

# Full wwPDB X-ray Structure Validation Report (i)

### Sep 13, 2020 - 06:00 PM BST

PDB ID : 4PU6

Title : Crystal structure of potassium-dependent plant-type L-asparaginase from

Phaseolus vulgaris in complex with K+ cations

Authors : Bejger, M.; Gilski, M.; Imiolczyk, B.; Jaskolski, M.

Deposited on : 2014-03-12

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 following versions of software and data (see references (1)) 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 : 2.14.4.dev1

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)

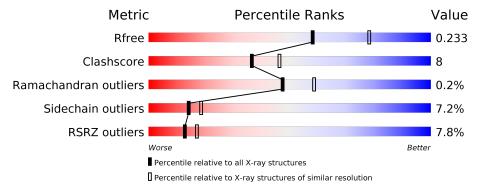
Validation Pipeline (wwPDB-VP) : 2.14.4.dev1

## 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
$R_{free}$	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 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	197	65%	14% 20%					
1	С	197	66%	12% • 20%					
2	В	131	76%	23%					
2	D	131	15%	25% •					



## 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4361 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 L-ASPARAGINASE ALPHA SUBUNIT.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	157	Total			0	S	0	0	0
			1173	731	205	231	6			
1	C	157	Total	С	N	Ο	$\mathbf{S}$	0	0	0
1		197	1173	731	205	231	6		0	

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	_	EXPRESSION TAG	UNP V7CU13
A	0	ALA	-	EXPRESSION TAG	UNP V7CU13
A	17	THR	ASN	SEE REMARK 999	UNP V7CU13
С	-1	GLY	_	EXPRESSION TAG	UNP V7CU13
С	0	ALA	_	EXPRESSION TAG	UNP V7CU13
С	17	THR	ASN	SEE REMARK 999	UNP V7CU13

• Molecule 2 is a protein called L-ASPARAGINASE BETA SUBUNIT.

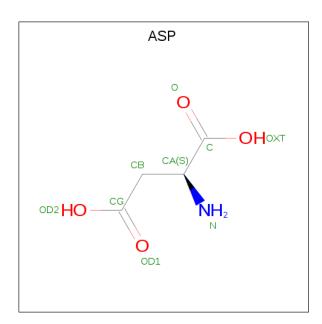
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	D	131	Total	С	N	О	S	0	0	0
	Б	191	944	580	167	184	13	U		U
9	D	131	Total	С	N	О	S	0	0	Ω
	ע	131	944	580	167	184	13	0		U

• Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total K 2 2	0	0
3	С	2	Total K 2 2	0	0

• Molecule 4 is ASPARTIC ACID (three-letter code: ASP) (formula: C<sub>4</sub>H<sub>7</sub>NO<sub>4</sub>).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	В	1	Total	C 1	N 1	O 1	0	0

#### • Molecule 5 is water.

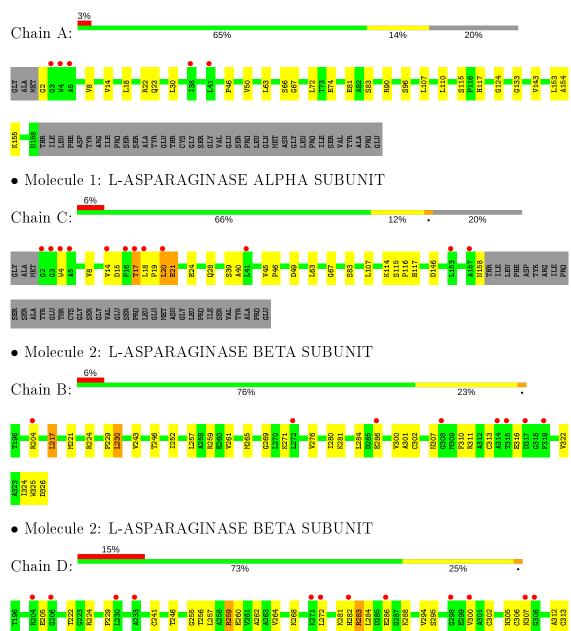
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	48	Total O 48 48	0	0
5	В	22	Total O 22 22	0	0
5	С	34	Total O 34 34	0	0
5	D	10	Total O 10 10	0	0



