Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2020 – 09:42 pm BST

PDB ID	:	4C0B
Title	:	Structure of wild-type Clp1p-Pcf11p (454 -563) complex
Authors	:	Fribourg, S.; Dupin, A.F.
Deposited on	:	2013-08-01
Resolution	:	2.77 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 following versions of software and data (see references ⓘ) were used in the production of this report:

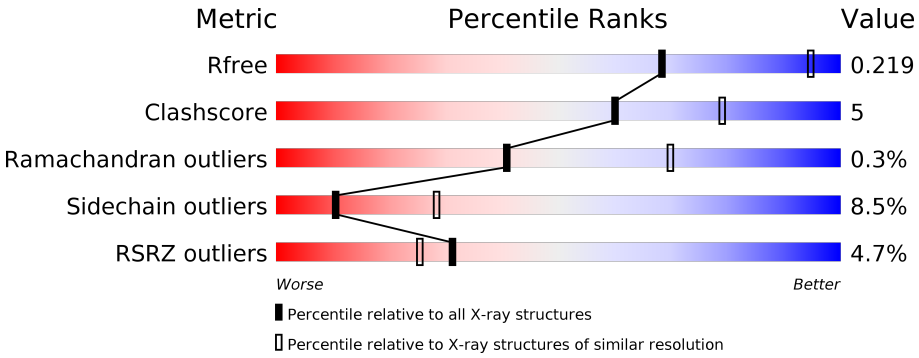
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.77 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	4107 (2.80-2.76)
Clashscore	141614	4575 (2.80-2.76)
Ramachandran outliers	138981	4487 (2.80-2.76)
Sidechain outliers	138945	4489 (2.80-2.76)
RSRZ outliers	127900	4027 (2.80-2.76)

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 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	446	5% 81% 13%
1	B	446	3% 80% 15%
2	C	110	4% 22% 75%
2	D	110	5% 25% 6% 67%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7464 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 MRNA CLEAVAGE AND POLYADENYLATION FACTOR CLP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	428	Total	C	N	O	S	0	0	0
			3410	2191	571	636	12			
1	B	430	Total	C	N	O	S	0	0	0
			3426	2201	574	639	12			

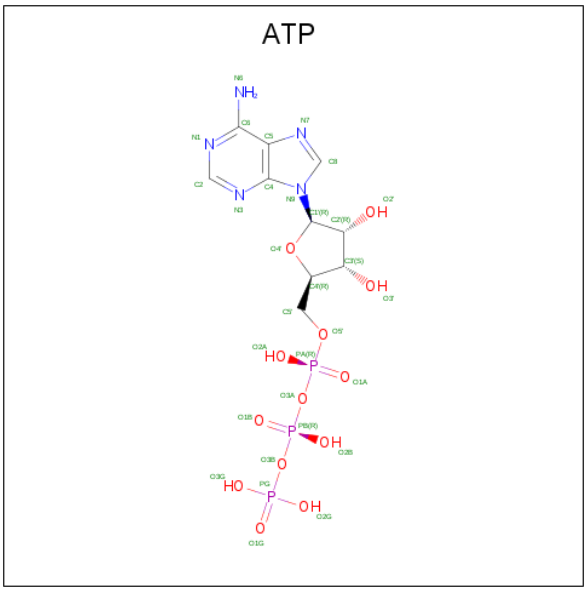
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	446	GLN	-	expression tag	UNP Q08685
B	446	GLN	-	expression tag	UNP Q08685

- Molecule 2 is a protein called PCF11P.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	27	Total	C	N	O	0	0	0
			230	143	41	46			
2	D	36	Total	C	N	O	0	0	0
			290	177	51	62			

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O P 31 10 5 13 3	0	0
3	B	1	Total C N O P 31 10 5 13 3	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Mg 1 1	0	0
4	A	1	Total Mg 1 1	0	0

- Molecule 5 is water.

