



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:11 AM UTC

PDB ID : 7LFK / pdb_00007lfk
Title : MODEL OF MHC CLASS Ib H2-M3 WITH MOUSE ND1 N-TERMINAL
HEPTAPEPTIDE, THR MUTANT, REFINED AT 1.60 ANGSTROMS RES-
OLUTION
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Deposited on : 2021-01-17
Resolution : 1.60 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

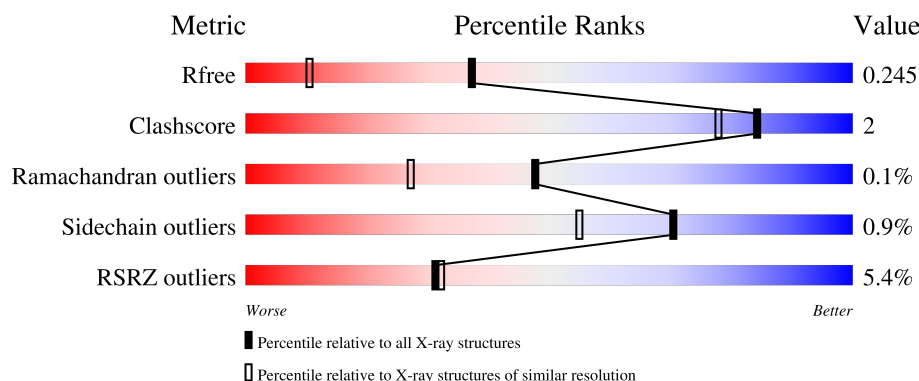
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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}	180053	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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 $\leq 5\%$. 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	282	3% 93% • •
1	D	282	7% 93% • •
2	B	99	% 93% 7%
2	E	99	6% 88% 12%
3	C	7	43% 57% 29% 14%

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Mol	Chain	Length	Quality of chain
3	F	7	29% 100%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12797 atoms, of which 6062 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 Histocompatibility 2, M region locus 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	275	Total	C	H	N	O	S	0	1	0
			4396	1412	2158	396	418	12			
1	D	275	Total	C	H	N	O	S	0	1	0
			4396	1412	2158	396	418	12			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLY	deletion	UNP Q31093
A	277	HIS	-	expression tag	UNP Q31093
A	278	HIS	-	expression tag	UNP Q31093
A	279	HIS	-	expression tag	UNP Q31093
A	280	HIS	-	expression tag	UNP Q31093
A	281	HIS	-	expression tag	UNP Q31093
A	282	HIS	-	expression tag	UNP Q31093
D	?	-	GLY	deletion	UNP Q31093
D	277	HIS	-	expression tag	UNP Q31093
D	278	HIS	-	expression tag	UNP Q31093
D	279	HIS	-	expression tag	UNP Q31093
D	280	HIS	-	expression tag	UNP Q31093
D	281	HIS	-	expression tag	UNP Q31093
D	282	HIS	-	expression tag	UNP Q31093

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	99	Total	C	H	N	O	S	0	1	0
			1629	527	804	138	153	7			
2	E	99	Total	C	H	N	O	S	0	1	0
			1628	527	803	138	153	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	85	ASP	ALA	variant	UNP P01887
E	85	ASP	ALA	variant	UNP P01887

