



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:21 PM GMT

PDB ID : 4LDW  
Title : Crystal structure of the DNA Binding Domain of arabidopsis thaliana auxin response factor 1, P21 structure  
Authors : boer, D.R.; Coll, M.  
Deposited on : 2013-06-25  
Resolution : 2.67 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](mailto: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.

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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)  
Xtriage (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

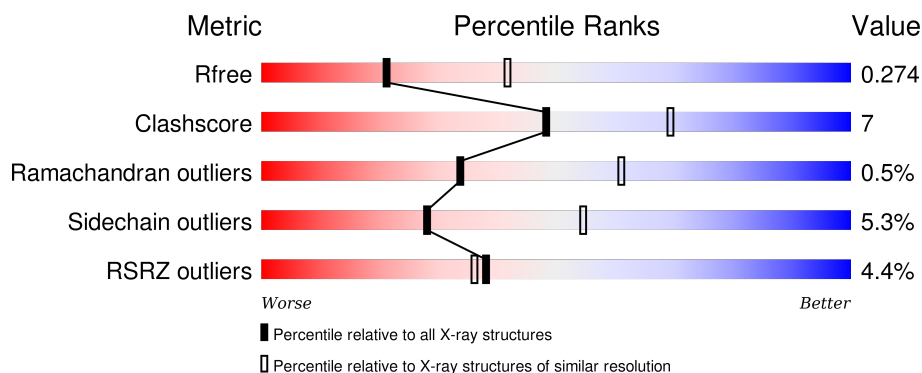
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.67 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	2780 (2.70-2.66)
Clashscore	102246	3138 (2.70-2.66)
Ramachandran outliers	100387	3089 (2.70-2.66)
Sidechain outliers	100360	3089 (2.70-2.66)
RSRZ outliers	91569	2789 (2.70-2.66)

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  $\geq 3$ , 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	362	
1	B	362	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5160 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 Auxin response factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	311	Total	C	N	O	S	0	0	0
			2505	1586	450	456	13			
1	B	324	Total	C	N	O	S	0	0	0
			2599	1641	465	480	13			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	356	ASN	-	EXPRESSION TAG	UNP Q8L7G0
A	357	SER	-	EXPRESSION TAG	UNP Q8L7G0
A	358	TYR	-	EXPRESSION TAG	UNP Q8L7G0
A	359	SER	-	EXPRESSION TAG	UNP Q8L7G0
A	360	GLN	-	EXPRESSION TAG	UNP Q8L7G0
A	361	SER	-	EXPRESSION TAG	UNP Q8L7G0
A	362	MET	-	EXPRESSION TAG	UNP Q8L7G0
B	356	ASN	-	EXPRESSION TAG	UNP Q8L7G0
B	357	SER	-	EXPRESSION TAG	UNP Q8L7G0
B	358	TYR	-	EXPRESSION TAG	UNP Q8L7G0
B	359	SER	-	EXPRESSION TAG	UNP Q8L7G0
B	360	GLN	-	EXPRESSION TAG	UNP Q8L7G0
B	361	SER	-	EXPRESSION TAG	UNP Q8L7G0
B	362	MET	-	EXPRESSION TAG	UNP Q8L7G0

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Cl	0	0
			2	2		

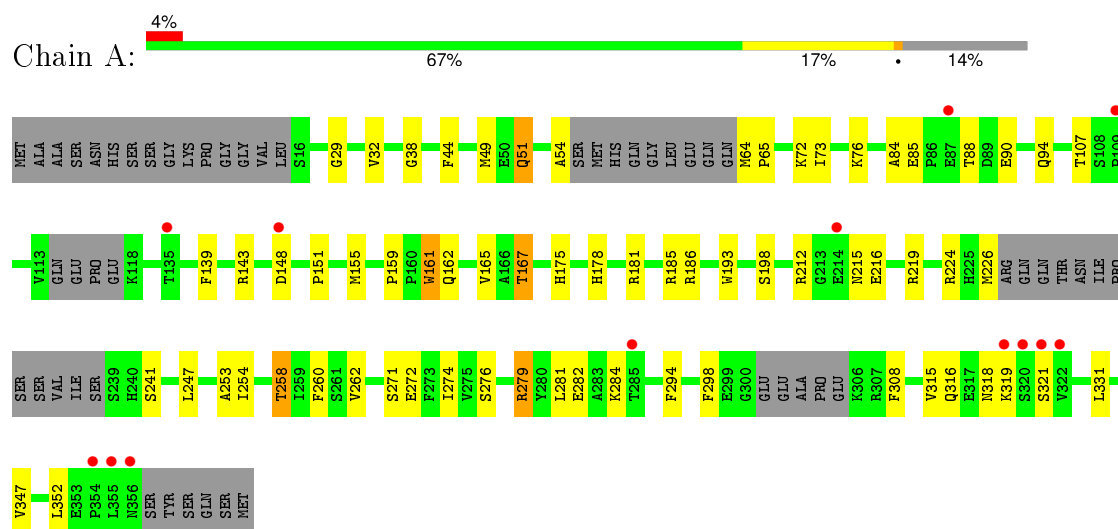
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	25	Total 25	O 25	0	0
3	B	29	Total 29	O 29	0	0