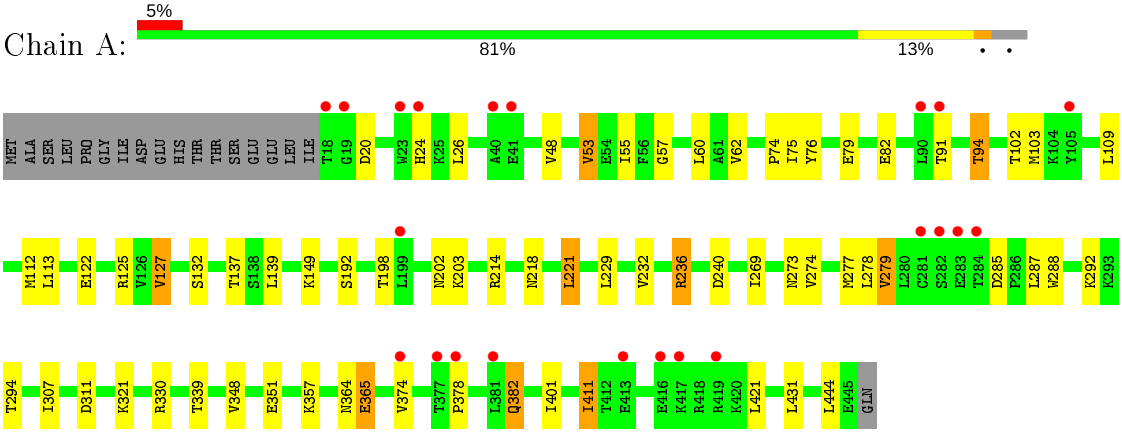
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	19	Total O 19 19	0	0
5	B	18	Total O 18 18	0	0
5	C	1	Total O 1 1	0	0
5	D	6	Total O 6 6	0	0

3 Residue-property plots

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.

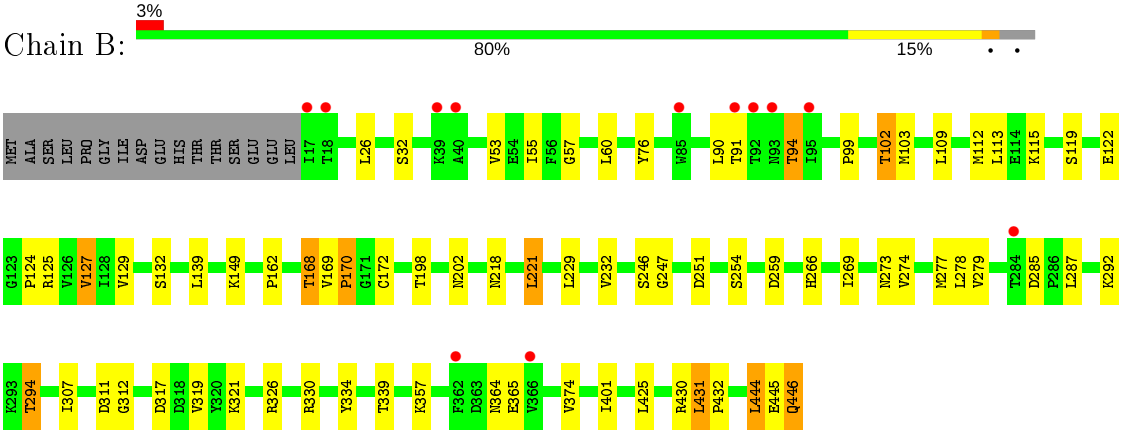
- Molecule 1: MRNA CLEAVAGE AND POLYADENYLATION FACTOR CLP1

Chain A:



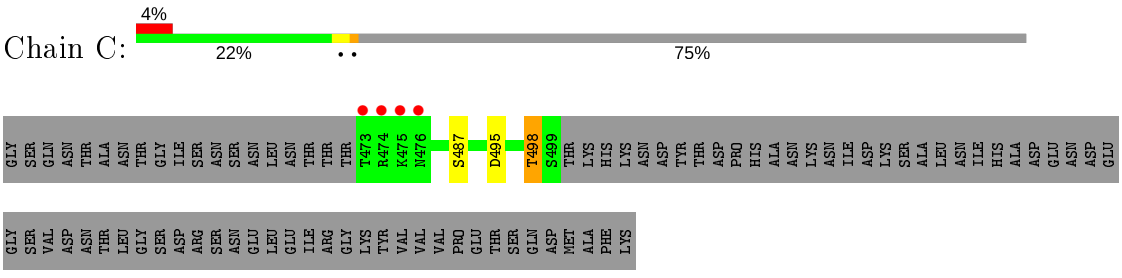
- Molecule 1: MRNA CLEAVAGE AND POLYADENYLATION FACTOR CLP1

Chain B:

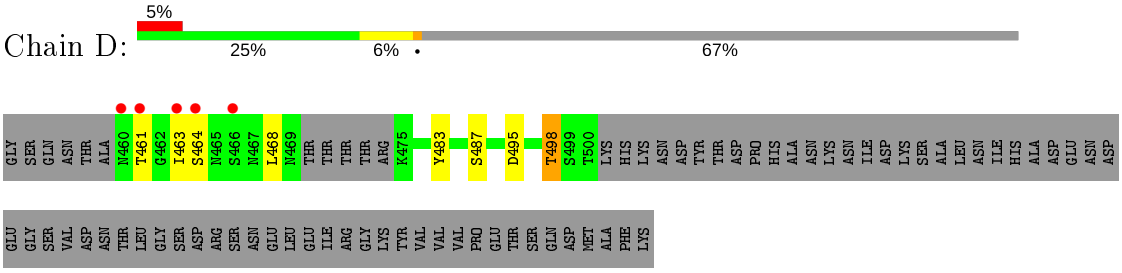


- Molecule 2: PCF11P

Chain C:



• Molecule 2: PCF11P



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	89.35Å 95.41Å 182.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.55 – 2.77 40.46 – 2.77	Depositor EDS
% Data completeness (in resolution range)	99.6 (40.55-2.77) 99.6 (40.46-2.77)	Depositor EDS
R_{merge}	0.01	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.54 (at 2.77Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.179 , 0.214 0.191 , 0.219	Depositor DCC
R_{free} test set	2018 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	58.4	Xtriage
Anisotropy	0.213	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 52.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7464	wwPDB-VP
Average B, all atoms (Å^2)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ATP

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	0.48	0/3487	0.78	0/4744
1	B	0.51	0/3503	0.81	3/4766 (0.1%)
2	C	0.53	0/235	0.69	0/317
2	D	0.71	0/294	0.90	0/397
All	All	0.51	0/7519	0.79	3/10224 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	246	SER	C-N-CA	-6.03	109.64	122.30
1	B	172	CYS	N-CA-C	5.36	125.48	111.00
1	B	170	PRO	N-CA-C	5.27	125.81	112.10

There are no chirality outliers.

There are no planarity outliers.

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	3410	0	3443	33	0
1	B	3426	0	3461	34	0
2	C	230	0	212	1	0
2	D	290	0	264	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	31	0	12	1	0
3	B	31	0	12	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	19	0	0	0	0
5	B	18	0	0	0	0
5	C	1	0	0	0	0
5	D	6	0	0	0	0
All	All	7464	0	7404	68	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 (68) 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:364:ASN:O	1:A:365:GLU:HB2	1.61	1.00
1:A:127:VAL:HG22	1:A:274:VAL:HG11	1.53	0.90
1:B:127:VAL:HG22	1:B:274:VAL:HG11	1.51	0.89
1:B:168:THR:HG23	2:D:483:TYR:OH	1.76	0.83
1:A:364:ASN:O	1:A:365:GLU:CB	2.36	0.74
1:B:364:ASN:O	1:B:365:GLU:HB2	1.87	0.73
1:B:278:LEU:HB3	1:B:307:ILE:HD11	1.70	0.73
1:A:278:LEU:HB3	1:A:307:ILE:HD11	1.70	0.72
2:D:463:ILE:HG12	2:D:464:SER:H	1.63	0.63
1:A:55:ILE:HD12	1:A:60:LEU:HD21	1.84	0.60
1:B:55:ILE:HD12	1:B:60:LEU:HD21	1.85	0.58
1:A:48:VAL:HG23	1:A:62:VAL:HA	1.84	0.58
1:B:326:ARG:NH2	1:B:444:LEU:O	2.36	0.58
1:A:378:PRO:O	1:A:382:GLN:HB2	2.04	0.58
1:A:57:GLY:O	1:A:149:LYS:NZ	2.34	0.56
1:B:168:THR:HG22	1:B:169:VAL:H	1.71	0.55
1:B:91:THR:H	1:B:94:THR:HG22	1.72	0.54
1:B:162:PRO:O	1:B:170:PRO:O	2.25	0.54
1:B:278:LEU:HB3	1:B:307:ILE:CD1	2.38	0.54
1:B:57:GLY:O	1:B:149:LYS:NZ	2.34	0.54
1:B:102:THR:HG21	1:B:311:ASP:H	1.73	0.53
2:D:495:ASP:HA	2:D:498:THR:HB	1.90	0.53
1:B:312:GLY:HA3	3:B:1447:ATP:N6	2.24	0.53
1:A:125:ARG:NH2	1:B:122:GLU:OE2	2.42	0.53
1:B:168:THR:HG23	2:D:483:TYR:HH	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:ILE:HD13	1:A:421:LEU:HD23	1.92	0.52
1:A:278:LEU:HB3	1:A:307:ILE:CD1	2.39	0.52