## 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: L-ASPARAGINASE ALPHA SUBUNIT









# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	56.94Å 102.67Å 127.03Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.60 - 2.30	Depositor
Resolution (A)	47.60 - 2.30	EDS
% Data completeness	96.3 (47.60-2.30)	Depositor
(in resolution range)	96.2 (47.60-2.30)	EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.19 (at 2.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
D D	0.176 , 0.231	Depositor
$R, R_{free}$	0.178 , $0.233$	DCC
$R_{free}$ test set	1009 reflections $(3.10\%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	47.7	Xtriage
Anisotropy	0.651	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.34 , 48.7	EDS
L-test for twinning <sup>2</sup>	$< L >=0.49, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4361	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.79% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



 $<sup>^{1}</sup>$ Intensities estimated from amplitudes.

## 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:

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		
MIOI	Chain	RMSZ	# Z >5	RMSZ	# Z  > 5	
1	A	0.65	0/1190	0.74	0/1613	
1	С	0.64	0/1190	0.72	0/1613	
2	В	0.67	0/954	0.76	1/1283 (0.1%)	
2	D	0.54	0/954	0.67	0/1283	
All	All	0.63	0/4288	0.72	$1/5792 \ (0.0\%)$	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
2	В	217	LEU	CA-CB-CG	5.31	127.52	115.30

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	1173	0	1176	20	0
1	С	1173	0	1176	16	0
2	В	944	0	930	22	0
2	D	944	0	930	25	0
3	A	2	0	0	0	0
3	С	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	В	9	0	3	1	0
5	A	48	0	0	4	0
5	В	22	0	0	0	0
5	С	34	0	0	0	0
5	D	10	0	0	0	0
All	All	4361	0	4215	67	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 8.

All (67) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A	A.1. 0	Interatomic	Clash
Atom-1	Atom-2	${\rm distance} \ ({\rm \AA})$	overlap (Å)
1:C:14:VAL:O	2:D:307:ASN:ND2	2.20	0.71
2:B:311:ARG:HH22	2:B:326:ASP:HB3	1.55	0.71
1:A:2:GLY:N	5:A:336:HOH:O	2.28	0.66
2:B:259:ARG:HD3	2:D:256:THR:HG21	1.76	0.66
2:B:259:ARG:CD	2:D:256:THR:HG21	2.29	0.62
1:A:22:ARG:HH22	1:A:63:LEU:HD11	1.67	0.59
1:C:40:ALA:O	1:C:45:VAL:HG13	2.03	0.59
1:A:23:GLN:HG3	2:B:324:ILE:HD12	1.85	0.58
2:D:315:THR:OG1	2:D:319:PHE:HB3	2.04	0.57
1:A:2:GLY:N	5:A:335:HOH:O	2.37	0.57
1:C:24:GLU:O	1:C:28:GLN:HG2	2.04	0.56
1:A:30:LEU:HD11	2:B:310:PHE:HB3	1.86	0.56
1:A:133:GLY:HA2	5:A:327:HOH:O	2.04	0.56
2:D:255:GLY:O	2:D:283:ARG:NH1	2.41	0.54
1:C:15:ASP:OD2	1:C:17:THR:HG22	2.09	0.52
1:A:74:GLU:O	1:A:155:LYS:NZ	2.36	0.52
1:A:81:GLU:HB3	1:A:96:SER:HA	1.91	0.52
2:D:205:GLU:OE1	2:D:205:GLU:N	2.39	0.52
1:A:72:LEU:HD21	1:A:143:VAL:HG13	1.91	0.52
2:D:284:LEU:HD13	2:D:305:ASN:ND2	2.25	0.51
1:A:14:VAL:O	2:B:307:ASN:ND2	2.27	0.51
2:B:300:VAL:HG21	2:B:313:CYS:HB2	1.92	0.50
1:A:90:ARG:HH12	2:D:283:ARG:NH1	2.11	0.49
4:B:501:ASP:OD1	4:B:501:ASP:N	2.45	0.48
2:D:272:LEU:HD22	2:D:295:SER:HB3	1.94	0.48
2:B:229:PRO:HG2	2:B:230:LEU:HD13	1.95	0.48
1:A:117:HIS:CG	2:D:224:ARG:HG3	2.49	0.47
1:A:90:ARG:HH12	2:D:283:ARG:HH12	1.61	0.47

