



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:28 AM GMT

PDB ID : 3ERR
Title : Microtubule binding domain from mouse cytoplasmic dynein as a fusion with seryl-tRNA synthetase
Authors : Carter, A.P.
Deposited on : 2008-10-03
Resolution : 2.27 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtrriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

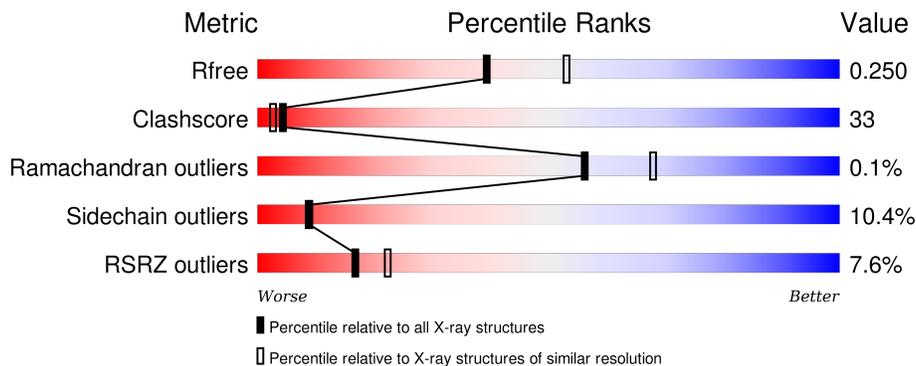
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.27 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	5193 (2.30-2.26)
Clashscore	102246	5929 (2.30-2.26)
Ramachandran outliers	100387	5851 (2.30-2.26)
Sidechain outliers	100360	5850 (2.30-2.26)
RSRZ outliers	91569	5204 (2.30-2.26)

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	536	 4% (poor fit), 65% (0-1 outliers), 28% (2-3 outliers), 5% (4+ outliers)
1	B	536	 10% (poor fit), 54% (0-1 outliers), 38% (2-3 outliers), 5% (4+ outliers)

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 8589 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 fusion protein of microtubule binding domain from mouse cytoplasmic dynein and seryl-tRNA synthetase from *Thermus thermophilus*.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	527	4210	2677	741	776	16	0	0	0
1	B	527	4210	2677	741	776	16	0	0	0

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP Q9JHU4
A	2	VAL	-	EXPRESSION TAG	UNP Q9JHU4
A	3	ASP	-	EXPRESSION TAG	UNP Q9JHU4
A	4	LEU	-	EXPRESSION TAG	UNP Q9JHU4
A	5	LYS	-	EXPRESSION TAG	UNP Q9JHU4
A	6	ARG	-	EXPRESSION TAG	UNP Q9JHU4
A	7	LEU	-	EXPRESSION TAG	UNP Q9JHU4
A	8	ARG	-	EXPRESSION TAG	UNP Q9JHU4
A	9	GLN	-	EXPRESSION TAG	UNP Q9JHU4
A	10	GLU	-	EXPRESSION TAG	UNP Q9JHU4
A	11	PRO	-	EXPRESSION TAG	UNP Q9JHU4
A	12	GLU	-	EXPRESSION TAG	UNP Q9JHU4
A	13	VAL	-	EXPRESSION TAG	UNP Q9JHU4
A	14	PHE	-	EXPRESSION TAG	UNP Q9JHU4
A	15	HIS	-	EXPRESSION TAG	UNP Q9JHU4
A	16	ARG	-	EXPRESSION TAG	UNP Q9JHU4
A	17	ALA	-	EXPRESSION TAG	UNP Q9JHU4
A	18	ILE	-	EXPRESSION TAG	UNP Q9JHU4
A	19	ARG	-	EXPRESSION TAG	UNP Q9JHU4
A	20	GLU	-	EXPRESSION TAG	UNP Q9JHU4
A	21	LYS	-	EXPRESSION TAG	UNP Q9JHU4
A	22	GLY	-	EXPRESSION TAG	UNP Q9JHU4
A	23	VAL	-	EXPRESSION TAG	UNP Q9JHU4
A	24	ALA	-	EXPRESSION TAG	UNP Q9JHU4

