Full wwPDB X-ray Structure Validation Report (i)

Sep 5, 2023 – 03:53 PM EDT

PDB ID	:	4ELY
Title	:	CCDBVFI:GYRA14EC
Authors	:	De Jonge, N.; Simic, R.; Buts, L.; Haesaerts, S.; Roelants, K.; Garcia-Pino, A.; Sterckx, Y.; De Greve, H.; Lah, J.; Loris, R.
Deposited on	:	2012-04-11
Resolution	:	1.93 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:

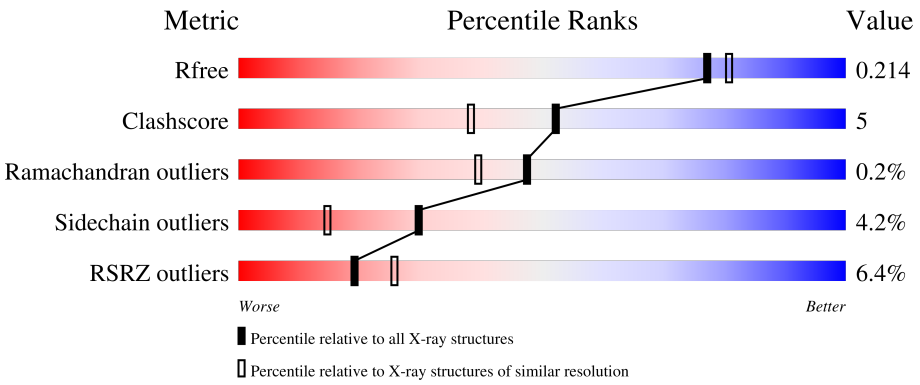
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 1.93 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	4310 (1.96-1.92)
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)
RSRZ outliers	127900	4250 (1.96-1.92)

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	156	7%, 82%, • •, 13%
1	B	156	7%, 72%, 13%, •, 13%
2	C	105	4%, 76%, 15%, •, 7%
2	D	105	4%, 79%, 13%, •, 7%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3906 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 DNA gyrase subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	135	1053	672	181	199	1	0	3	1
1	B	135	1058	672	186	199	1	0	2	1

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	342	MET	-	initiating methionine	UNP P0AES5
A	343	GLY	-	expression tag	UNP P0AES5
A	344	SER	-	expression tag	UNP P0AES5
A	345	SER	-	expression tag	UNP P0AES5
A	346	HIS	-	expression tag	UNP P0AES5
A	347	HIS	-	expression tag	UNP P0AES5
A	348	HIS	-	expression tag	UNP P0AES5
A	349	HIS	-	expression tag	UNP P0AES5
A	350	HIS	-	expression tag	UNP P0AES5
A	351	HIS	-	expression tag	UNP P0AES5
A	352	SER	-	expression tag	UNP P0AES5
A	353	SER	-	expression tag	UNP P0AES5
A	354	GLY	-	expression tag	UNP P0AES5
A	355	LEU	-	expression tag	UNP P0AES5
A	356	VAL	-	expression tag	UNP P0AES5
A	357	PRO	-	expression tag	UNP P0AES5
A	358	ARG	-	expression tag	UNP P0AES5
A	359	GLY	-	expression tag	UNP P0AES5
A	360	SER	-	expression tag	UNP P0AES5
A	361	HIS	-	expression tag	UNP P0AES5
A	362	MET	-	expression tag	UNP P0AES5
B	342	MET	-	initiating methionine	UNP P0AES5
B	343	GLY	-	expression tag	UNP P0AES5
B	344	SER	-	expression tag	UNP P0AES5
B	345	SER	-	expression tag	UNP P0AES5

