Full wwPDB X-ray Structure Validation Report (i)

Nov 14, 2023 – 08:09 PM JST

PDB ID	:	6A4B
Title	:	Structure of TREX2 in complex with a duplex DNA with 2 nucleotide 3'-overhang
Authors	:	Hsiao, Y.Y.
Deposited on	:	2018-06-19
Resolution	:	2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

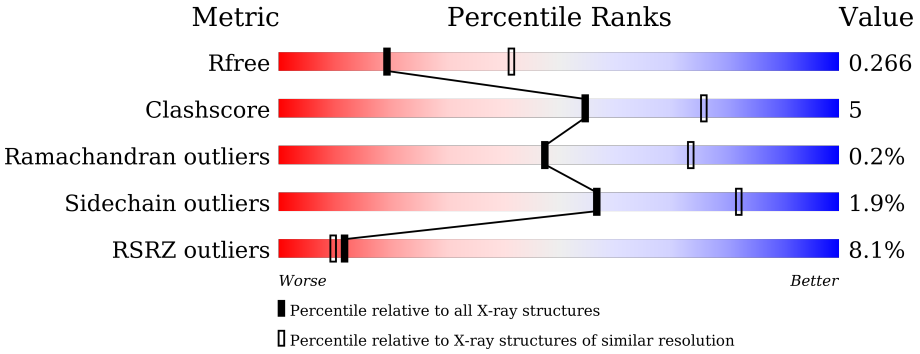
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 of 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	256	6%, 70%, 12%, •, 17%
1	B	256	4%, 67%, 16%, •, 16%
1	C	256	8%, 72%, 12%, 16%
1	D	256	12%, 71%, 13%, 16%
1	E	256	7%, 71%, 13%, 15%
1	F	256	2%, 71%, 13%, 15%

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Mol	Chain	Length	Quality of chain
2	G	18	17% 67% 17% 17%
2	H	18	22% 67% 17% 17%
2	I	18	6% 61% 22% 17%
2	J	18	11% 89% 11%
2	K	18	6% 72% 6% 22%
2	L	18	11% 56% 28% 17%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 11982 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 Three prime repair exonuclease 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	213	1661	1055	287	309	10	0	0	0
1	B	216	1680	1067	291	312	10	0	0	0
1	C	215	1677	1063	293	311	10	0	0	0
1	D	215	1684	1069	295	310	10	0	0	0
1	E	217	1690	1071	295	314	10	0	0	0
1	F	217	1690	1071	295	314	10	0	0	0