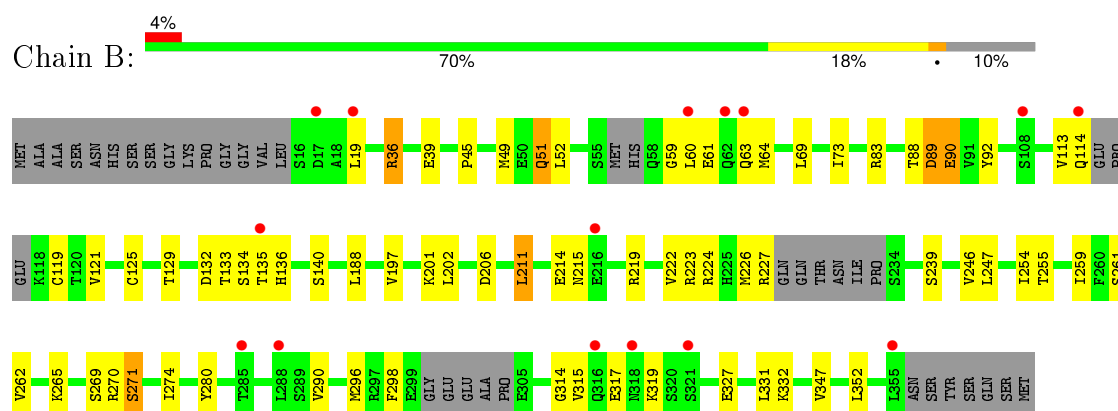
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Auxin response factor 1



- Molecule 1: Auxin response factor 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.26 Å 83.67 Å 79.03 Å 90.00° 117.61° 90.00°	Depositor
Resolution (Å)	35.94 – 2.67 35.91 – 2.67	Depositor EDS
% Data completeness (in resolution range)	96.1 (35.94-2.67) 96.1 (35.91-2.67)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.06 (at 2.68 Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, $R_{free}$	0.216 , 0.279 0.216 , 0.274	Depositor DCC
$R_{free}$ test set	1234 reflections (5.59%)	DCC
Wilson B-factor (Å <sup>2</sup> )	66.1	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 43.5	EDS
Estimated twinning fraction	0.039 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 23313 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5160	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.33% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 5.1 Standard geometry

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

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	0.61	0/2571	0.74	0/3482
1	B	0.58	0/2665	0.73	0/3610
All	All	0.59	0/5236	0.74	0/7092

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

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	2505	0	2449	36	0
1	B	2599	0	2529	40	0
2	A	2	0	0	0	0
3	A	25	0	0	0	0
3	B	29	0	0	1	0
All	All	5160	0	4978	74	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 7.