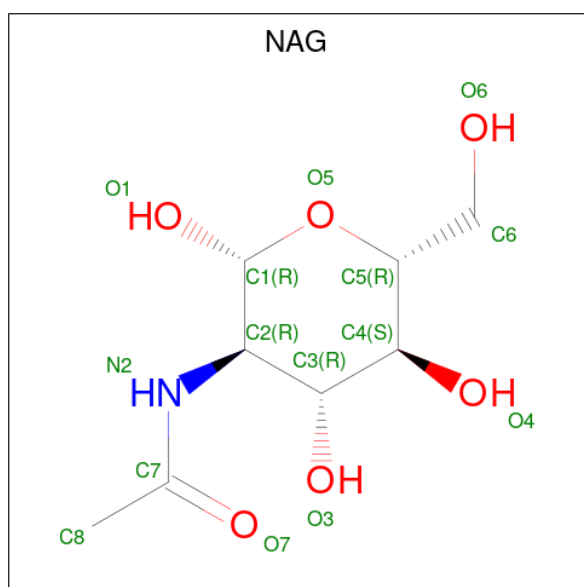
- Molecule 3 is a protein called Heptapeptide from NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	7	Total	C	H	N	O	S	0	0	0
			127	44	63	8	11	1			
3	F	7	Total	C	H	N	O	S	0	0	0
			127	44	63	8	11	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	6	THR	ILE	engineered mutation	UNP P03888
F	6	THR	ILE	engineered mutation	UNP P03888

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	H	N	O		0	0
			27	8	13	1	5			

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total 3	Na 3	0	0
5	D	2	Total 2	Na 2	0	0
5	E	1	Total 1	Na 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	164	Total 164	O 164	0	0
6	B	84	Total 84	O 84	0	0
6	C	5	Total 5	O 5	0	0
6	D	163	Total 163	O 163	0	0
6	E	43	Total 43	O 43	0	0
6	F	2	Total 2	O 2	0	0

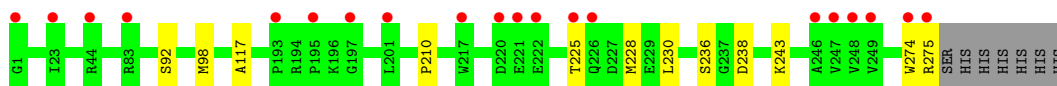
3 Residue-property plots

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: Histocompatibility 2, M region locus 3



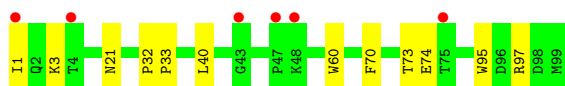
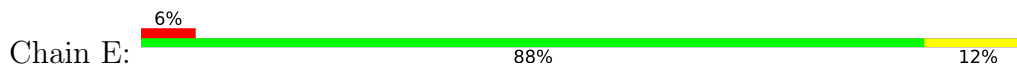
- Molecule 1: Histocompatibility 2, M region locus 3



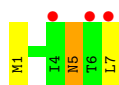
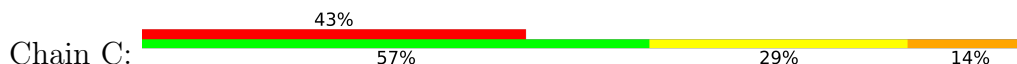
- Molecule 2: Beta-2-microglobulin



- Molecule 2: Beta-2-microglobulin



- Molecule 3: Heptapeptide from NADH-ubiquinone oxidoreductase chain 1



- Molecule 3: Heptapeptide from NADH-ubiquinone oxidoreductase chain 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	63.43Å 69.10Å 54.80Å 102.54° 93.86° 114.10°	Depositor
Resolution (Å)	31.62 – 1.60 31.62 – 1.60	Depositor EDS
% Data completeness (in resolution range)	86.6 (31.62-1.60) 86.6 (31.62-1.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.80 (at 1.60Å)	Xtriage
Refinement program	PHENIX 1.18.2-3874	Depositor
R, R_{free}	0.208 , 0.244 0.209 , 0.245	Depositor DCC
R_{free} test set	2001 reflections (1.86%)	wwPDB-VP
Wilson B-factor (Å ²)	19.1	Xtriage
Anisotropy	0.337	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 41.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12797	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.63% 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: NAG, FME, NA

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	0.94	0/2301	0.87	0/3121
1	D	0.86	0/2301	0.83	0/3121
2	B	1.07	0/854	0.94	0/1158
2	E	0.70	0/854	0.75	0/1159
3	C	0.86	0/55	0.82	0/72
3	F	1.00	0/55	0.72	0/72
All	All	0.90	0/6420	0.85	0/8703

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	2238	2158	2157	8	0
1	D	2238	2158	2158	8	0
2	B	825	804	803	5	0
2	E	825	803	803	9	0
3	C	64	63	63	3	0
3	F	64	63	63	0	0
4	A	14	13	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	3	0	0	0	0
5	D	2	0	0	0	0
5	E	1	0	0	0	0
6	A	164	0	0	0	0
6	B	84	0	0	1	0
6	C	5	0	0	0	0
6	D	163	0	0	1	0
6	E	43	0	0	0	0
6	F	2	0	0	0	0
All	All	6735	6062	6060	28	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 2.

