



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 19, 2017 – 11:28 AM EDT

PDB ID : 5XFR
Title : Ternary complex of MTF2, DNA and histone
Authors : Wang, Z.; Li, H.
Deposited on : unknown
Resolution : 2.25 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

<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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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-20029824

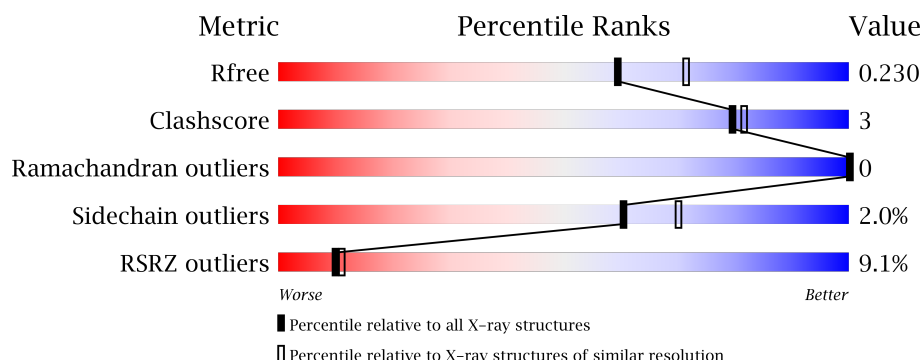
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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.



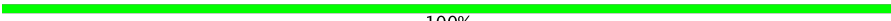
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	1062 (2.26-2.26)
Clashscore	112137	1178 (2.26-2.26)
Ramachandran outliers	110173	1145 (2.26-2.26)
Sidechain outliers	110143	1146 (2.26-2.26)
RSRZ outliers	101464	1066 (2.26-2.26)

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	317	<div> <div>5%</div> <div>88%</div> <div>10%</div> <div>.</div> </div>
1	B	317	<div> <div>11%</div> <div>84%</div> <div>9%</div> <div>6%</div> </div>
2	C	8	<div> <div>25%</div> <div>25%</div> <div>13%</div> <div>63%</div> </div>
2	D	8	<div> <div>25%</div> <div>25%</div> <div>13%</div> <div>63%</div> </div>
3	E	13	<div> <div>15%</div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	13	 100%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5844 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 Metal-response element-binding transcription factor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	309	Total	C	N	O	S	0	0	0
			2500	1603	419	449	29			
1	B	298	Total	C	N	O	S	0	0	0
			2423	1558	408	430	27			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	42	SER	-	expression tag	UNP Q9Y483
B	42	SER	-	expression tag	UNP Q9Y483

- Molecule 2 is a protein called Peptide from Histone H3.1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			28	20	5	3			
2	D	3	Total	C	N	O	0	0	0
			28	20	5	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	13	Total	C	N	O	P	0	0	0
			263	124	50	77	12			
3	F	13	Total	C	N	O	P	0	0	0
			263	124	50	77	12			

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	4	Total 4	Zn 4	0	0
4	A	4	Total 4	Zn 4	0	0

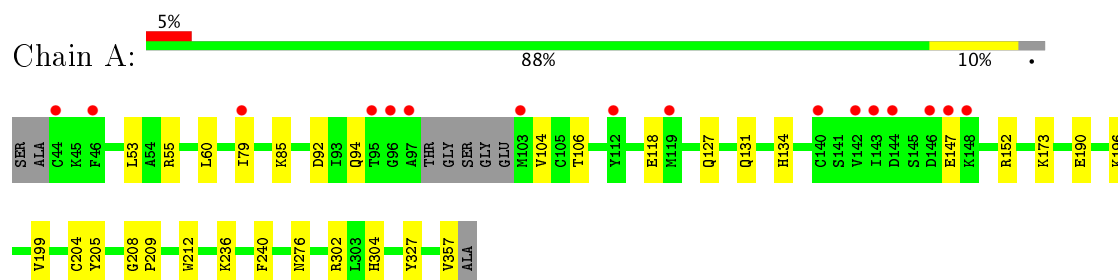
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	151	Total 151	O 151	0	0
5	B	146	Total 146	O 146	0	0
5	C	1	Total 1	O 1	0	0
5	D	1	Total 1	O 1	0	0
5	E	12	Total 12	O 12	0	0
5	F	20	Total 20	O 20	0	0