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q9R1A9
A	-18	GLY	-	expression tag	UNP Q9R1A9
A	-17	SER	-	expression tag	UNP Q9R1A9
A	-16	SER	-	expression tag	UNP Q9R1A9
A	-15	HIS	-	expression tag	UNP Q9R1A9
A	-14	HIS	-	expression tag	UNP Q9R1A9
A	-13	HIS	-	expression tag	UNP Q9R1A9
A	-12	HIS	-	expression tag	UNP Q9R1A9
A	-11	HIS	-	expression tag	UNP Q9R1A9
A	-10	HIS	-	expression tag	UNP Q9R1A9
A	-9	SER	-	expression tag	UNP Q9R1A9
A	-8	SER	-	expression tag	UNP Q9R1A9
A	-7	GLY	-	expression tag	UNP Q9R1A9
A	-6	LEU	-	expression tag	UNP Q9R1A9
A	-5	VAL	-	expression tag	UNP Q9R1A9
A	-4	PRO	-	expression tag	UNP Q9R1A9
A	-3	ARG	-	expression tag	UNP Q9R1A9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q9R1A9
A	-1	SER	-	expression tag	UNP Q9R1A9
A	0	HIS	-	expression tag	UNP Q9R1A9
B	-19	MET	-	initiating methionine	UNP Q9R1A9
B	-18	GLY	-	expression tag	UNP Q9R1A9
B	-17	SER	-	expression tag	UNP Q9R1A9
B	-16	SER	-	expression tag	UNP Q9R1A9
B	-15	HIS	-	expression tag	UNP Q9R1A9
B	-14	HIS	-	expression tag	UNP Q9R1A9
B	-13	HIS	-	expression tag	UNP Q9R1A9
B	-12	HIS	-	expression tag	UNP Q9R1A9
B	-11	HIS	-	expression tag	UNP Q9R1A9
B	-10	HIS	-	expression tag	UNP Q9R1A9
B	-9	SER	-	expression tag	UNP Q9R1A9
B	-8	SER	-	expression tag	UNP Q9R1A9
B	-7	GLY	-	expression tag	UNP Q9R1A9
B	-6	LEU	-	expression tag	UNP Q9R1A9
B	-5	VAL	-	expression tag	UNP Q9R1A9
B	-4	PRO	-	expression tag	UNP Q9R1A9
B	-3	ARG	-	expression tag	UNP Q9R1A9
B	-2	GLY	-	expression tag	UNP Q9R1A9
B	-1	SER	-	expression tag	UNP Q9R1A9
B	0	HIS	-	expression tag	UNP Q9R1A9
C	-19	MET	-	initiating methionine	UNP Q9R1A9
C	-18	GLY	-	expression tag	UNP Q9R1A9
C	-17	SER	-	expression tag	UNP Q9R1A9
C	-16	SER	-	expression tag	UNP Q9R1A9
C	-15	HIS	-	expression tag	UNP Q9R1A9
C	-14	HIS	-	expression tag	UNP Q9R1A9
C	-13	HIS	-	expression tag	UNP Q9R1A9
C	-12	HIS	-	expression tag	UNP Q9R1A9
C	-11	HIS	-	expression tag	UNP Q9R1A9
C	-10	HIS	-	expression tag	UNP Q9R1A9
C	-9	SER	-	expression tag	UNP Q9R1A9
C	-8	SER	-	expression tag	UNP Q9R1A9
C	-7	GLY	-	expression tag	UNP Q9R1A9
C	-6	LEU	-	expression tag	UNP Q9R1A9
C	-5	VAL	-	expression tag	UNP Q9R1A9
C	-4	PRO	-	expression tag	UNP Q9R1A9
C	-3	ARG	-	expression tag	UNP Q9R1A9
C	-2	GLY	-	expression tag	UNP Q9R1A9
C	-1	SER	-	expression tag	UNP Q9R1A9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	HIS	-	expression tag	UNP Q9R1A9
D	-19	MET	-	initiating methionine	UNP Q9R1A9
D	-18	GLY	-	expression tag	UNP Q9R1A9
D	-17	SER	-	expression tag	UNP Q9R1A9
D	-16	SER	-	expression tag	UNP Q9R1A9
D	-15	HIS	-	expression tag	UNP Q9R1A9
D	-14	HIS	-	expression tag	UNP Q9R1A9
D	-13	HIS	-	expression tag	UNP Q9R1A9
D	-12	HIS	-	expression tag	UNP Q9R1A9
D	-11	HIS	-	expression tag	UNP Q9R1A9
D	-10	HIS	-	expression tag	UNP Q9R1A9
D	-9	SER	-	expression tag	UNP Q9R1A9
D	-8	SER	-	expression tag	UNP Q9R1A9
D	-7	GLY	-	expression tag	UNP Q9R1A9
D	-6	LEU	-	expression tag	UNP Q9R1A9
D	-5	VAL	-	expression tag	UNP Q9R1A9
D	-4	PRO	-	expression tag	UNP Q9R1A9
D	-3	ARG	-	expression tag	UNP Q9R1A9
D	-2	GLY	-	expression tag	UNP Q9R1A9
D	-1	SER	-	expression tag	UNP Q9R1A9
D	0	HIS	-	expression tag	UNP Q9R1A9
E	-19	MET	-	initiating methionine	UNP Q9R1A9
E	-18	GLY	-	expression tag	UNP Q9R1A9
E	-17	SER	-	expression tag	UNP Q9R1A9
E	-16	SER	-	expression tag	UNP Q9R1A9
E	-15	HIS	-	expression tag	UNP Q9R1A9
E	-14	HIS	-	expression tag	UNP Q9R1A9
E	-13	HIS	-	expression tag	UNP Q9R1A9
E	-12	HIS	-	expression tag	UNP Q9R1A9
E	-11	HIS	-	expression tag	UNP Q9R1A9
E	-10	HIS	-	expression tag	UNP Q9R1A9
E	-9	SER	-	expression tag	UNP Q9R1A9
E	-8	SER	-	expression tag	UNP Q9R1A9
E	-7	GLY	-	expression tag	UNP Q9R1A9
E	-6	LEU	-	expression tag	UNP Q9R1A9
E	-5	VAL	-	expression tag	UNP Q9R1A9
E	-4	PRO	-	expression tag	UNP Q9R1A9
E	-3	ARG	-	expression tag	UNP Q9R1A9
E	-2	GLY	-	expression tag	UNP Q9R1A9
E	-1	SER	-	expression tag	UNP Q9R1A9
E	0	HIS	-	expression tag	UNP Q9R1A9
F	-19	MET	-	initiating methionine	UNP Q9R1A9

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-18	GLY	-	expression tag	UNP Q9R1A9
F	-17	SER	-	expression tag	UNP Q9R1A9
F	-16	SER	-	expression tag	UNP Q9R1A9
F	-15	HIS	-	expression tag	UNP Q9R1A9
F	-14	HIS	-	expression tag	UNP Q9R1A9
F	-13	HIS	-	expression tag	UNP Q9R1A9
F	-12	HIS	-	expression tag	UNP Q9R1A9
F	-11	HIS	-	expression tag	UNP Q9R1A9
F	-10	HIS	-	expression tag	UNP Q9R1A9
F	-9	SER	-	expression tag	UNP Q9R1A9
F	-8	SER	-	expression tag	UNP Q9R1A9
F	-7	GLY	-	expression tag	UNP Q9R1A9
F	-6	LEU	-	expression tag	UNP Q9R1A9
F	-5	VAL	-	expression tag	UNP Q9R1A9
F	-4	PRO	-	expression tag	UNP Q9R1A9
F	-3	ARG	-	expression tag	UNP Q9R1A9
F	-2	GLY	-	expression tag	UNP Q9R1A9
F	-1	SER	-	expression tag	UNP Q9R1A9
F	0	HIS	-	expression tag	UNP Q9R1A9