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Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}\;({ m \AA})$	$ m overlap~(\AA)$
2:D:241:CYS:SG	2:D:262:ALA:HB2	2.55	0.47
1:A:83:SER:HB3	2:B:229:PRO:HA	1.96	0.47
2:B:204:ARG:NH2	2:B:316:GLU:OE2	2.45	0.47
1:C:20:LEU:HD13	1:C:21:GLU:N	2.30	0.47
2:B:224:ARG:HG3	1:C:117:HIS:CG	2.50	0.46
1:A:124:GLY:HA3	2:D:222:THR:O	2.16	0.46
2:D:256:THR:HG23	2:D:260:GLU:HG2	1.97	0.46
2:D:315:THR:C	2:D:317:ASP:H	2.18	0.46
1:C:8:VAL:HG22	2:D:312:ALA:HB3	1.97	0.45
2:D:288:LYS:HA	2:D:305:ASN:OD1	2.16	0.45
2:D:255:GLY:HA2	2:D:283:ARG:HH12	1.82	0.45
1:A:46:PRO:O	1:A:50:VAL:HG23	2.16	0.45
2:B:221:MET:CE	1:C:116:PRO:HD2	2.47	0.45
2:B:311:ARG:NH2	2:B:326:ASP:HB3	2.29	0.45
1:A:154:ALA:HA	5:A:344:HOH:O	2.17	0.45
2:B:252:ILE:HG23	2:B:257:LEU:HB2	1.98	0.44
2:B:276:VAL:HG21	2:B:301:ALA:HB3	2.00	0.44
2:B:284:LEU:HD13	2:B:284:LEU:HA	1.79	0.44
2:D:260:GLU:O	2:D:264:VAL:HG13	2.18	0.44
2:B:280:ILE:HA	2:B:284:LEU:HD23	1.99	0.44
2:B:204:ARG:NE	2:B:316:GLU:OE2	2.41	0.44
2:D:255:GLY:O	2:D:256:THR:HG22	2.17	0.44
1:A:110:LEU:HD23	1:A:110:LEU:HA	1.91	0.44
1:C:4:TRP:CE2	2:D:316:GLU:HB2	2.52	0.44
2:B:243:VAL:HG21	2:B:261:VAL:HB	1.98	0.44
2:B:325:TRP:O	2:B:326:ASP:HB3	2.18	0.44
2:D:264:VAL:O	2:D:268:LYS:HB2	2.19	0.43
2:D:281:LYS:HD3	2:D:282:HIS:NE2	2.34	0.43
1:C:18:LEU:HA	1:C:19:PRO:HD3	1.85	0.43
1:C:83:SER:HB3	2:D:229:PRO:HA	2.01	0.42
2:D:259:ARG:O	2:D:259:ARG:HD3	2.19	0.42
1:C:107:LEU:HD12	1:C:107:LEU:HA	1.84	0.41
1:C:46:PRO:HD2	1:C:49:ASP:OD2	2.21	0.41
1:C:114:LYS:HE3	1:C:114:LYS:HB3	1.83	0.41
2:B:265:MET:O	2:B:269:GLY:HA2	2.21	0.41
1:C:20:LEU:HD13	1:C:21:GLU:H	1.85	0.41
1:A:107:LEU:HD12	1:A:107:LEU:HA	1.72	0.41
2:B:221:MET:HE1	1:C:116:PRO:HD2	2.03	0.40
1:A:66:SER:O	1:A:67:GLY:C	2.59	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	Perce	ntiles
1	A	155/197 (79%)	149 (96%)	6 (4%)	0	100	100
1	C	155/197~(79%)	149 (96%)	5 (3%)	1 (1%)	25	31
2	В	129/131~(98%)	120 (93%)	9 (7%)	0	100	100
2	D	129/131~(98%)	118 (92%)	11 (8%)	0	100	100
All	All	568/656 (87%)	536 (94%)	31 (6%)	1 (0%)	47	58

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	С	67	GLY

#### 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	Perc	entiles
1	A	127/160 (79%)	123 (97%)	4 (3%)	40	55
1	С	$127/160 \ (79\%)$	119 (94%)	8 (6%)	18	24
2	В	96/96 (100%)	88 (92%)	8 (8%)	11	14
2	D	96/96 (100%)	85 (88%)	11 (12%)	5	6
All	All	$446/512 \ (87\%)$	415 (93%)	31 (7%)	14	19