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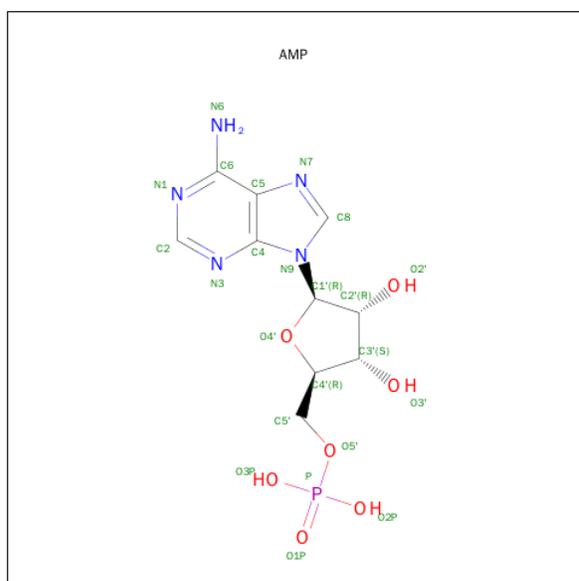
Chain	Residue	Modelled	Actual	Comment	Reference
A	25	LEU	-	EXPRESSION TAG	UNP Q9JHU4
A	26	ASP	-	EXPRESSION TAG	UNP Q9JHU4
A	27	LEU	-	EXPRESSION TAG	UNP Q9JHU4
A	28	GLU	-	EXPRESSION TAG	UNP Q9JHU4
A	29	ALA	-	EXPRESSION TAG	UNP Q9JHU4
A	30	LEU	-	EXPRESSION TAG	UNP Q9JHU4
A	31	LEU	-	EXPRESSION TAG	UNP Q9JHU4
A	32	ALA	-	EXPRESSION TAG	UNP Q9JHU4
A	33	VAL	-	EXPRESSION TAG	UNP Q9JHU4
A	34	ASP	-	EXPRESSION TAG	UNP Q9JHU4
A	3323	ALA	CYS	ENGINEERED	UNP Q9JHU4
A	3387	ALA	CYS	ENGINEERED	UNP Q9JHU4
A	420	GLY	-	EXPRESSION TAG	UNP P34945
A	421	ALA	-	EXPRESSION TAG	UNP P34945
A	422	HIS	-	EXPRESSION TAG	UNP P34945
A	423	HIS	-	EXPRESSION TAG	UNP P34945
A	424	HIS	-	EXPRESSION TAG	UNP P34945
A	425	HIS	-	EXPRESSION TAG	UNP P34945
A	426	HIS	-	EXPRESSION TAG	UNP P34945
A	427	HIS	-	EXPRESSION TAG	UNP P34945
B	1	MET	-	EXPRESSION TAG	UNP Q9JHU4
B	2	VAL	-	EXPRESSION TAG	UNP Q9JHU4
B	3	ASP	-	EXPRESSION TAG	UNP Q9JHU4
B	4	LEU	-	EXPRESSION TAG	UNP Q9JHU4
B	5	LYS	-	EXPRESSION TAG	UNP Q9JHU4
B	6	ARG	-	EXPRESSION TAG	UNP Q9JHU4
B	7	LEU	-	EXPRESSION TAG	UNP Q9JHU4
B	8	ARG	-	EXPRESSION TAG	UNP Q9JHU4
B	9	GLN	-	EXPRESSION TAG	UNP Q9JHU4
B	10	GLU	-	EXPRESSION TAG	UNP Q9JHU4
B	11	PRO	-	EXPRESSION TAG	UNP Q9JHU4
B	12	GLU	-	EXPRESSION TAG	UNP Q9JHU4
B	13	VAL	-	EXPRESSION TAG	UNP Q9JHU4
B	14	PHE	-	EXPRESSION TAG	UNP Q9JHU4
B	15	HIS	-	EXPRESSION TAG	UNP Q9JHU4
B	16	ARG	-	EXPRESSION TAG	UNP Q9JHU4
B	17	ALA	-	EXPRESSION TAG	UNP Q9JHU4
B	18	ILE	-	EXPRESSION TAG	UNP Q9JHU4
B	19	ARG	-	EXPRESSION TAG	UNP Q9JHU4
B	20	GLU	-	EXPRESSION TAG	UNP Q9JHU4
B	21	LYS	-	EXPRESSION TAG	UNP Q9JHU4
B	22	GLY	-	EXPRESSION TAG	UNP Q9JHU4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	23	VAL	-	EXPRESSION TAG	UNP Q9JHU4
B	24	ALA	-	EXPRESSION TAG	UNP Q9JHU4
B	25	LEU	-	EXPRESSION TAG	UNP Q9JHU4
B	26	ASP	-	EXPRESSION TAG	UNP Q9JHU4
B	27	LEU	-	EXPRESSION TAG	UNP Q9JHU4
B	28	GLU	-	EXPRESSION TAG	UNP Q9JHU4
B	29	ALA	-	EXPRESSION TAG	UNP Q9JHU4
B	30	LEU	-	EXPRESSION TAG	UNP Q9JHU4
B	31	LEU	-	EXPRESSION TAG	UNP Q9JHU4
B	32	ALA	-	EXPRESSION TAG	UNP Q9JHU4
B	33	VAL	-	EXPRESSION TAG	UNP Q9JHU4
B	34	ASP	-	EXPRESSION TAG	UNP Q9JHU4
B	3323	ALA	CYS	ENGINEERED	UNP Q9JHU4
B	3387	ALA	CYS	ENGINEERED	UNP Q9JHU4
B	420	GLY	-	EXPRESSION TAG	UNP P34945
B	421	ALA	-	EXPRESSION TAG	UNP P34945
B	422	HIS	-	EXPRESSION TAG	UNP P34945
B	423	HIS	-	EXPRESSION TAG	UNP P34945
B	424	HIS	-	EXPRESSION TAG	UNP P34945
B	425	HIS	-	EXPRESSION TAG	UNP P34945
B	426	HIS	-	EXPRESSION TAG	UNP P34945
B	427	HIS	-	EXPRESSION TAG	UNP P34945