- Molecule 2 is a DNA chain called DNA (5'-D(*GP*GP*CP*CP*CP*TP*TP*AP*GP*GP*GP*CP*CP*TP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	G	15	303	145	53	91	14	0	0	0
2	H	15	303	145	53	91	14	0	0	0
2	I	15	303	145	53	91	14	0	0	0
2	J	18	362	174	60	111	17	0	0	0
2	K	14	283	135	51	84	13	0	0	0
2	L	15	303	145	53	91	14	0	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	A	2	2	2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0
3	E	2	Total Mg 2 2	0	0
3	F	1	Total Mg 1 1	0	0
3	G	1	Total Mg 1 1	0	0
3	I	1	Total Mg 1 1	0	0
3	L	1	Total Mg 1 1	0	0

- Molecule 4 is water.

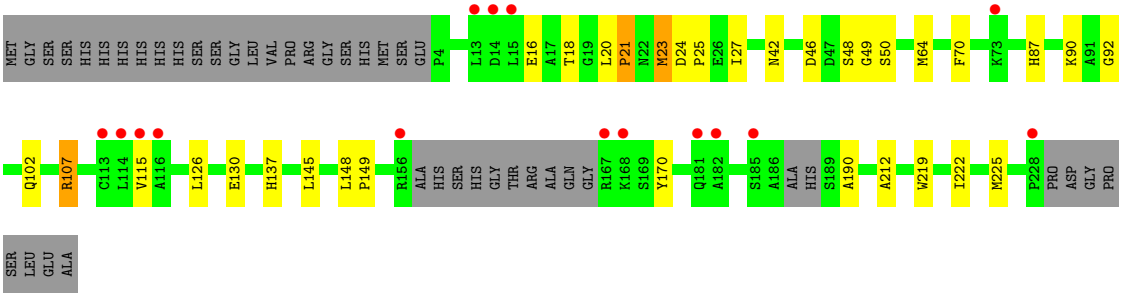
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	5	Total O 5 5	0	0
4	B	5	Total O 5 5	0	0
4	C	5	Total O 5 5	0	0
4	D	5	Total O 5 5	0	0
4	E	5	Total O 5 5	0	0
4	F	2	Total O 2 2	0	0
4	G	3	Total O 3 3	0	0
4	L	2	Total O 2 2	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

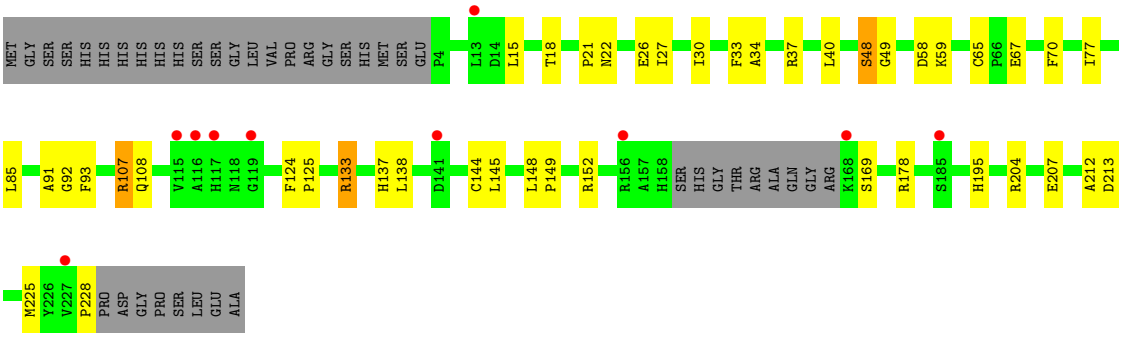
• Molecule 1: Three prime repair exonuclease 2

Chain A:



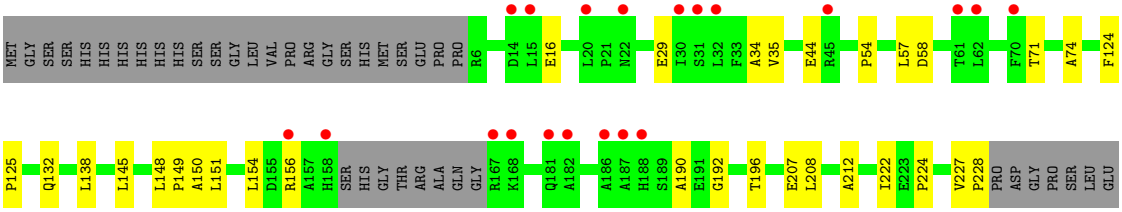
• Molecule 1: Three prime repair exonuclease 2

Chain B:



• Molecule 1: Three prime repair exonuclease 2

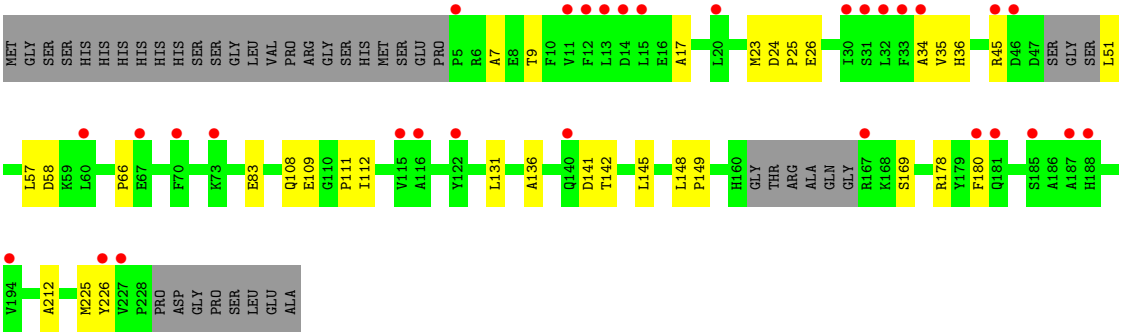
Chain C:



ALA

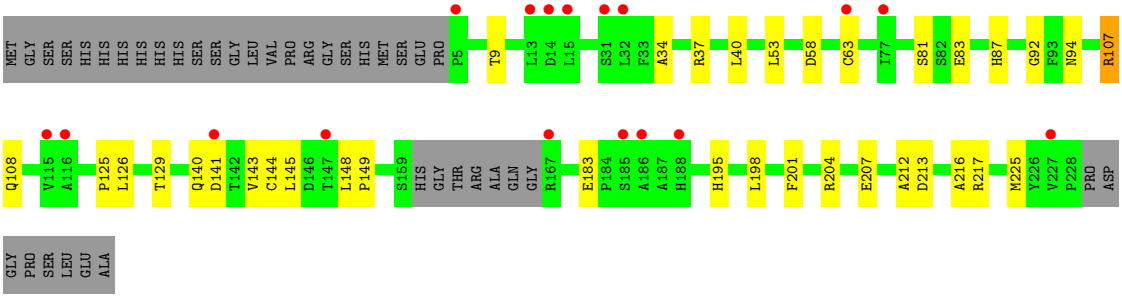
• Molecule 1: Three prime repair exonuclease 2

Chain D:



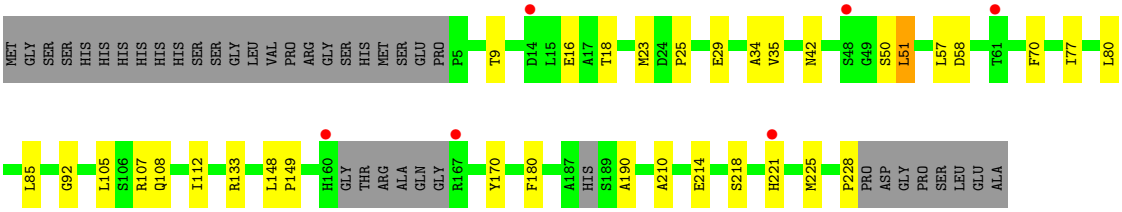
• Molecule 1: Three prime repair exonuclease 2

Chain E:



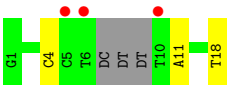
• Molecule 1: Three prime repair exonuclease 2

Chain F:



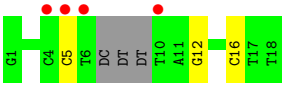
• Molecule 2: DNA (5'-D(*GP*GP*CP*CP*CP*TP*TP*AP*GP*GP*GP*CP*CP*TP*T)-3')

Chain G:



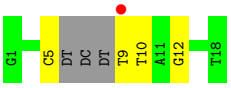
• Molecule 2: DNA (5'-D(*GP*GP*CP*CP*CP*TP*TP*AP*GP*GP*GP*CP*CP*TP*T)-3')

Chain H:



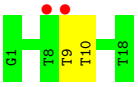
• Molecule 2: DNA (5'-D(*GP*GP*CP*CP*CP*TP*TP*AP*GP*GP*GP*CP*CP*TP*T)-3')

Chain I:



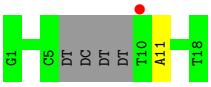
• Molecule 2: DNA (5'-D(*GP*GP*CP*CP*CP*TP*TP*AP*GP*GP*GP*CP*CP*TP*T)-3')

Chain J:



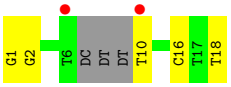
• Molecule 2: DNA (5'-D(*GP*GP*CP*CP*CP*TP*TP*AP*GP*GP*GP*CP*CP*TP*T)-3')

Chain K:



• Molecule 2: DNA (5'-D(*GP*GP*CP*CP*CP*TP*TP*AP*GP*GP*GP*CP*CP*TP*T)-3')