All (28) 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:D:230:LEU:HD11	1:D:243:LYS:HE3	1.85	0.57
1:D:236:SER:OG	1:D:238:ASP:OD1	2.21	0.57
1:D:117:ALA:HB2	2:E:60:TRP:CE2	2.40	0.56
2:E:73:THR:HG22	2:E:74:GLU:N	2.20	0.55
2:B:74:GLU:HG3	2:B:75:THR:HG23	1.89	0.54
2:B:32:PRO:HB2	2:B:33:PRO:HD2	1.90	0.53
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.43	0.52
1:D:210:PRO:HG3	6:D:548:HOH:O	2.13	0.48
1:A:80:THR:HG21	3:C:7:LEU:CB	2.44	0.47
1:A:219:LYS:O	1:A:220:ASP:C	2.57	0.47
1:A:260:TYR:CE1	1:A:271:ALA:HB2	2.52	0.44
2:E:1:ILE:HD12	2:E:3:LYS:CE	2.48	0.44
2:B:33:PRO:O	2:B:54:MET:HE1	2.17	0.44
2:E:1:ILE:HD12	2:E:3:LYS:HE2	2.00	0.43
1:D:98[A]:MET:HE2	2:E:60:TRP:CZ3	2.53	0.43
2:E:32:PRO:HB2	2:E:33:PRO:HD2	1.99	0.43
2:B:74:GLU:HG2	6:B:132:HOH:O	2.18	0.42
2:E:73:THR:CG2	2:E:74:GLU:N	2.82	0.42
1:D:225:THR:HA	1:D:228:MET:HE2	2.01	0.42
1:A:262:HIS:CD2	1:A:269:PRO:HG3	2.55	0.42
1:A:260:TYR:HA	1:A:270:LEU:O	2.20	0.42
1:A:80:THR:HG21	3:C:7:LEU:HB3	2.01	0.42
1:D:274:TRP:O	1:D:275:ARG:HB2	2.19	0.41
1:D:274:TRP:O	1:D:275:ARG:CB	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:5:ASN:OD1	3:C:5:ASN:N	2.54	0.41
2:E:95:TRP:CH2	2:E:97:ARG:HG2	2.56	0.40
1:A:258:THR:OG1	1:A:273:LYS:HE2	2.21	0.40
2:E:21:ASN:HB3	2:E:70:PHE:CE1	2.56	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	274/282 (97%)	269 (98%)	4 (2%)	1 (0%)	30	14
1	D	274/282 (97%)	267 (97%)	7 (3%)	0	100	100
2	B	98/99 (99%)	98 (100%)	0	0	100	100
2	E	98/99 (99%)	97 (99%)	1 (1%)	0	100	100
3	C	5/7 (71%)	5 (100%)	0	0	100	100
3	F	5/7 (71%)	5 (100%)	0	0	100	100
All	All	754/776 (97%)	741 (98%)	12 (2%)	1 (0%)	48	27

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	220	ASP

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	238/244 (98%)	236 (99%)	2 (1%)	73	59
1	D	238/244 (98%)	237 (100%)	1 (0%)	84	75
2	B	95/94 (101%)	94 (99%)	1 (1%)	65	46
2	E	95/94 (101%)	94 (99%)	1 (1%)	65	46
3	C	6/6 (100%)	5 (83%)	1 (17%)	2	0
3	F	6/6 (100%)	6 (100%)	0	100	100
All	All	678/688 (98%)	672 (99%)	6 (1%)	70	55