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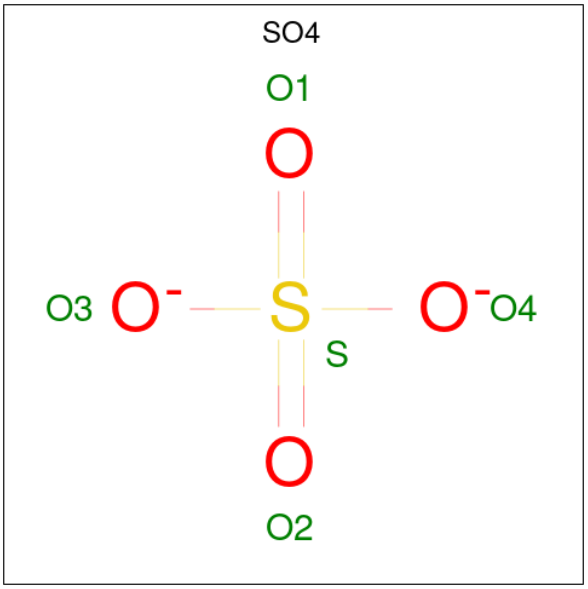
Chain	Residue	Modelled	Actual	Comment	Reference
B	346	HIS	-	expression tag	UNP P0AES5
B	347	HIS	-	expression tag	UNP P0AES5
B	348	HIS	-	expression tag	UNP P0AES5
B	349	HIS	-	expression tag	UNP P0AES5
B	350	HIS	-	expression tag	UNP P0AES5
B	351	HIS	-	expression tag	UNP P0AES5
B	352	SER	-	expression tag	UNP P0AES5
B	353	SER	-	expression tag	UNP P0AES5
B	354	GLY	-	expression tag	UNP P0AES5
B	355	LEU	-	expression tag	UNP P0AES5
B	356	VAL	-	expression tag	UNP P0AES5
B	357	PRO	-	expression tag	UNP P0AES5
B	358	ARG	-	expression tag	UNP P0AES5
B	359	GLY	-	expression tag	UNP P0AES5
B	360	SER	-	expression tag	UNP P0AES5
B	361	HIS	-	expression tag	UNP P0AES5
B	362	MET	-	expression tag	UNP P0AES5

- Molecule 2 is a protein called CcdB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	98	766	494	119	150	3	0	0	0
			Total	C	N	O	S			
2	D	98	766	493	119	151	3	0	1	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
3	A	1	5	4	1	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
4	A	1	1	1	0	0
			Total	Cl		
4	D	1	1	1	0	0

- Molecule 5 is water.

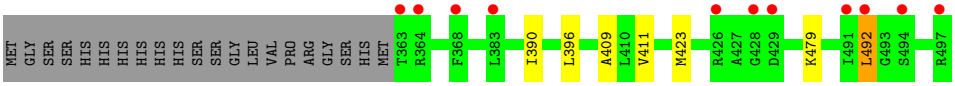
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	105	105	105	0	0
			Total	O		
5	B	83	83	83	0	0
			Total	O		
5	C	40	40	40	0	0
			Total	O		
5	D	28	28	28	0	0

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.

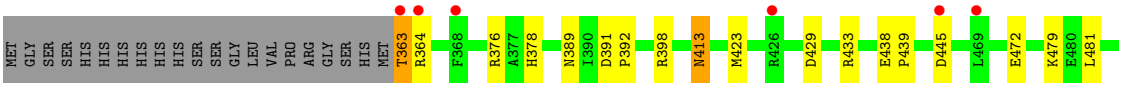
• Molecule 1: DNA gyrase subunit A

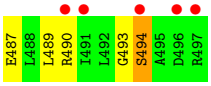
Chain A:



• Molecule 1: DNA gyrase subunit A

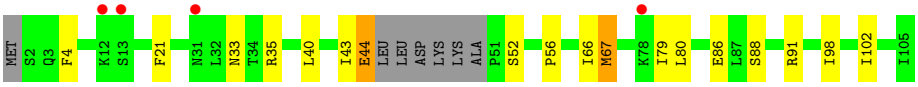
Chain B:





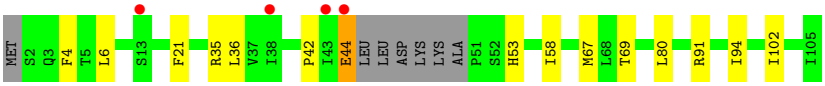
• Molecule 2: CcdB

Chain C:



• Molecule 2: CcdB

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	130.07Å 90.83Å 58.13Å 90.00° 102.59° 90.00°	Depositor
Resolution (Å)	24.62 – 1.93 24.62 – 1.93	Depositor EDS
% Data completeness (in resolution range)	98.9 (24.62-1.93) 98.9 (24.62-1.93)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	3.53 (at 1.93Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.185 , 0.217 0.181 , 0.214	Depositor DCC
R_{free} test set	2470 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	36.9	Xtriage
Anisotropy	0.302	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 55.6	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	0.97	EDS
Total number of atoms	3906	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.25% 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: SO4, 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	0.38	0/1072	0.53	1/1460 (0.1%)
1	B	0.34	0/1082	0.50	0/1471
2	C	0.37	0/781	0.57	0/1065
2	D	0.34	0/784	0.54	0/1069
All	All	0.36	0/3719	0.53	1/5065 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	492	LEU	CA-CB-CG	5.58	128.13	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	1053	0	1051	6	0
1	B	1058	0	1062	14	0
2	C	766	0	757	12	0
2	D	766	0	757	10	0
3	A	5	0	0	0	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1	0	0	1	0
5	A	105	0	0	1	0
5	B	83	0	0	2	0
5	C	40	0	0	1	0
5	D	28	0	0	2	0
All	All	3906	0	3627	40	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 (40) 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)
4:D:201:CL:CL	5:D:319:HOH:O	2.19	0.97
1:B:493:GLY:H	1:B:494:SER:HB3	1.30	0.94
1:A:390:ILE:HG21	1:B:398[A]:ARG:HD3	1.77	0.66
2:C:35:ARG:HG3	2:C:80:LEU:HD11	1.77	0.66
2:C:102:ILE:HD11	2:D:36:LEU:HD23	1.77	0.65
2:C:86:GLU:OE2	2:C:88:SER:OG	2.10	0.64
1:A:423:MET:HE3	1:A:479:LYS:HE3	1.82	0.61
1:A:423:MET:HE2	1:A:479:LYS:HG3	1.82	0.60
2:C:21:PHE:HE1	2:C:80:LEU:HD22	1.67	0.59
2:C:43:ILE:O	2:C:44:GLU:HB2	2.04	0.58
1:B:493:GLY:N	1:B:494:SER:HB3	2.11	0.55
1:B:423:MET:HE2	1:B:479:LYS:HG3	1.89	0.54
1:B:433:ARG:NH2	1:B:438:GLU:O	2.40	0.54
1:B:378:HIS:HE1	5:B:517:HOH:O	1.91	0.53
1:A:423:MET:CE	1:A:479:LYS:HG3	2.40	0.52
1:B:423:MET:HE3	1:B:479:LYS:HE3	1.92	0.51
2:C:33:ASN:ND2	5:C:231:HOH:O	2.42	0.51
1:B:391:ASP:HB2	1:B:392:PRO:HD3	1.94	0.50
2:D:91:ARG:NH1	5:D:314:HOH:O	2.45	0.49
2:D:21:PHE:HE1	2:D:80:LEU:HD22	1.78	0.48
2:C:67:MET:HE3	2:C:67:MET:HB3	1.80	0.48
1:A:396:LEU:HD21	1:A:409:ALA:HB3	1.94	0.47
2:D:67:MET:SD	2:D:94:ILE:HG12	2.54	0.47
2:D:4:PHE:CZ	2:D:91:ARG:HG3	2.51	0.45
2:D:35:ARG:HG3	2:D:80:LEU:HD11	1.97	0.45
1:B:363:THR:OG1	1:B:364:ARG:N	2.48	0.45
2:D:42:PRO:C	2:D:44:GLU:H	2.18	0.45
2:C:40:LEU:HD22	2:C:67:MET:HG2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:56:PRO:HD2	2:C:67:MET:HB2	1.99	0.43
1:A:411[A]:VAL:HG23	5:A:638:HOH:O	2.17	0.43
2:C:4:PHE:CZ	2:C:91:ARG:HG3	2.54	0.43
1:B:376:ARG:HG2	1:B:481:LEU:HD11	2.01	0.43
1:B:389:ASN:O	1:B:392:PRO:HD2	2.19	0.42
1:B:413:ASN:HB3	5:B:511:HOH:O	2.19	0.42
2:C:98:ILE:HD13	2:D:102:ILE:HD13	2.02	0.41
1:B:433:ARG:NH2	1:B:439:PRO:HA	2.36	0.41
2:D:58:ILE:HD11	2:D:67:MET:HE3	2.03	0.41
2:D:67:MET:HG2	2:D:69:THR:HG22	2.03	0.41
1:B:493:GLY:HA2	1:B:494:SER:O	2.21	0.41
2:C:43:ILE:HG12	2:C:66:ILE:HG13	2.02	0.41