All (74) 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:63:GLN:NE2	3:B:405:HOH:O	2.13	0.80
1:B:73:ILE:CD1	1:B:254:ILE:HD11	2.12	0.79
1:B:73:ILE:HD11	1:B:254:ILE:HD11	1.74	0.70
1:A:253:ALA:HA	1:A:258:THR:HG22	1.79	0.65
1:B:49:MET:CE	1:B:247:LEU:HD11	2.30	0.61
1:B:347:VAL:HG21	1:B:352:LEU:HD21	1.82	0.61
1:B:121:VAL:HG21	1:B:211:LEU:HD21	1.83	0.61
1:A:347:VAL:HG21	1:A:352:LEU:HD21	1.82	0.60
1:A:143:ARG:CD	1:A:185:ARG:HG3	2.33	0.58
1:B:259:ILE:C	1:B:259:ILE:HD12	2.24	0.58
1:A:143:ARG:HD2	1:A:185:ARG:HG3	1.86	0.57
1:B:89:ASP:O	1:B:90:GLU:C	2.43	0.56
1:B:135:THR:HG23	1:B:136:HIS:CE1	2.42	0.54
1:A:139:PHE:HB2	1:A:193:TRP:CE2	2.43	0.54
1:B:270:ARG:O	1:B:271:SER:C	2.47	0.53
1:B:49:MET:HE1	1:B:247:LEU:HD11	1.92	0.52
1:B:315:VAL:HG12	1:B:331:LEU:HD22	1.92	0.52
1:B:317:GLU:O	1:B:319:LYS:HG3	2.09	0.52
1:A:44:PHE:CE2	1:A:72:LYS:HB3	2.45	0.52
1:A:161:TRP:HA	1:A:178:HIS:O	2.09	0.52
1:A:29:GLY:O	1:A:32:VAL:HG12	2.09	0.52
1:B:45:PRO:O	1:B:49:MET:HG2	2.10	0.52
1:B:202:LEU:HD21	1:B:222:VAL:CG2	2.40	0.51
1:B:262:VAL:HG21	1:B:274:ILE:HD11	1.92	0.51
1:B:19:LEU:HD23	1:B:219:ARG:NH2	2.26	0.51
1:B:280:TYR:OH	1:B:327:GLU:OE1	2.16	0.51
1:A:262:VAL:HG21	1:A:274:ILE:HD11	1.92	0.51
1:A:32:VAL:O	1:A:32:VAL:HG13	2.11	0.50
1:A:315:VAL:HG23	1:A:331:LEU:HD23	1.93	0.50
1:B:140:SER:HA	1:B:188:LEU:HD23	1.93	0.49
1:A:215:ASN:O	1:A:216:GLU:HB2	2.12	0.49
1:A:49:MET:CE	1:A:247:LEU:HD21	2.42	0.49
1:B:317:GLU:HG3	1:B:332:LYS:HB2	1.94	0.49
1:A:51:GLN:O	1:A:54:ALA:HB3	2.13	0.48
1:B:317:GLU:HA	1:B:317:GLU:OE1	2.15	0.47
1:B:73:ILE:HD13	1:B:254:ILE:HD11	1.90	0.47
1:B:36:ARG:O	1:B:39:GLU:HB2	2.15	0.46
1:A:64:MET:N	1:A:65:PRO:CD	2.78	0.46
1:A:260:PHE:HA	1:B:61:GLU:HG2	1.96	0.46
1:A:315:VAL:HG23	1:A:331:LEU:CD2	2.45	0.46
1:B:214:GLU:O	1:B:215:ASN:OD1	2.33	0.46
1:B:206:ASP:OD2	1:B:224:ARG:NH1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:ILE:HG12	1:A:254:ILE:HD11	1.97	0.46
1:B:51:GLN:OE1	1:B:265:LYS:N	2.37	0.45
1:B:202:LEU:HD21	1:B:222:VAL:HG21	1.99	0.44
1:B:49:MET:HE2	1:B:247:LEU:HD21	2.00	0.44
1:A:49:MET:HE3	1:A:247:LEU:HD21	2.00	0.44
1:A:143:ARG:HD3	1:A:185:ARG:HG3	1.99	0.43
1:A:159:PRO:HG2	1:A:161:TRP:CZ3	2.53	0.43
1:A:294:PHE:C	1:A:294:PHE:CD1	2.92	0.43
1:A:94:GLN:NE2	1:B:59:GLY:HA2	2.33	0.43
1:A:298:PHE:CD2	1:A:308:PHE:HD2	2.37	0.43
1:A:165:VAL:HG22	1:A:175:HIS:CE1	2.54	0.42
1:A:281:LEU:O	1:A:282:GLU:C	2.57	0.42
1:A:315:VAL:O	1:A:316:GLN:C	2.56	0.42
1:B:290:VAL:HG23	1:B:314:GLY:N	2.34	0.42
1:A:151:PRO:O	1:A:162:GLN:NE2	2.47	0.42
1:B:88:THR:O	1:B:90:GLU:N	2.52	0.42
1:A:276:SER:OG	1:A:279:ARG:HB2	2.19	0.42
1:A:38:GLY:HA2	1:A:76:LYS:HE2	2.01	0.42
1:B:197:VAL:O	1:B:201:LYS:N	2.53	0.42
1:B:296:MET:HG2	1:B:298:PHE:CE1	2.55	0.42
1:A:281:LEU:O	1:A:284:LYS:N	2.47	0.41
1:B:113:VAL:HG12	1:B:114:GLN:N	2.35	0.41
1:A:85:GLU:O	1:A:88:THR:O	2.39	0.41
1:B:83:ARG:HD2	1:B:92:TYR:OH	2.20	0.41
1:A:271:SER:O	1:A:272:GLU:HB2	2.21	0.41
1:A:167:THR:HG23	1:A:219:ARG:HD2	2.02	0.41
1:A:148:ASP:O	1:A:212:ARG:NH2	2.51	0.41
1:B:129:THR:O	1:B:133:THR:HG23	2.21	0.41
1:A:84:ALA:HA	1:A:90:GLU:O	2.20	0.41
1:B:52:LEU:HD11	1:B:246:VAL:HG21	2.03	0.41
1:B:255:THR:O	1:B:255:THR:HG22	2.20	0.40
1:B:226:MET:O	1:B:227:ARG:CB	2.69	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	301/362 (83%)	280 (93%)	21 (7%)	0	100	100
1	B	314/362 (87%)	293 (93%)	18 (6%)	3 (1%)	19	42
All	All	615/724 (85%)	573 (93%)	39 (6%)	3 (0%)	34	61