All (31) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	A	8	VAL
1	A	18	LEU
1	A	115	SER
1	A	153	LEU
2	В	217	LEU
2	В	230	LEU
2	В	246	THR
2	В	271	LYS
2	В	281	LYS
2	В	286	GLU
2	В	302	CYS
2	B C	322	VAL
1	С	17	THR LEU
1	С	20	LEU
1	С	21	GLU
1	С	39	SER
1	C C C C C D	63	LEU
1	С	115	SER
1	С	146	ASP
1	С	158	ASN
2		246	THR
2	D	257	LEU
2	D	259	ARG
2	D	283	ARG
2	D	286	GLU
2	D	294	VAL
2	D	300	VAL
2	D	302	CYS
2	D	306	CYS
2	D	313	CYS
2	D	322	VAL

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 monosaccharides in this entry.

## 5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 4 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	Mol Type Chain Res	n   Res   Link		Link BNG7   WH7		Bond angles		gles		
WIOI		Chain	Tites Lillik	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	ASP	В	501	_	2,8,8	0.15	0	1,10,10	0.46	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	ASP	В	501	-	_	1/2/8/8	_

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	В	501	ASP	N-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	В	501	ASP	1	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,  $95^{th}$  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 $>$	$\#\mathrm{RSRZ}{>}2$	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	A	157/197 (79%)	-0.01	5 (3%) 47 54	20, 41, 70, 105	2 (1%)
1	С	157/197 (79%)	0.18	12 (7%) 13 18	22, 48, 86, 109	5 (3%)
2	В	131/131 (100%)	0.38	8 (6%) 21 27	20, 53, 77, 103	1 (0%)
2	D	131/131 (100%)	0.90	20 (15%) 2 3	27, 66, 93, 106	8 (6%)
All	All	576/656 (87%)	0.34	45 (7%) 13 17	20, 49, 87, 109	16 (2%)

All (45) RSRZ outliers are listed below:

Mol	Chain	Res Type		RSRZ
1	A	3	GLY	4.9
2	D	272	LEU	4.4
2	D	308	GLY	4.0
2	В	319	PHE	4.0
2	В	315	THR	3.9
2	D	318	GLY	3.7
2	D	271	LYS	3.6
1	A	38	ILE	3.5
2	D	319	PHE	3.5
2	D	314	ALA	3.5
2	D	315	THR	3.4
1	С	153	LEU	3.4
1	A	4	TRP	3.4
2	D	326	ASP	3.3
1	С	3	GLY	3.3
1	A	41	LEU	3.1
1	С	18	LEU	3.1
1	С	17	THR	3.1
2	D	204	ARG	3.0
2	D	317	ASP	3.0
2	В	317	ASP	2.8

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Mol	Chain	Res	Type	RSRZ	
1	С	4	TRP	2.8	
2	В	204	ARG	2.6	
1	С	41	LEU	2.6	
1	С	157	ALA	2.6	
1	С	16	PRO	2.5	
2	D	320	MET	2.5	
2	D	206	GLY	2.5	
2	D	282	HIS	2.5	
2	D	286	GLU	2.5	
2	D	325	TRP	2.5	
2	D	230	LEU	2.5	
1	С	5	ALA	2.4	
2	В	314	ALA	2.4	
1	С	14	VAL	2.4	
2	D	300	VAL	2.4	
1	С	20	LEU	2.4	
1	С	2	GLY	2.3	
2	В	272	LEU	2.3	
2	В	308	GLY	2.3	
2	D	307	ASN	2.3	
1	A	5	ALA	2.2	
2	В	286	GLU	2.2	
2	D	298	GLY	2.1	
2	D	233	ALA	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 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,  $95^{th}$  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	${f B-factors}({f A}^2)$	Q<0.9
4	ASP	В	501	9/9	0.87	0.23	25,37,47,50	9
3	K	С	201	1/1	0.96	0.09	57,57,57	0
3	K	A	201	1/1	0.97	0.08	41,41,41,41	0
3	K	A	202	1/1	0.99	0.07	44,44,44,44	0
3	K	С	202	1/1	0.99	0.07	47,47,47,47	0

# 6.5 Other polymers (i)

There are no such residues in this entry.