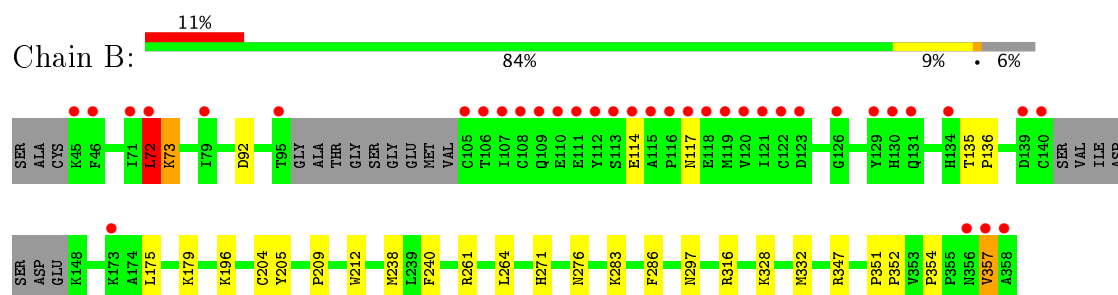
3 Residue-property plots [i](#)

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.

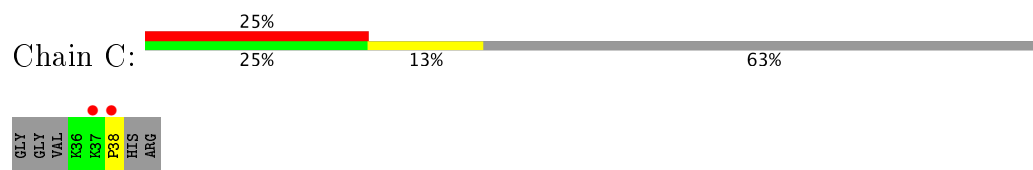
- Molecule 1: Metal-response element-binding transcription factor 2



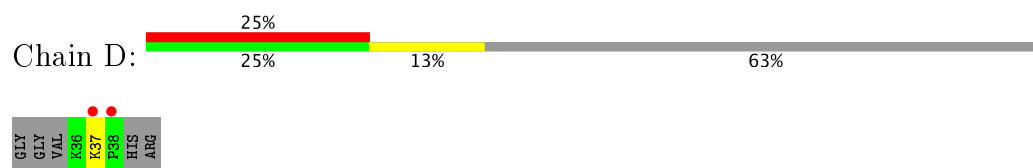
- Molecule 1: Metal-response element-binding transcription factor 2



- Molecule 2: Peptide from Histone H3.1



- Molecule 2: Peptide from Histone H3.1



- Molecule 3: DNA (5'-D(*GP*GP*GP*CP*GP*GP*CP*CP*GP*CP*CP*CP*T)-3')





- Molecule 3: DNA (5'-D(*GP*GP*GP*CP*GP*GP*CP*CP*GP*CP*CP*CP*T)-3')

Chain F:  100%

There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	137.74Å 137.74Å 101.23Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.59 – 2.25 46.59 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.59-2.25) 100.0 (46.59-2.25)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.96 (at 2.24Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.203 , 0.231 0.199 , 0.230	Depositor DCC
R_{free} test set	2690 reflections (5.10%)	DCC
Wilson B-factor (Å ²)	32.5	Xtriage
Anisotropy	0.152	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 43.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5844	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.58% 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, M3L

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	0/2566	0.37	0/3466
1	B	0.22	0/2488	0.41	1/3359 (0.0%)
2	C	0.19	0/17	0.44	0/23
2	D	0.27	0/17	0.59	0/23
3	E	0.52	0/294	0.91	0/452
3	F	0.50	0/294	0.93	0/452
All	All	0.27	0/5676	0.48	1/7775 (0.0%)

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	B	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	72	LEU	CA-CB-CG	6.56	130.39	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	72	LEU	Peptide

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	2500	0	2449	16	0
1	B	2423	0	2380	18	0
2	C	28	0	40	1	0
2	D	28	0	40	0	0
3	E	263	0	146	0	0
3	F	263	0	146	0	0
4	A	4	0	0	0	0
4	B	4	0	0	0	0
5	A	151	0	0	1	0
5	B	146	0	0	1	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	12	0	0	0	0
5	F	20	0	0	0	0
All	All	5844	0	5201	34	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 3.