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	48.72Å 87.32Å 432.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.23 – 2.70 29.23 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.2 (29.23-2.70) 96.7 (29.23-2.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	2.08 (at 2.72Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.224 , 0.263 0.230 , 0.266	Depositor DCC
R_{free} test set	3961 reflections (7.80%)	wwPDB-VP
Wilson B-factor (Å^2)	74.1	Xtriage
Anisotropy	0.289	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 39.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	11982	wwPDB-VP
Average B, all atoms (Å^2)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.22	0/1701	0.41	0/2310
1	B	0.22	0/1723	0.39	0/2343
1	C	0.22	0/1718	0.38	0/2334
1	D	0.22	0/1726	0.39	0/2344
1	E	0.21	0/1732	0.37	0/2353
1	F	0.22	0/1731	0.38	0/2350
2	G	0.56	0/337	0.92	0/516
2	H	0.50	0/337	0.91	0/516
2	I	0.55	0/337	0.90	0/516
2	J	0.51	0/403	0.94	0/620
2	K	0.56	0/315	0.88	0/482
2	L	0.55	0/337	0.89	0/516
All	All	0.30	0/12397	0.52	0/17200

There are no bond length outliers.

There are no bond angle outliers.

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	1661	0	1631	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1680	0	1643	25	0
1	C	1677	0	1641	16	0
1	D	1684	0	1647	17	0
1	E	1690	0	1654	18	0
1	F	1690	0	1653	19	0
2	G	303	0	172	3	0
2	H	303	0	172	2	0
2	I	303	0	172	3	0
2	J	362	0	206	2	0
2	K	283	0	160	1	0
2	L	303	0	172	4	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	2	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	I	1	0	0	0	0
3	L	1	0	0	0	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
4	C	5	0	0	0	0
4	D	5	0	0	0	0
4	E	5	0	0	0	0
4	F	2	0	0	0	0
4	G	3	0	0	0	0
4	L	2	0	0	0	0
All	All	11982	0	10923	118	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 5.