1:A:91:THR:H	1:A:94:THR:HG22	1.73	0.52
1:A:53:VAL:CG2	1:A:75:ILE:HG22	2.40	0.52
1:A:102:THR:HG21	1:A:311:ASP:H	1.75	0.51
2:C:495:ASP:HA	2:C:498:THR:HB	1.91	0.51
1:B:124:PRO:O	1:B:247:GLY:HA3	2.12	0.50
1:B:125:ARG:HD2	1:B:273:ASN:O	2.12	0.49
1:A:236:ARG:NH1	1:A:240:ASP:OD2	2.45	0.49
1:A:357:LYS:HB2	1:A:374:VAL:HG22	1.94	0.49
1:B:218:ASN:CG	1:B:221:LEU:HB2	2.33	0.49
1:B:266:HIS:HE2	1:B:294:THR:HG22	1.78	0.49
1:A:279:VAL:CG1	1:A:288:TRP:HZ3	2.26	0.48
1:B:364:ASN:O	1:B:365:GLU:CB	2.57	0.48
1:A:122:GLU:OE2	1:B:125:ARG:NH2	2.46	0.48
1:B:357:LYS:HB2	1:B:374:VAL:HG22	1.94	0.48
1:A:127:VAL:HG22	1:A:274:VAL:CG1	2.36	0.47
1:B:127:VAL:CG2	1:B:274:VAL:HG11	2.35	0.47
1:B:269:ILE:HD11	1:B:277:MET:HE1	1.96	0.46
1:A:74:PRO:HG3	3:A:1446:ATP:C6	2.51	0.46
1:A:279:VAL:HG13	1:A:288:TRP:HZ3	1.81	0.45
1:A:269:ILE:HD11	1:A:277:MET:HE1	1.99	0.45
1:B:127:VAL:HG22	1:B:274:VAL:CG1	2.34	0.45
1:B:198:THR:HG21	1:B:202:ASN:HD21	1.82	0.44
1:A:53:VAL:HG21	1:A:75:ILE:HG22	2.00	0.43
1:B:334:TYR:OH	2:D:468:LEU:HD23	2.19	0.43
1:B:76:TYR:CZ	1:B:103:MET:HG3	2.53	0.43
1:A:76:TYR:CZ	1:A:103:MET:HG3	2.53	0.43
1:A:198:THR:HG21	1:A:202:ASN:HD21	1.83	0.42
1:B:269:ILE:HD11	1:B:277:MET:CE	2.48	0.42
1:A:269:ILE:HD11	1:A:277:MET:CE	2.48	0.42
1:A:53:VAL:HG22	1:A:75:ILE:HG22	2.00	0.42
1:B:129:VAL:HG12	1:B:279:VAL:HG13	2.02	0.42
1:B:431:LEU:HD22	1:B:432:PRO:HD2	2.02	0.41
1:A:218:ASN:CG	1:A:221:LEU:HB2	2.39	0.41
1:A:279:VAL:HG13	1:A:288:TRP:CZ3	2.55	0.41
1:B:446:GLN:HG3	1:B:446:GLN:H	1.69	0.41
1:A:269:ILE:HA	1:A:274:VAL:HB	2.03	0.41
1:B:317:ASP:OD2	1:B:319:VAL:HB	2.20	0.41
1:B:32:SER:HA	1:B:99:PRO:HA	2.03	0.40
1:A:192:SER:HA	1:A:203:LYS:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:ASP:HB3	1:A:24:HIS:HE1	1.86	0.40
1:A:279:VAL:CG1	1:A:288:TRP:CZ3	3.05	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	426/446 (96%)	408 (96%)	18 (4%)	0	100 100
1	B	428/446 (96%)	407 (95%)	21 (5%)	0	100 100
2	C	25/110 (23%)	23 (92%)	1 (4%)	1 (4%)	3 8
2	D	32/110 (29%)	26 (81%)	4 (12%)	2 (6%)	1 3
All	All	911/1112 (82%)	864 (95%)	44 (5%)	3 (0%)	41 70

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	498	THR
2	D	498	THR
2	D	461	THR

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	384/401 (96%)	350 (91%)	34 (9%)	9 26
1	B	386/401 (96%)	352 (91%)	34 (9%)	10 27
2	C	25/98 (26%)	24 (96%)	1 (4%)	31 62
2	D	33/98 (34%)	32 (97%)	1 (3%)	41 72
All	All	828/998 (83%)	758 (92%)	70 (8%)	10 28

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	LEU
1	A	53	VAL
1	A	79	GLU
1	A	82	GLU
1	A	94	THR
1	A	109	LEU
1	A	112	MET
1	A	113	LEU
1	A	127	VAL
1	A	132	SER
1	A	137	THR
1	A	139	LEU
1	A	214	ARG
1	A	221	LEU
1	A	229	LEU
1	A	232	VAL
1	A	236	ARG
1	A	273	ASN
1	A	279	VAL
1	A	285	ASP
1	A	287	LEU
1	A	292	LYS
1	A	294	THR
1	A	321	LYS
1	A	330	ARG
1	A	339	THR
1	A	348	VAL
1	A	351	GLU
1	A	365	GLU
1	A	382	GLN
1	A	401	ILE
1	A	411	ILE
1	A	431	LEU

