Full wwPDB X-ray Structure Validation Report (i)

Sep 6, 2023 – 03:12 PM EDT

PDB ID	:	4H1U
Title	:	Nucleotide-free human dynamin-1-like protein GTPase-GED fusion
Authors	:	Wenger, J.; Klinglmayr, E.; Puehringer, S.; Goettig, P.
Deposited on	:	2012-09-11
Resolution	:	2.30 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 (i)) were used in the production of this report:

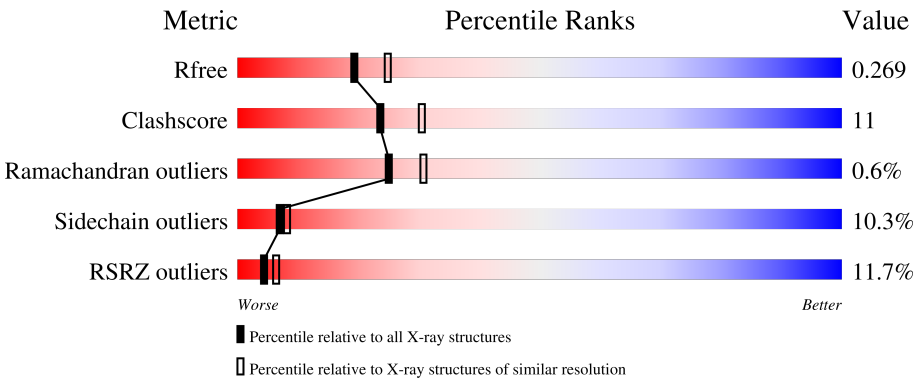
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

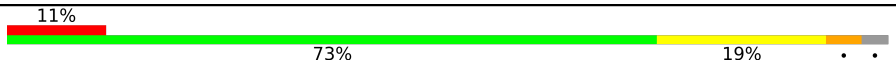
The reported resolution of this entry is 2.30 Å.

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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	369	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2908 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.

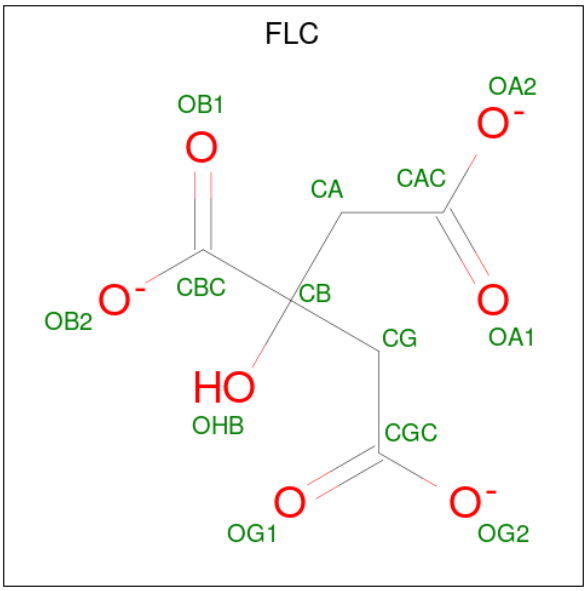
- Molecule 1 is a protein called Dynamin-1-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	358	2766	1731	489	537	9	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	703	GLY	-	linker	UNP O00429
A	704	SER	-	linker	UNP O00429
A	705	GLY	-	linker	UNP O00429
A	706	SER	-	linker	UNP O00429
A	707	GLY	-	linker	UNP O00429
A	708	SER	-	linker	UNP O00429
A	709	GLY	-	linker	UNP O00429
A	710	SER	-	linker	UNP O00429
A	737	LEU	-	expression tag	UNP O00429
A	738	GLU	-	expression tag	UNP O00429
A	739	HIS	-	expression tag	UNP O00429
A	740	HIS	-	expression tag	UNP O00429
A	741	HIS	-	expression tag	UNP O00429
A	742	HIS	-	expression tag	UNP O00429
A	743	HIS	-	expression tag	UNP O00429
A	744	HIS	-	expression tag	UNP O00429

- Molecule 2 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 13 6 7	0	0

- Molecule 3 is water.

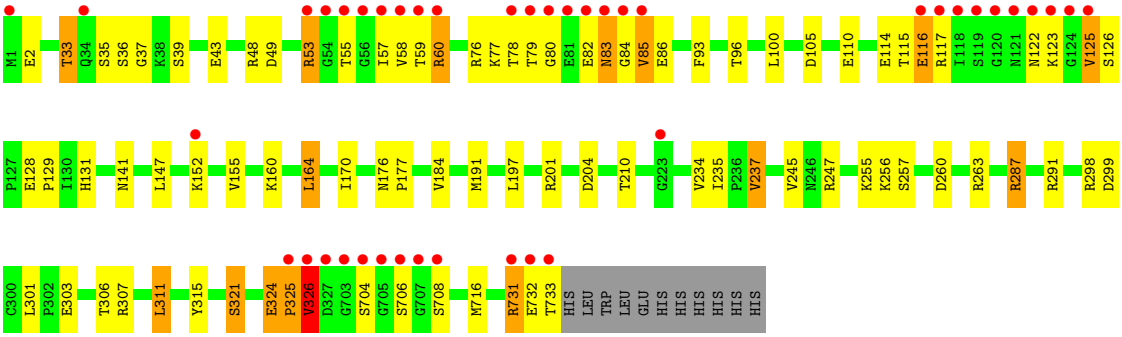
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	129	Total O 129 129	0	0