All (118) 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:E:125:PRO:HB2	1:E:225:MET:HG3	1.66	0.76
1:D:45:ARG:HA	1:D:51:LEU:HA	1.72	0.71
1:A:92:GLY:O	1:B:107:ARG:NH2	2.23	0.71
1:F:16:GLU:HG2	1:F:190:ALA:HB2	1.72	0.71
1:B:34:ALA:HB3	1:B:58:ASP:HB2	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:37:ARG:NH2	1:B:213:ASP:OD2	2.24	0.70
1:D:169:SER:O	1:D:178:ARG:NH2	2.24	0.70
1:A:107:ARG:NH2	1:B:92:GLY:O	2.25	0.69
1:B:125:PRO:HB2	1:B:225:MET:HG3	1.77	0.66
1:E:107:ARG:NH2	1:F:92:GLY:O	2.29	0.66
1:A:90:LYS:NZ	1:B:108:GLN:OE1	2.29	0.65
1:B:204:ARG:NH1	1:B:207:GLU:OE2	2.33	0.61
1:A:107:ARG:HH12	1:B:91:ALA:HB3	1.65	0.61
1:E:34:ALA:HB3	1:E:58:ASP:HB2	1.82	0.60
1:C:154:LEU:HD21	1:C:207:GLU:HB3	1.83	0.60
1:D:7:ALA:HA	1:D:111:PRO:HG2	1.84	0.59
1:F:18:THR:HB	1:F:70:PHE:HA	1.84	0.59
1:B:48:SER:N	1:B:49:GLY:HA2	2.18	0.59
1:D:51:LEU:HD21	1:D:180:PHE:HE1	1.68	0.58
1:C:34:ALA:HB3	1:C:58:ASP:HB2	1.85	0.58
1:D:9:THR:HG21	1:D:108:GLN:HB3	1.86	0.58
1:D:34:ALA:HB3	1:D:58:ASP:HB2	1.86	0.58
1:E:53:LEU:HD22	1:E:198:LEU:HD23	1.84	0.58
2:H:5:DC:O2	2:H:12:DG:N2	2.27	0.58
1:E:9:THR:HG21	1:E:108:GLN:HB3	1.85	0.57
1:F:9:THR:HG21	1:F:108:GLN:HB3	1.85	0.57
1:D:26:GLU:HB2	1:D:66:PRO:HB3	1.87	0.57
1:F:34:ALA:HB3	1:F:58:ASP:HB2	1.87	0.56
1:E:37:ARG:NH2	1:E:213:ASP:OD2	2.36	0.56
1:F:51:LEU:HD13	1:F:180:PHE:HE1	1.72	0.55
1:A:48:SER:N	1:A:49:GLY:HA2	2.22	0.55
2:I:9:DT:H2"	2:I:10:DT:H5"	1.89	0.54
1:D:36:HIS:NE2	1:D:109:GLU:OE1	2.35	0.54
1:C:156:ARG:NH1	2:I:5:DC:OP1	2.41	0.54
1:B:152:ARG:HH21	2:G:4:DC:H4'	1.73	0.54
1:B:15:LEU:HD22	1:B:30:ILE:HG22	1.90	0.53
1:C:145:LEU:HD22	1:C:212:ALA:HB2	1.90	0.53
1:B:33:PHE:CZ	1:B:59:LYS:HE3	2.44	0.53
1:B:145:LEU:HD22	1:B:212:ALA:HB2	1.91	0.52
1:C:150:ALA:O	1:C:154:LEU:HB2	2.10	0.52
1:C:44:GLU:HG3	1:C:54:PRO:HA	1.90	0.52
2:J:9:DT:H1'	2:J:10:DT:C4	2.45	0.52
1:E:144:CYS:N	1:E:217:ARG:O	2.42	0.52
1:F:133:ARG:HG2	1:F:228:PRO:HG3	1.91	0.51
2:K:11:DA:N3	2:K:11:DA:H2'	2.25	0.51
1:A:102:GLN:NE2	1:A:137:HIS:O	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:169:SER:O	1:B:178:ARG:NH2	2.43	0.51
1:B:148:LEU:HB3	1:B:149:PRO:HD3	1.93	0.51
1:A:115:VAL:HG22	1:A:145:LEU:HB3	1.92	0.50
2:L:1:DG:H2'	2:L:2:DG:C8	2.46	0.50
1:B:77:ILE:HD11	2:G:18:DT:H2'	1.94	0.50
1:F:16:GLU:HB2	1:F:29:GLU:HB3	1.94	0.50
1:A:18:THR:HB	1:A:70:PHE:HA	1.92	0.49
1:D:148:LEU:HB3	1:D:149:PRO:HD3	1.94	0.49
1:B:65:CYS:HA	1:B:85:LEU:HD13	1.95	0.49
1:F:210:ALA:O	1:F:214:GLU:HG2	2.12	0.49
1:A:46:ASP:HB2	1:A:50:SER:H	1.77	0.49
1:B:21:PRO:HA	1:B:225:MET:HE1	1.95	0.49
1:E:148:LEU:HB3	1:E:149:PRO:HD3	1.95	0.49
1:C:148:LEU:HB3	1:C:149:PRO:HD3	1.95	0.48
1:A:25:PRO:HG2	1:A:225:MET:HE1	1.96	0.48
1:F:35:VAL:HG22	1:F:57:LEU:HD13	1.95	0.48
1:C:16:GLU:HB2	1:C:29:GLU:HB3	1.95	0.48
1:A:27:ILE:HG13	1:A:130:GLU:HG3	1.96	0.47
1:B:26:GLU:OE1	1:B:67:GLU:N	2.43	0.47
1:F:148:LEU:HB3	1:F:149:PRO:HD3	1.97	0.47
1:D:112:ILE:HB	1:D:142:THR:HG22	1.96	0.47
1:C:35:VAL:HG22	1:C:57:LEU:HD13	1.96	0.47
1:C:132:GLN:HE22	1:C:224:PRO:HG3	1.80	0.46
1:F:170:TYR:N	2:L:16:DC:OP1	2.30	0.46
1:A:23:MET:N	1:A:24:ASP:HA	2.30	0.46
1:F:77:ILE:HD11	2:L:18:DT:H2'	1.96	0.46
1:E:92:GLY:O	1:E:94:ASN:ND2	2.49	0.46
1:E:140:GLN:HA	1:E:141:ASP:HA	1.53	0.46
1:F:80:LEU:HD22	1:F:85:LEU:HD21	1.98	0.46
1:A:16:GLU:HG2	1:A:190:ALA:HB2	1.98	0.46
1:C:151:LEU:HD22	1:C:208:LEU:HD21	1.97	0.46
1:E:63:CYS:O	1:F:107:ARG:NH2	2.48	0.46
1:F:105:LEU:HD22	1:F:112:ILE:HD13	1.98	0.45
1:C:192:GLY:O	1:C:196:THR:HG23	2.16	0.45
1:A:148:LEU:HB3	1:A:149:PRO:HD3	1.98	0.45
1:B:133:ARG:HH21	1:B:228:PRO:HB2	1.82	0.45
1:D:17:ALA:HB1	1:D:25:PRO:HB2	1.99	0.45
1:D:131:LEU:HB3	1:D:136:ALA:HB3	1.98	0.45
1:A:64:MET:HG2	1:B:107:ARG:NH2	2.32	0.45
2:G:11:DA:N3	2:G:11:DA:H2'	2.32	0.45
1:C:16:GLU:HG2	1:C:190:ALA:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:THR:HB	1:B:70:PHE:HA	1.99	0.44
1:A:219:TRP:HA	1:A:222:ILE:HD13	1.99	0.44
1:A:20:LEU:HB3	1:A:21:PRO:HD2	2.00	0.43
1:A:18:THR:HA	1:A:70:PHE:CD2	2.53	0.43
1:C:124:PHE:HB2	1:C:125:PRO:HD3	2.00	0.43
1:D:24:ASP:OD1	1:D:226:TYR:HB2	2.18	0.43
1:C:227:VAL:HA	1:C:228:PRO:HD3	1.90	0.43
1:E:126:LEU:O	1:E:129:THR:OG1	2.32	0.43
1:E:53:LEU:HD11	1:E:195:HIS:ND1	2.34	0.43
1:B:27:ILE:HG21	1:B:30:ILE:HG23	2.00	0.43
2:I:12:DG:H8	2:I:12:DG:OP2	2.01	0.43
2:J:9:DT:H4'	2:J:10:DT:H5'	2.01	0.43
1:D:35:VAL:HG22	1:D:57:LEU:HD13	2.00	0.42
1:E:40:LEU:HD13	1:E:201:PHE:CE1	2.53	0.42
1:E:145:LEU:HD22	1:E:212:ALA:HB2	2.01	0.42
1:D:225:MET:HG2	1:D:226:TYR:CD2	2.54	0.42
1:E:204:ARG:HE	1:E:207:GLU:CD	2.23	0.42
1:F:42:ASN:OD1	1:F:42:ASN:N	2.52	0.42
1:A:42:ASN:N	1:A:42:ASN:OD1	2.53	0.42
1:A:170:TYR:N	2:H:16:DC:OP1	2.48	0.41
1:F:25:PRO:HG2	1:F:225:MET:HE1	2.02	0.41
1:B:22:ASN:OD1	1:B:22:ASN:N	2.54	0.41
1:E:143:VAL:HB	1:E:216:ALA:HB1	2.02	0.41
1:D:145:LEU:HD22	1:D:212:ALA:HB2	2.02	0.41
2:L:10:DT:H6	2:L:10:DT:H2'	1.72	0.41
1:F:218:SER:OG	1:F:221:HIS:ND1	2.46	0.40
1:A:145:LEU:HD22	1:A:212:ALA:HB2	2.03	0.40
1:E:81:SER:OG	1:E:83:GLU:OE1	2.39	0.40
1:B:124:PHE:CE2	1:B:144:CYS:HB3	2.57	0.40
1:C:71:THR:HG23	1:C:74:ALA:H	1.87	0.40
1:D:141:ASP:N	1:D:141:ASP:OD1	2.37	0.40