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Mol	Chain	Res	Type
1	A	444	LEU
1	B	26	LEU
1	B	53	VAL
1	B	90	LEU
1	B	94	THR
1	B	102	THR
1	B	109	LEU
1	B	112	MET
1	B	113	LEU
1	B	115	LYS
1	B	119	SER
1	B	127	VAL
1	B	132	SER
1	B	139	LEU
1	B	168	THR
1	B	221	LEU
1	B	229	LEU
1	B	232	VAL
1	B	251	ASP
1	B	254	SER
1	B	259	ASP
1	B	285	ASP
1	B	287	LEU
1	B	292	LYS
1	B	294	THR
1	B	321	LYS
1	B	330	ARG
1	B	339	THR
1	B	401	ILE
1	B	425	LEU
1	B	430	ARG
1	B	431	LEU
1	B	444	LEU
1	B	445	GLU
1	B	446	GLN
2	C	487	SER
2	D	487	SER

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

Mol	Chain	Res	Type
1	A	24	HIS

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Mol	Chain	Res	Type
1	A	202	ASN
1	A	257	GLN
1	B	202	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)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\#\|Z\| > 2$
3	ATP	B	1447	4	26,33,33	0.71	0	31,52,52	0.75	1 (3%)
3	ATP	A	1446	4	26,33,33	0.71	0	31,52,52	0.73	1 (3%)

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	ATP	B	1447	4	-	1/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ATP	A	1446	4	-	0/18/38/38	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	1447	ATP	C5-C6-N6	2.27	123.80	120.35
3	A	1446	ATP	C5-C6-N6	2.23	123.74	120.35

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1447	ATP	PA-O3A-PB-O2B

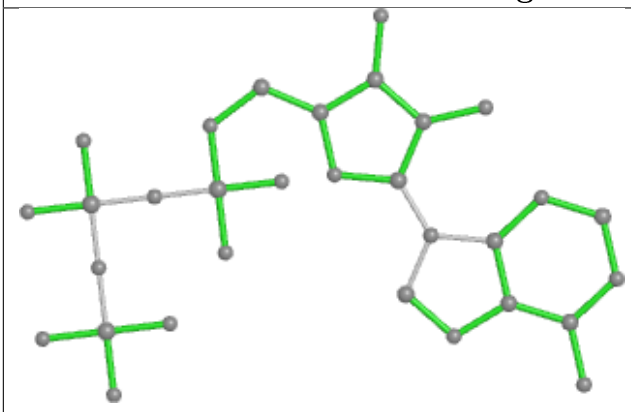
There are no ring outliers.

2 monomers are involved in 2 short contacts:

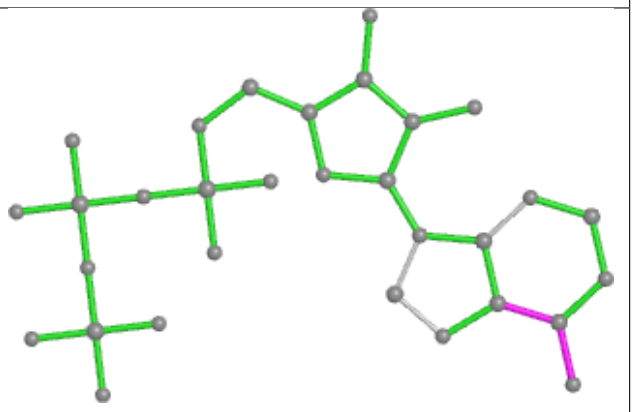
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1447	ATP	1	0
3	A	1446	ATP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