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	136/156 (87%)	132 (97%)	4 (3%)	0	100	100
1	B	135/156 (86%)	131 (97%)	3 (2%)	1 (1%)	22	11
2	C	94/105 (90%)	93 (99%)	1 (1%)	0	100	100
2	D	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
All	All	460/522 (88%)	450 (98%)	9 (2%)	1 (0%)	47	39

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	494	SER

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	103/127 (81%)	102 (99%)	1 (1%)	76	71
1	B	106/127 (84%)	97 (92%)	9 (8%)	10	2
2	C	89/99 (90%)	85 (96%)	4 (4%)	27	12
2	D	90/99 (91%)	87 (97%)	3 (3%)	38	24
All	All	388/452 (86%)	371 (96%)	17 (4%)	30	13

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	492	LEU
1	B	363	THR
1	B	413	ASN
1	B	429	ASP
1	B	445	ASP
1	B	472[A]	GLU
1	B	472[B]	GLU
1	B	487	GLU
1	B	489	LEU
1	B	490	ARG
2	C	44	GLU
2	C	52	SER
2	C	67	MET
2	C	79	ILE
2	D	6	LEU
2	D	44	GLU
2	D	53	HIS

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)

Of 3 ligands modelled in this entry, 2 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	SO4	A	501	-	4,4,4	0.15	0	6,6,6	0.26	0

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 (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	135/156 (86%)	0.29	11 (8%)	12	17	26, 40, 80, 109	0
1	B	135/156 (86%)	0.40	11 (8%)	12	17	26, 47, 79, 103	0
2	C	98/105 (93%)	0.24	4 (4%)	37	44	30, 45, 73, 80	0
2	D	98/105 (93%)	0.30	4 (4%)	37	44	33, 49, 80, 92	0
All	All	466/522 (89%)	0.31	30 (6%)	19	26	26, 45, 79, 109	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	368	PHE	5.0
1	B	490	ARG	4.1
1	A	494	SER	4.0
1	B	491	ILE	3.8
1	B	363	THR	3.7
2	C	13	SER	3.5
1	A	426	ARG	3.2
1	A	428	GLY	3.2
1	B	497	ARG	2.8
2	C	78	LYS	2.8
1	A	368	PHE	2.7
1	A	363	THR	2.7
2	D	38	ILE	2.7
2	D	43	ILE	2.7
1	B	426	ARG	2.5
1	B	494	SER	2.5
1	B	496	ASP	2.5
1	A	429	ASP	2.4
1	B	445	ASP	2.4
2	D	44	GLU	2.4
2	D	13	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	492	LEU	2.3
1	A	497	ARG	2.3
1	B	364	ARG	2.2
1	A	383	LEU	2.2
1	B	469	LEU	2.1
2	C	12	LYS	2.1
2	C	31	ASN	2.1
1	A	364	ARG	2.1
1	A	491	ILE	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, 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
4	CL	D	201	1/1	0.75	0.16	85,85,85,85	0
4	CL	A	502	1/1	0.84	0.05	84,84,84,84	0
3	SO4	A	501	5/5	0.99	0.05	41,52,54,65	0

6.5 Other polymers (i)

There are no such residues in this entry.