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	207/256 (81%)	201 (97%)	5 (2%)	1 (0%)	29	54
1	B	212/256 (83%)	203 (96%)	8 (4%)	1 (0%)	29	54
1	C	211/256 (82%)	202 (96%)	9 (4%)	0	100	100
1	D	209/256 (82%)	201 (96%)	8 (4%)	0	100	100
1	E	213/256 (83%)	204 (96%)	9 (4%)	0	100	100
1	F	211/256 (82%)	201 (95%)	10 (5%)	0	100	100
All	All	1263/1536 (82%)	1212 (96%)	49 (4%)	2 (0%)	47	73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	93	PHE
1	A	21	PRO

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	181/214 (85%)	177 (98%)	4 (2%)	52	79
1	B	182/214 (85%)	175 (96%)	7 (4%)	33	62
1	C	181/214 (85%)	179 (99%)	2 (1%)	73	90
1	D	182/214 (85%)	180 (99%)	2 (1%)	73	90
1	E	183/214 (86%)	180 (98%)	3 (2%)	62	85
1	F	183/214 (86%)	180 (98%)	3 (2%)	62	85
All	All	1092/1284 (85%)	1071 (98%)	21 (2%)	57	82

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	MET
1	A	87	HIS
1	A	107	ARG
1	A	126	LEU
1	B	40	LEU
1	B	48	SER
1	B	107	ARG
1	B	133	ARG
1	B	137	HIS
1	B	138	LEU
1	B	195	HIS
1	C	138	LEU
1	C	222	ILE
1	D	23	MET
1	D	83	GLU
1	E	87	HIS
1	E	107	ARG
1	E	183	GLU
1	F	23	MET
1	F	50	SER
1	F	51	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	181	GLN
1	B	140	GLN
1	B	188	HIS
1	C	108	GLN
1	C	132	GLN
1	D	87	HIS
1	F	22	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 11 ligands modelled in this entry, 11 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)

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	213/256 (83%)	0.31	15 (7%)	16	14	45, 68, 101, 122	0
1	B	216/256 (84%)	0.23	10 (4%)	32	31	44, 69, 103, 117	0
1	C	215/256 (83%)	0.46	20 (9%)	8	6	55, 79, 111, 149	0
1	D	215/256 (83%)	0.67	31 (14%)	2	1	49, 72, 116, 132	0
1	E	217/256 (84%)	0.47	17 (7%)	13	11	57, 83, 109, 131	0
1	F	217/256 (84%)	0.27	6 (2%)	53	54	61, 80, 110, 121	0
2	G	15/18 (83%)	0.52	3 (20%)	1	0	65, 98, 124, 133	0
2	H	15/18 (83%)	1.04	4 (26%)	0	0	76, 117, 142, 144	0
2	I	15/18 (83%)	0.18	1 (6%)	17	16	74, 98, 126, 145	0
2	J	18/18 (100%)	0.52	2 (11%)	5	4	84, 98, 124, 125	0
2	K	14/18 (77%)	0.32	1 (7%)	16	14	74, 97, 119, 119	0
2	L	15/18 (83%)	0.54	2 (13%)	3	2	69, 112, 137, 153	0
All	All	1385/1644 (84%)	0.41	112 (8%)	12	10	44, 78, 114, 153	0