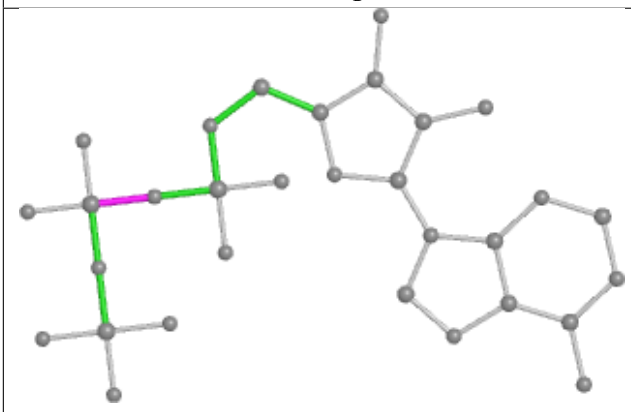
Ligand ATP B 1447



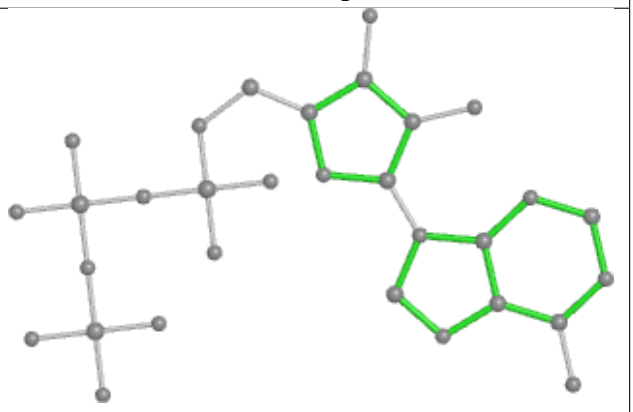
Bond lengths



Bond angles

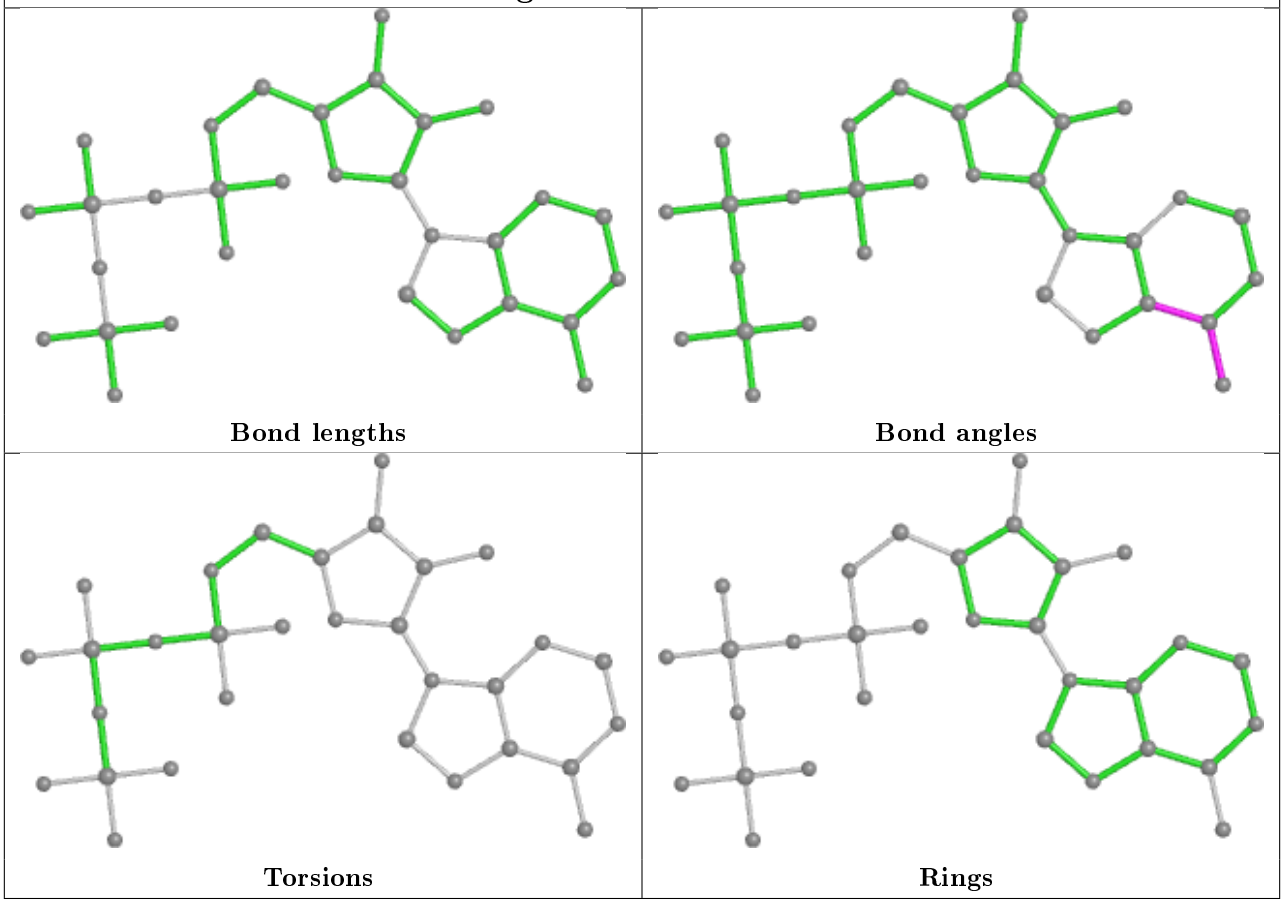


Torsions



Rings

Ligand ATP A 1446



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, 95^{th} 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	428/446 (95%)	0.13	22 (5%)	28	22	35, 70, 117, 144	0
1	B	430/446 (96%)	0.03	12 (2%)	53	48	33, 57, 93, 125	0
2	C	27/110 (24%)	0.49	4 (14%)	2	1	37, 54, 119, 128	0
2	D	36/110 (32%)	0.68	5 (13%)	2	2	35, 60, 122, 129	0
All	All	921/1112 (82%)	0.12	43 (4%)	31	25	33, 63, 111, 144	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	460	ASN	6.5
2	D	463	ILE	5.4
1	A	417	LYS	5.0
1	B	17	ILE	4.4
2	D	461	THR	4.0
2	C	474	ARG	4.0
1	A	18	THR	3.9
1	B	284	THR	3.8
1	A	378	PRO	3.7
2	D	464	SER	3.6
1	A	283	GLU	3.6
1	B	18	THR	3.5
2	C	473	THR	3.5
2	C	475	LYS	3.5
1	A	91	THR	3.4
2	C	476	ASN	3.4
1	B	366	VAL	3.2
1	A	374	VAL	3.0
1	B	91	THR	2.9