All (34) 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:B:332:MET:HG3	1:B:347:ARG:HG2	1.65	0.78
1:A:118:GLU:H	1:A:131:GLN:HE21	1.34	0.75
1:A:240:PHE:H	1:A:276:ASN:HD21	1.34	0.75
1:B:240:PHE:H	1:B:276:ASN:HD21	1.35	0.74
1:A:79:ILE:HG22	1:A:85:LYS:HG2	1.70	0.73
1:A:134:HIS:CE1	1:A:152:ARG:H	2.18	0.62
1:B:114:GLU:HB2	1:B:117:ASN:HB3	1.84	0.59
1:A:106:THR:HG21	1:A:127:GLN:HB3	1.86	0.58
1:B:261:ARG:HH21	1:B:264:LEU:HD11	1.69	0.58
1:A:134:HIS:HE1	1:A:152:ARG:H	1.53	0.56
1:A:60:LEU:HD13	2:C:38:PRO:HG3	1.88	0.56
1:A:302:ARG:NH1	5:A:502:HOH:O	2.33	0.55
1:B:354:PRO:HG2	1:B:357:VAL:HG23	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:LYS:HD3	1:A:302:ARG:HA	1.90	0.54
1:B:204:CYS:SG	1:B:205:TYR:N	2.83	0.51
1:B:297:ASN:HD22	1:B:316:ARG:HH11	1.59	0.49
1:A:204:CYS:SG	1:A:205:TYR:N	2.86	0.49
1:A:53:LEU:HB2	1:A:94:GLN:HB3	1.95	0.49
1:B:175:LEU:HG	1:B:179:LYS:HD3	1.94	0.48
1:A:196:LYS:HB3	1:A:212:TRP:CD1	2.49	0.47
1:B:261:ARG:NH2	1:B:264:LEU:HD11	2.30	0.46
1:B:328:LYS:NZ	5:B:511:HOH:O	2.49	0.46
1:B:271:HIS:CG	1:B:352:PRO:HG3	2.51	0.45
1:B:196:LYS:HB3	1:B:212:TRP:CD1	2.53	0.44
1:A:55:ARG:HD3	1:A:208:GLY:HA3	2.00	0.43
1:B:351:PRO:HA	1:B:352:PRO:HD3	1.90	0.42
1:A:190:GLU:HB2	1:A:199:VAL:HG22	2.00	0.42
1:A:55:ARG:HB3	1:A:92:ASP:HB3	2.02	0.41
1:B:73:LYS:HD2	1:B:73:LYS:HA	1.87	0.41
1:A:92:ASP:CG	1:A:209:PRO:HD3	2.41	0.41
1:B:135:THR:HA	1:B:136:PRO:HA	1.96	0.40
1:B:92:ASP:CG	1:B:209:PRO:HD3	2.41	0.40
1:B:283:LYS:HG3	1:B:286:PHE:CZ	2.57	0.40
1:B:297:ASN:ND2	1:B:316:ARG:HH11	2.20	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	305/317 (96%)	299 (98%)	6 (2%)	0	100	100
1	B	292/317 (92%)	281 (96%)	11 (4%)	0	100	100
2	C	1/8 (12%)	1 (100%)	0	0	100	100
2	D	1/8 (12%)	1 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	599/650 (92%)	582 (97%)	17 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	278/282 (99%)	272 (98%)	6 (2%)	57	67
1	B	268/282 (95%)	264 (98%)	4 (2%)	70	79
2	C	2/5 (40%)	2 (100%)	0	100	100
2	D	2/5 (40%)	1 (50%)	1 (50%)	0	0
All	All	550/574 (96%)	539 (98%)	11 (2%)	60	70

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	104	VAL
1	A	147	GLU
1	A	173	LYS
1	A	304	HIS
1	A	327	TYR
1	A	357	VAL
1	B	72	LEU
1	B	73	LYS
1	B	238	MET
1	B	357	VAL
2	D	37	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	GLN

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Mol	Chain	Res	Type
1	A	134	HIS
1	A	153	GLN
1	A	201	GLN
1	A	232	GLN
1	A	276	ASN
1	A	299	ASN
1	A	319	HIS
1	A	356	ASN
1	B	180	GLN
1	B	276	ASN
1	B	297	ASN
1	B	299	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	M3L	C	36	2	11,11,12	0.80	1 (9%)	11,14,16	0.99	1 (9%)
2	M3L	D	36	2	11,11,12	0.80	1 (9%)	11,14,16	0.87	1 (9%)