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: Dynamin-1-like protein

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	53.50Å 151.43Å 42.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.85 – 2.30 19.85 – 2.30	Depositor EDS
% Data completeness (in resolution range)	95.2 (19.85-2.30) 95.3 (19.85-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	2.59 (at 2.30Å)	Xtriage
Refinement program	PHENIX 1.8_1069	Depositor
R, R_{free}	0.230 , 0.269 0.231 , 0.269	Depositor DCC
R_{free} test set	772 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	25.2	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 43.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	2908	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.30% 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: FLC

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	0.30	1/2800 (0.0%)	0.49	0/3789

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	321	SER	CB-OG	-5.78	1.34	1.42

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	2766	0	2860	63	0
2	A	13	0	5	3	0
3	A	129	0	0	4	0
All	All	2908	0	2865	63	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 11.

All (63) 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:324:GLU:HG3	1:A:325:PRO:HA	1.40	1.03
1:A:324:GLU:CG	1:A:325:PRO:HA	1.94	0.97
1:A:37:GLY:HA2	2:A:801:FLC:HA2	1.52	0.89
1:A:324:GLU:CB	1:A:325:PRO:HA	2.06	0.82
1:A:49:ASP:OD1	1:A:247:ARG:NH2	2.13	0.80
1:A:58:VAL:HG22	1:A:59:THR:H	1.52	0.75
1:A:53:ARG:HH21	2:A:801:FLC:HG2	1.57	0.70
1:A:298:ARG:NH1	1:A:299:ASP:OD1	2.24	0.69
1:A:325:PRO:O	1:A:326:VAL:HG12	1.91	0.69
1:A:116:GLU:OE1	1:A:117:ARG:N	2.28	0.66
1:A:247:ARG:NH1	1:A:256:LYS:O	2.27	0.66
1:A:125:VAL:CG1	1:A:125:VAL:O	2.45	0.64
1:A:83:ASN:OD1	1:A:83:ASN:N	2.33	0.62
1:A:33:THR:HG22	1:A:36:SER:HB3	1.81	0.62
1:A:82:GLU:HG3	1:A:83:ASN:N	2.16	0.60
1:A:60:ARG:HE	1:A:116:GLU:HG2	1.66	0.60
1:A:160:LYS:NZ	3:A:1014:HOH:O	2.35	0.60
1:A:326:VAL:O	1:A:326:VAL:HG13	2.02	0.59
1:A:43:GLU:OE1	1:A:53:ARG:NH1	2.37	0.57
1:A:33:THR:HG23	1:A:35:SER:H	1.70	0.57
1:A:260:ASP:OD1	1:A:263:ARG:NH1	2.38	0.57
1:A:257:SER:OG	1:A:260:ASP:OD2	2.24	0.55
1:A:155:VAL:HG21	1:A:164:LEU:HD13	1.90	0.54
1:A:53:ARG:NH2	2:A:801:FLC:HG2	2.22	0.54
1:A:126:SER:OG	1:A:128:GLU:OE1	2.22	0.53
1:A:60:ARG:HH21	1:A:116:GLU:HB2	1.74	0.52
1:A:83:ASN:CB	1:A:84:GLY:HA2	2.40	0.51
1:A:115:THR:O	1:A:117:ARG:HG3	2.11	0.51
1:A:287:ARG:O	1:A:291:ARG:HG2	2.11	0.51
1:A:60:ARG:HE	1:A:116:GLU:HB3	1.77	0.50
1:A:324:GLU:CB	1:A:325:PRO:CA	2.85	0.50
1:A:324:GLU:HB3	1:A:325:PRO:HA	1.93	0.50
1:A:82:GLU:HG3	1:A:83:ASN:H	1.75	0.49
1:A:315:TYR:CZ	1:A:716:MET:HG2	2.48	0.49
1:A:210:THR:O	1:A:237:VAL:HG13	2.13	0.49
1:A:76:ARG:CZ	1:A:100:LEU:HD11	2.43	0.48
1:A:78:THR:OG1	1:A:85:VAL:O	2.24	0.48
1:A:125:VAL:O	1:A:125:VAL:HG13	2.12	0.48
1:A:122:ASN:HB3	1:A:123:LYS:H	1.48	0.47
1:A:82:GLU:CG	1:A:83:ASN:N	2.77	0.47
1:A:210:THR:HB	1:A:237:VAL:HG22	1.97	0.47
1:A:57:ILE:HG13	1:A:58:VAL:H	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:GLU:O	1:A:114:GLU:HB2	2.18	0.44
1:A:201:ARG:HA	1:A:204:ASP:O	2.17	0.44
1:A:125:VAL:O	1:A:125:VAL:HG12	2.17	0.44
1:A:60:ARG:HE	1:A:116:GLU:CG	2.31	0.44
1:A:191:MET:CG	1:A:235:ILE:HD11	2.48	0.44
1:A:184:VAL:O	3:A:921:HOH:O	2.21	0.43
1:A:191:MET:HG2	1:A:235:ILE:HD11	1.99	0.43
1:A:197:LEU:O	1:A:201:ARG:HG3	2.18	0.43
1:A:197:LEU:HD11	1:A:235:ILE:HD13	2.00	0.43
1:A:60:ARG:HE	1:A:116:GLU:CB	2.31	0.43
1:A:731:ARG:HB2	1:A:732:GLU:H	1.65	0.42
1:A:307:ARG:O	1:A:311:LEU:HB2	2.19	0.42
1:A:79:THR:HG23	1:A:80:GLY:HA2	2.01	0.42
1:A:77:LYS:HD2	1:A:77:LYS:H	1.85	0.42
1:A:131:HIS:HB3	3:A:961:HOH:O	2.20	0.41
1:A:147:LEU:HD13	1:A:170:ILE:HA	2.02	0.41
1:A:128:GLU:HA	1:A:129:PRO:HD3	1.91	0.41
1:A:141:ASN:ND2	3:A:1016:HOH:O	2.50	0.41
1:A:176:ASN:HA	1:A:177:PRO:HD3	1.95	0.40
1:A:325:PRO:O	1:A:326:VAL:CG1	2.66	0.40
1:A:93:PHE:HB2	1:A:96:THR:OG1	2.22	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	356/369 (96%)	338 (95%)	16 (4%)	2 (1%)	25 31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	326	VAL
1	A	325	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	312/323 (97%)	280 (90%)	32 (10%)	7 8