1	B	93	ASN	2.6
1	A	413	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	284	THR	2.6
1	A	199	LEU	2.6
1	B	40	ALA	2.5
2	D	466	SER	2.4
1	B	362	PHE	2.4
1	A	281	CYS	2.4
1	A	381	LEU	2.4
1	A	19	GLY	2.3
1	B	95	ILE	2.3
1	A	282	SER	2.3
1	A	24	HIS	2.3
1	B	39	LYS	2.3
1	A	41	GLU	2.2
1	B	85	TRP	2.2
1	A	419	ARG	2.2
1	B	92	THR	2.2
1	A	416	GLU	2.1
1	A	377	THR	2.1
1	A	40	ALA	2.1
1	A	23	TRP	2.1
1	A	105	TYR	2.1
1	A	90	LEU	2.1

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. The B-factors column lists the minimum, median, 95^{th} 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
4	MG	B	1448	1/1	0.90	0.43	66,66,66,66	0

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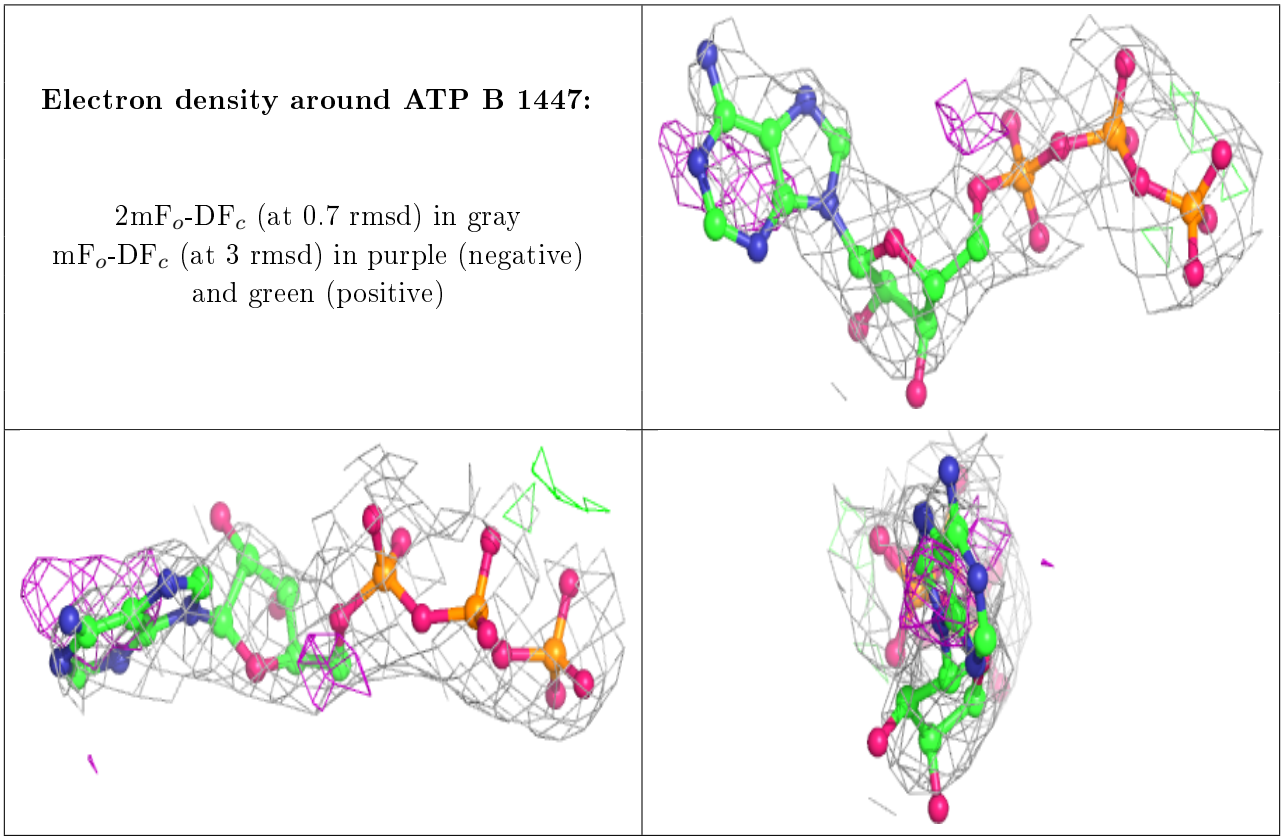
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	ATP	B	1447	31/31	0.91	0.21	103,110,117,118	0
3	ATP	A	1446	31/31	0.93	0.19	120,124,134,136	0
4	MG	A	1447	1/1	0.95	0.43	67,67,67,67	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

