	4 (1%)	0	100	100
All	All	3258/3976 (82%)	3226 (99%)	31 (1%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	345	HIS

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	367/378 (97%)	344 (94%)	23 (6%)	18	46
1	B	360/378 (95%)	348 (97%)	12 (3%)	38	62
1	C	365/378 (97%)	350 (96%)	15 (4%)	30	57
1	D	365/378 (97%)	354 (97%)	11 (3%)	41	64
1	E	358/378 (95%)	346 (97%)	12 (3%)	37	61
1	F	358/378 (95%)	347 (97%)	11 (3%)	40	63
1	G	358/378 (95%)	349 (98%)	9 (2%)	47	68
1	H	358/378 (95%)	349 (98%)	9 (2%)	47	68
All	All	2889/3024 (96%)	2787 (96%)	102 (4%)	36	61

5 of 102 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	211	ASP
1	D	345	HIS
1	H	104	LEU
1	C	345	HIS
1	D	87	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	345	HIS
1	G	377	HIS
1	G	225	HIS
1	C	345	HIS
1	E	345	HIS

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)

8 ligands are 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	$\#\|Z\| > 2$
2	SO4	A	1001	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	B	1001	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	F	1001	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	D	1001	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	H	1001	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	E	1001	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	C	1001	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	G	1001	-	4,4,4	0.99	0	6,6,6	1.66	1 (16%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	G	1001	SO4	O4-S-O3	3.82	125.37	109.06

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1001	SO4	1	0
2	F	1001	SO4	1	0
2	H	1001	SO4	2	0
2	E	1001	SO4	1	0
2	C	1001	SO4	2	0

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	A	421/497 (84%)	-0.26	4 (0%) 82 74	51, 113, 166, 211	0
1	B	413/497 (83%)	-0.14	8 (1%) 66 58	62, 116, 177, 218	0
1	C	419/497 (84%)	-0.01	13 (3%) 49 38	71, 139, 209, 259	0
1	D	419/497 (84%)	-0.08	5 (1%) 79 70	75, 133, 193, 243	0
1	E	411/497 (82%)	-0.01	8 (1%) 66 58	83, 146, 198, 249	0
1	F	411/497 (82%)	-0.12	7 (1%) 70 60	65, 125, 176, 190	0
1	G	411/497 (82%)	0.27	28 (6%) 17 14	118, 167, 231, 259	0
1	H	411/497 (82%)	0.30	30 (7%) 15 12	102, 177, 223, 266	0
All	All	3316/3976 (83%)	-0.01	103 (3%) 49 38	51, 140, 209, 266	0

The worst 5 of 103 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	264	ASP	6.1
1	H	264	ASP	5.3
1	C	264	ASP	5.2
1	G	31	LEU	5.0
1	E	180	LYS	4.6

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

There are no carbohydrates in this entry.

6.4 Ligands

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, 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	B-factors(Å^2)	Q<0.9
2	SO4	C	1001	5/5	0.73	0.49	162,165,166,172	0
2	SO4	A	1001	5/5	0.88	0.31	119,122,146,154	0
2	SO4	B	1001	5/5	0.91	0.45	126,131,139,141	0
2	SO4	H	1001	5/5	0.92	0.39	152,157,161,166	0
2	SO4	G	1001	5/5	0.92	0.43	172,174,178,186	0
2	SO4	D	1001	5/5	0.94	0.29	104,115,144,156	0
2	SO4	F	1001	5/5	0.94	0.16	81,81,91,105	0
2	SO4	E	1001	5/5	0.95	0.24	133,135,137,145	0

6.5 Other polymers

There are no such residues in this entry.