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
2	M3L	C	36	2	-	0/8/10/12	0/0/0/0
2	M3L	D	36	2	-	0/8/10/12	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	36	M3L	CA-C	2.19	1.53	1.50
2	D	36	M3L	CA-C	2.22	1.53	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	36	M3L	CB-CA-C	-2.88	106.90	111.65
2	D	36	M3L	CB-CA-C	-2.47	107.59	111.65

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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	309/317 (97%)	0.30	16 (5%) 28 32	22, 34, 60, 87	0
1	B	298/317 (94%)	0.63	36 (12%) 5 4	21, 36, 73, 102	0
2	C	2/8 (25%)	3.90	2 (100%) 0 0	77, 77, 77, 88	0
2	D	2/8 (25%)	4.62	2 (100%) 0 0	77, 77, 77, 88	0
3	E	13/13 (100%)	0.44	2 (15%) 2 2	33, 36, 61, 68	0
3	F	13/13 (100%)	-0.03	0 100 100	30, 34, 48, 49	0
All	All	637/676 (94%)	0.48	58 (9%) 10 11	21, 35, 68, 102	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	97	ALA	7.0
1	A	146	ASP	7.0
1	B	112	TYR	6.9
1	A	112	TYR	6.8
1	B	111	GLU	6.7
1	B	109	GLN	6.3
1	B	105	CYS	5.9
1	B	113	SER	5.9
1	B	72	LEU	5.8
2	D	37	LYS	5.7
1	A	44	CYS	5.6
2	C	37	LYS	5.3
1	A	96	GLY	5.2
1	B	116	PRO	5.0
1	B	115	ALA	5.0
1	B	120	VAL	4.9
1	B	140	CYS	4.6
1	B	110	GLU	4.5
1	B	119	MET	4.4

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Mol	Chain	Res	Type	RSRZ
1	B	95	THR	4.2
1	B	357	VAL	4.2
1	B	71	ILE	3.9
1	B	114	GLU	3.7
1	A	95	THR	3.7
2	D	38	PRO	3.6
1	B	129	TYR	3.5
1	B	121	ILE	3.5
1	A	103	MET	3.4
3	E	13	DT	3.4
1	B	107	ILE	3.3
1	A	144	ASP	3.2
1	B	108	CYS	3.2
1	A	143	ILE	3.1
1	A	46	PHE	3.1
1	B	123	ASP	2.9
1	B	126	GLY	2.8
1	B	134	HIS	2.8
1	B	131	GLN	2.7
1	B	117	ASN	2.6
1	B	358	ALA	2.6
1	B	122	CYS	2.6
1	A	147	GLU	2.6
3	E	12	DC	2.5
2	C	38	PRO	2.5
1	A	142	VAL	2.4
1	B	356	ASN	2.4
1	B	118	GLU	2.3
1	B	46	PHE	2.3
1	B	139	ASP	2.3
1	B	106	THR	2.2
1	A	119	MET	2.2
1	B	79	ILE	2.2
1	A	79	ILE	2.2
1	B	173	LYS	2.1
1	A	148	LYS	2.1
1	B	45	LYS	2.1
1	B	130	HIS	2.0
1	A	140	CYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
2	M3L	C	36	12/13	0.81	0.29	-	39,57,74,76	0
2	M3L	D	36	12/13	0.76	0.21	-	43,52,75,81	0

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
4	ZN	A	404	1/1	0.99	0.15	0.73	25,25,25,25	0
4	ZN	B	403	1/1	0.99	0.15	0.68	24,24,24,24	0
4	ZN	B	404	1/1	1.00	0.16	0.37	22,22,22,22	0
4	ZN	A	403	1/1	0.99	0.12	-0.51	26,26,26,26	0
4	ZN	A	402	1/1	0.98	0.12	-0.57	38,38,38,38	0
4	ZN	A	401	1/1	0.98	0.09	-0.77	41,41,41,41	0
4	ZN	B	402	1/1	0.94	0.06	-	75,75,75,75	0
4	ZN	B	401	1/1	0.97	0.07	-	54,54,54,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.