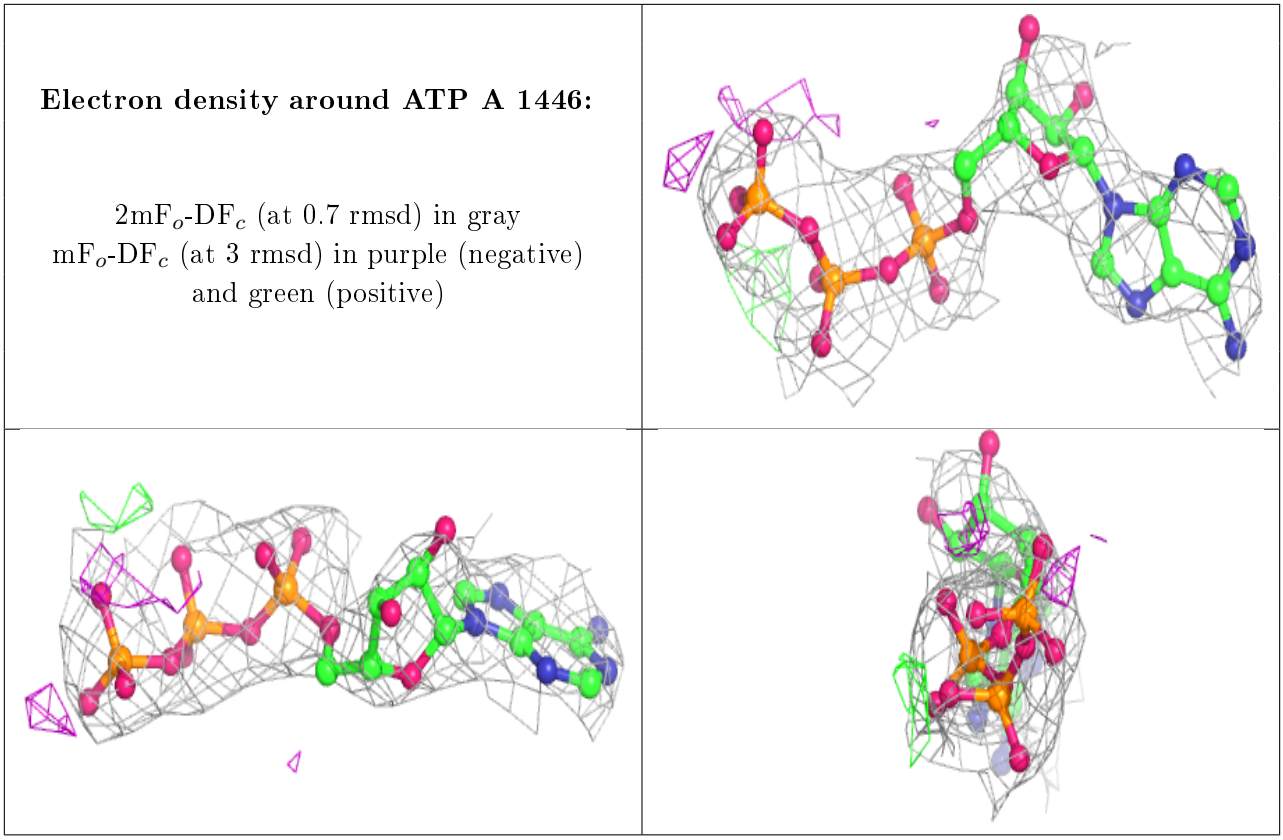
Electron density around ATP B 1447:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around ATP A 1446:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.