All (112) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	186	ALA	8.1
1	D	227	VAL	6.0
1	D	226	TYR	5.4
1	D	14	ASP	5.0
1	C	45	ARG	4.5
1	E	116	ALA	4.1
1	D	46	ASP	4.0
1	C	187	ALA	4.0
1	E	188	HIS	4.0
1	E	115	VAL	4.0
1	C	168	LYS	4.0

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Mol	Chain	Res	Type	RSRZ
1	C	188	HIS	3.8
1	D	13	LEU	3.8
1	E	167	ARG	3.8
1	D	185	SER	3.8
1	C	30	ILE	3.8
2	L	10	DT	3.7
1	D	30	ILE	3.6
1	E	5	PRO	3.6
1	C	32	LEU	3.5
1	C	61	THR	3.5
1	B	141	ASP	3.4
1	B	116	ALA	3.4
2	G	6	DT	3.3
1	A	182	ALA	3.3
1	D	115	VAL	3.3
2	H	6	DT	3.3
1	C	22	ASN	3.2
1	C	31	SER	3.2
1	A	156	ARG	3.2
1	B	168	LYS	3.2
1	D	31	SER	3.2
1	D	116	ALA	3.2
2	I	9	DT	3.2
1	C	181	GLN	3.2
1	E	186	ALA	3.1
1	D	73	LYS	3.1
1	D	32	LEU	3.0
2	G	5	DC	3.0
1	D	45	ARG	2.9
1	D	180	PHE	2.9
1	B	156	ARG	2.9
2	K	10	DT	2.9
1	A	167	ARG	2.9
1	F	167	ARG	2.9
1	D	188	HIS	2.8
1	E	185	SER	2.8
1	C	182	ALA	2.8
1	C	167	ARG	2.8
1	D	60	LEU	2.8
2	H	10	DT	2.8
2	J	9	DT	2.8
1	A	181	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	181	GLN	2.7
1	E	13	LEU	2.7
1	E	141	ASP	2.7
1	A	114	LEU	2.7
2	H	5	DC	2.7
1	A	14	ASP	2.7
1	D	122	TYR	2.6
1	A	13	LEU	2.6
1	D	33	PHE	2.6
1	C	62	LEU	2.6
2	J	8	DT	2.6
1	A	73	LYS	2.6
1	F	160	HIS	2.6
1	B	115	VAL	2.5
1	F	221	HIS	2.5
1	D	12	PHE	2.5
1	E	31	SER	2.5
1	B	227	VAL	2.5
2	G	10	DT	2.4
1	E	63	CYS	2.4
1	C	20	LEU	2.4
1	D	140	GLN	2.4
1	C	70	PHE	2.4
1	E	15	LEU	2.4
1	A	116	ALA	2.4
1	E	14	ASP	2.4
1	D	11	VAL	2.3
1	E	227	VAL	2.3
1	D	15	LEU	2.3
1	D	34	ALA	2.3
1	D	67	GLU	2.3
1	C	14	ASP	2.3
1	A	168	LYS	2.3
1	B	185	SER	2.3
1	E	77	ILE	2.3
1	A	113	CYS	2.3
1	E	32	LEU	2.2
1	E	147	THR	2.2
1	C	158	HIS	2.2
1	A	115	VAL	2.2
1	D	187	ALA	2.2
1	B	119	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	20	LEU	2.1
1	F	14	ASP	2.1
1	F	48	SER	2.1
2	L	6	DT	2.1
1	D	70	PHE	2.1
1	B	13	LEU	2.1
1	D	167	ARG	2.1
1	B	117	HIS	2.1
1	C	156	ARG	2.1
1	A	15	LEU	2.0
2	H	4	DC	2.0
1	A	228	PRO	2.0
1	A	185	SER	2.0
1	D	5	PRO	2.0
1	F	61	THR	2.0
1	C	15	LEU	2.0
1	D	194	VAL	2.0

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 monosaccharides 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(Å^2)	Q<0.9
3	MG	A	301	1/1	0.87	0.84	75,75,75,75	0
3	MG	A	302	1/1	0.88	0.12	75,75,75,75	0
3	MG	D	301	1/1	0.89	0.85	75,75,75,75	0
3	MG	B	301	1/1	0.90	0.16	69,69,69,69	0
3	MG	E	301	1/1	0.93	0.47	75,75,75,75	0
3	MG	L	101	1/1	0.93	0.45	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	MG	E	302	1/1	0.94	0.06	83,83,83,83	0
3	MG	C	301	1/1	0.94	0.32	87,87,87,87	0
3	MG	I	101	1/1	0.95	0.34	66,66,66,66	0
3	MG	F	301	1/1	0.95	0.13	76,76,76,76	0
3	MG	G	101	1/1	0.97	0.29	62,62,62,62	0

6.5 Other polymers (i)

There are no such residues in this entry.