- Molecule 2 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C₁₀H₁₄N₅O₇P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	71	Total	O	0	0
			71	71		
3	B	52	Total	O	0	0
			52	52		

4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	144.30Å 144.30Å 159.95Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.27 - 2.27 49.24 - 2.27	Depositor EDS
% Data completeness (in resolution range)	99.1 (49.27-2.27) 99.1 (49.24-2.27)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 2.27Å)	Xtriage
Refinement program	REFMAC 5.4.0067	Depositor
R, R_{free}	0.197 , 0.247 0.217 , 0.250	Depositor DCC
R_{free} test set	2856 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	51.6	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 60.7	EDS
Estimated twinning fraction	0.021 for h,-h-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 57094 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8589	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% 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, 0.375 respectively for untwinned datasets, and 0.333, 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:
AMP

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	0.99	6/4301 (0.1%)	0.99	16/5828 (0.3%)
1	B	0.90	6/4301 (0.1%)	0.93	14/5828 (0.2%)
All	All	0.95	12/8602 (0.1%)	0.96	30/11656 (0.3%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	369	GLY	CA-C	7.26	1.63	1.51
1	A	349	CYS	CB-SG	-6.83	1.70	1.82
1	B	115	GLU	CD-OE2	6.31	1.32	1.25
1	A	115	GLU	CG-CD	6.02	1.60	1.51
1	A	3278	GLU	CB-CG	-5.92	1.40	1.52