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	77	ASN
1	A	222	GLU
2	B	1	ILE
3	C	5	ASN
1	D	92	SER
2	E	40	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	GLN
1	A	113	HIS
1	D	115	GLN
1	D	262	HIS

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	$\# Z > 2$
3	FME	C	1	3	8,9,10	1.04	0	8,9,11	1.14	1 (12%)
3	FME	F	1	3	8,9,10	0.96	0	8,9,11	0.54	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
3	FME	C	1	3	-	1/7/9/11	-
3	FME	F	1	3	-	1/7/9/11	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	C	1	FME	CA-N-CN	-2.25	119.36	122.82

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	F	1	FME	CB-CA-N-CN
3	C	1	FME	CB-CA-N-CN

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 6 are monoatomic - leaving 1 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	$\# Z > 2$
4	NAG	A	2001	1	14,14,15	0.43	0	17,19,21	0.57	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
4	NAG	A	2001	1	-	0/6/23/26	0/1/1/1

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	275/282 (97%)	0.52	9 (3%)	49	52	12, 30, 54, 78	1 (0%)
1	D	275/282 (97%)	0.72	20 (7%)	21	21	12, 31, 65, 87	1 (0%)
2	B	99/99 (100%)	0.41	1 (1%)	79	83	15, 25, 49, 60	1 (1%)
2	E	99/99 (100%)	0.89	6 (6%)	27	27	23, 36, 59, 70	1 (1%)
3	C	6/7 (85%)	2.13	3 (50%)	0	0	30, 40, 52, 60	0
3	F	6/7 (85%)	1.29	2 (33%)	1	1	23, 31, 51, 56	0
All	All	760/776 (97%)	0.65	41 (5%)	31	32	12, 31, 57, 87	4 (0%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	1	ILE	5.0
1	D	225	THR	3.8
3	C	7	LEU	3.7
1	D	274	TRP	3.7
2	E	75	THR	3.7
2	E	1	ILE	3.6
1	D	195	PRO	3.3
1	D	275	ARG	3.3
1	D	248	VAL	3.3
3	C	4	ILE	3.0
1	A	220	ASP	3.0
1	A	146	ARG	2.9
1	A	90	GLY	2.7
1	D	221	GLU	2.7
1	A	1	GLY	2.6
1	D	222	GLU	2.6
1	D	1	GLY	2.5
2	E	48	LYS	2.5
1	D	247	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	226	GLN	2.5
1	D	193	PRO	2.4
1	D	246	ALA	2.4
3	F	7	LEU	2.4
3	F	6	THR	2.4
2	E	47	PRO	2.3
1	A	275	ARG	2.3
2	E	43	GLY	2.3
1	D	201	LEU	2.3
1	D	249	VAL	2.3
1	D	197	GLY	2.3
2	E	4[A]	THR	2.2
1	D	217	TRP	2.2
1	D	23	ILE	2.2
1	D	220	ASP	2.2
1	D	44	ARG	2.2
1	A	271	ALA	2.1
1	A	151	GLY	2.1
1	D	83	ARG	2.1
3	C	6	THR	2.1
1	A	107	MET	2.0
1	A	260	TYR	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. 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	FME	C	1	10/11	0.97	0.07	14,20,25,25	0
3	FME	F	1	10/11	0.98	0.05	16,20,24,24	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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($\text{\AA}^2$)	Q<0.9
4	NAG	A	2001	14/15	0.63	0.18	57,68,81,87	0
5	NA	A	2003	1/1	0.88	0.13	48,48,48,48	0
5	NA	D	301	1/1	0.88	0.13	50,50,50,50	0
5	NA	A	2004	1/1	0.91	0.12	47,47,47,47	0
5	NA	D	302	1/1	0.93	0.13	36,36,36,36	0
5	NA	E	101	1/1	0.93	0.12	52,52,52,52	0
5	NA	A	2002	1/1	0.95	0.12	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.