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	89	ASP
1	B	90	GLU
1	B	271	SER

### 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	278/322 (86%)	262 (94%)	16 (6%)	25	49
1	B	289/322 (90%)	275 (95%)	14 (5%)	31	59
All	All	567/644 (88%)	537 (95%)	30 (5%)	28	54

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	GLN
1	A	107	THR
1	A	155	MET
1	A	161	TRP
1	A	167	THR
1	A	181	ARG
1	A	186	ARG
1	A	198	SER
1	A	224	ARG

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Mol	Chain	Res	Type
1	A	226	MET
1	A	241	SER
1	A	258	THR
1	A	279	ARG
1	A	318	ASN
1	A	319	LYS
1	A	321	SER
1	B	36	ARG
1	B	51	GLN
1	B	60	LEU
1	B	64	MET
1	B	69	LEU
1	B	119	CYS
1	B	125	CYS
1	B	132	ASP
1	B	134	SER
1	B	211	LEU
1	B	223	ARG
1	B	239	SER
1	B	261	SER
1	B	269	SER

Some 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	311/362 (85%)	0.20	13 (4%) 40 38	37, 67, 105, 143	0
1	B	324/362 (89%)	0.22	15 (4%) 36 34	38, 64, 108, 136	0
All	All	635/724 (87%)	0.21	28 (4%) 38 36	37, 66, 108, 143	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	321	SER	7.3
1	A	322	VAL	4.6
1	A	355	LEU	4.3
1	B	321	SER	4.2
1	A	214	GLU	4.1
1	B	318	ASN	4.0
1	B	114	GLN	4.0
1	A	285	THR	3.8
1	A	319	LYS	3.8
1	A	356	ASN	3.6
1	A	320	SER	3.4
1	B	135	THR	3.2
1	B	216	GLU	2.8
1	B	285	THR	2.8
1	B	17	ASP	2.7
1	B	108	SER	2.7
1	A	354	PRO	2.6
1	B	19	LEU	2.6
1	B	316	GLN	2.5
1	B	355	LEU	2.4
1	A	87	GLU	2.4
1	A	109	PRO	2.3
1	A	148	ASP	2.3
1	B	288	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	60	LEU	2.2
1	B	62	GLN	2.2
1	B	63	GLN	2.2
1	A	135	THR	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 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	CL	A	401	1/1	0.97	0.07	-	62,62,62,62	0
2	CL	A	402	1/1	0.87	0.23	-	84,84,84,84	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.