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	A	33	THR
1	A	39	SER
1	A	48	ARG
1	A	53	ARG
1	A	55	THR
1	A	60	ARG
1	A	83	ASN
1	A	85	VAL
1	A	86	GLU
1	A	105	ASP
1	A	116	GLU
1	A	125	VAL
1	A	152	LYS
1	A	164	LEU
1	A	234	VAL
1	A	237	VAL
1	A	245	VAL
1	A	255	LYS
1	A	287	ARG
1	A	301	LEU
1	A	303	GLU
1	A	306	THR
1	A	311	LEU
1	A	321	SER

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Mol	Chain	Res	Type
1	A	324	GLU
1	A	326	VAL
1	A	704	SER
1	A	706	SER
1	A	708	SER
1	A	731	ARG
1	A	733	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

1 ligand is 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	FLC	A	801	-	12,12,12	1.64	2 (16%)	17,17,17	0.72	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
2	FLC	A	801	-	-	1/16/16/16	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	FLC	CB-CBC	3.94	1.57	1.53
2	A	801	FLC	CG-CB	2.17	1.56	1.53

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	FLC	OHB-CB-CG-CGC

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	FLC	3	0

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	358/369 (97%)	0.80	42 (11%) 4 6	4, 18, 79, 134	8 (2%)

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	703	GLY	22.4
1	A	704	SER	20.5
1	A	326	VAL	16.5
1	A	327	ASP	13.5
1	A	118	ILE	13.4
1	A	119	SER	12.4
1	A	325	PRO	9.7
1	A	80	GLY	9.3
1	A	81	GLU	9.3
1	A	707	GLY	7.6
1	A	117	ARG	7.5
1	A	1	MET	7.4
1	A	55	THR	7.0
1	A	121	ASN	7.0
1	A	58	VAL	6.7
1	A	733	THR	6.7
1	A	705	GLY	6.5
1	A	83	ASN	6.4
1	A	79	THR	6.4
1	A	706	SER	5.1
1	A	116	GLU	4.9
1	A	120	GLY	4.9
1	A	122	ASN	4.8
1	A	82	GLU	4.7
1	A	56	GLY	4.6
1	A	54	GLY	4.4
1	A	57	ILE	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	59	THR	4.2
1	A	84	GLY	4.2
1	A	123	LYS	4.0
1	A	85	VAL	3.8
1	A	732	GLU	3.5
1	A	124	GLY	3.2
1	A	708	SER	2.9
1	A	223	GLY	2.9
1	A	53	ARG	2.5
1	A	731	ARG	2.3
1	A	34	GLN	2.3
1	A	152	LYS	2.3
1	A	125	VAL	2.1
1	A	78	THR	2.1
1	A	60	ARG	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
2	FLC	A	801	13/13	0.77	0.28	22,30,42,44	0

6.5 Other polymers (i)

There are no such residues in this entry.