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	329	ARG	NE-CZ-NH1	12.33	126.46	120.30
1	A	344	ARG	NE-CZ-NH1	-12.18	114.21	120.30
1	A	329	ARG	NE-CZ-NH1	11.30	125.95	120.30
1	A	408	LEU	CA-CB-CG	-9.66	93.08	115.30
1	A	344	ARG	NE-CZ-NH2	9.39	124.99	120.30

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	4210	0	4230	238	0
1	B	4210	0	4230	323	0
2	A	23	0	12	0	0
2	B	23	0	12	0	0
3	A	71	0	0	2	0
3	B	52	0	0	5	0
All	All	8589	0	8484	558	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 33.

The worst 5 of 558 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:7:LEU:HD12	1:B:14:PHE:CD2	1.52	1.44
1:B:3308:MET:SD	1:B:3311:PRO:HB3	1.58	1.43
1:A:3339:ILE:HD13	1:A:3340:ILE:N	1.33	1.41
1:A:3308:MET:CE	1:A:3312:PRO:HD2	1.55	1.34
1:B:3340:ILE:HA	1:B:3345:PHE:CD1	1.64	1.32

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	525/536 (98%)	512 (98%)	12 (2%)	1 (0%)	52 63
1	B	525/536 (98%)	513 (98%)	12 (2%)	0	100 100
All	All	1050/1072 (98%)	1025 (98%)	24 (2%)	1 (0%)	56 68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	11	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	443/451 (98%)	400 (90%)	43 (10%)	10	11
1	B	443/451 (98%)	394 (89%)	49 (11%)	8	7
All	All	886/902 (98%)	794 (90%)	92 (10%)	9	9

5 of 92 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	390	MET
1	B	3334	LYS
1	B	348	SER
1	A	408	LEU
1	B	3294	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	15	HIS
1	B	3376	ASN
1	B	379	ASN
1	B	3301	HIS
1	B	3381	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 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	AMP	A	1507	-	20,25,25	1.54	2 (10%)	22,38,38	2.27	7 (31%)
2	AMP	B	1508	-	20,25,25	1.40	3 (15%)	22,38,38	2.16	6 (27%)

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	AMP	A	1507	-	-	0/6/26/26	0/3/3/3
2	AMP	B	1508	-	-	0/6/26/26	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1508	AMP	C2-N3	2.49	1.36	1.32
2	B	1508	AMP	O4'-C1'	3.32	1.45	1.41
2	A	1507	AMP	C5-C4	3.35	1.48	1.40
2	B	1508	AMP	C5-C4	3.68	1.48	1.40
2	A	1507	AMP	O4'-C1'	4.63	1.47	1.41

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	1507	AMP	N3-C2-N1	-7.43	123.21	128.89
2	B	1508	AMP	N3-C2-N1	-6.90	123.61	128.89
2	A	1507	AMP	C4'-O4'-C1'	-2.94	106.49	109.72
2	B	1508	AMP	C4-C5-N7	-2.78	106.92	109.48
2	A	1507	AMP	O3P-P-O5'	-2.58	99.12	106.56

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	527/536 (98%)	0.24	24 (4%) 36 44	23, 55, 90, 112	0
1	B	527/536 (98%)	0.55	56 (10%) 8 11	7, 68, 118, 162	0
All	All	1054/1072 (98%)	0.39	80 (7%) 17 22	7, 59, 110, 162	0

The worst 5 of 80 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3309	ALA	6.7
1	B	266	VAL	6.5
1	B	3306	ARG	6.1
1	B	3283	VAL	6.0
1	B	3276	VAL	5.8

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	AMP	A	1507	23/23	0.96	0.15	-0.97	36,43,66,71	0
2	AMP	B	1508	23/23	0.89	0.12	-2.02	63,72,90,92	0

6.5 Other polymers [i](#)

There are no such residues in this entry.