



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:31 AM GMT

PDB ID : 2HJG  
Title : The crystal structure of the B. subtilis YphC GTPase in complex with GDP  
Authors : Muench, S.P.; Xu, L.; Sedelnikova, S.E.; Rice, D.W  
Deposited on : 2006-06-30  
Resolution : 2.50 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

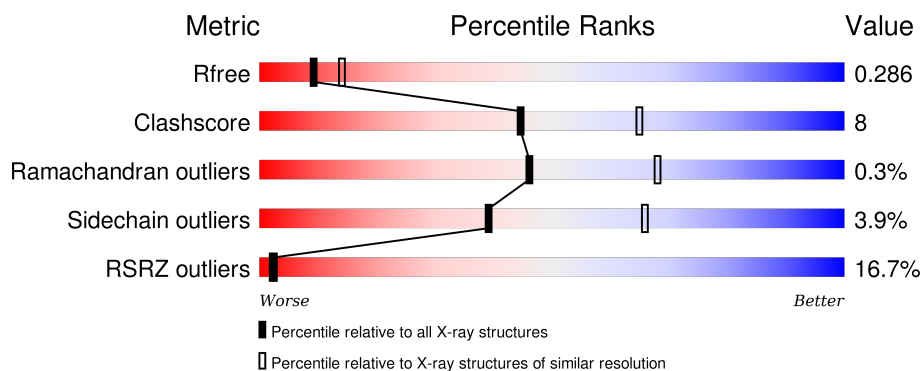
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	436	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3235 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 GTP-binding protein engA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	400	Total	C	N	O	S	Se	0	0	0
			3147	2018	527	591	1	10			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP P50743
A	80	MSE	MET	MODIFIED RESIDUE	UNP P50743
A	89	MSE	MET	MODIFIED RESIDUE	UNP P50743
A	126	MSE	MET	MODIFIED RESIDUE	UNP P50743
A	195	MSE	MET	MODIFIED RESIDUE	UNP P50743
A	233	MSE	MET	MODIFIED RESIDUE	UNP P50743
A	306	MSE	MET	MODIFIED RESIDUE	UNP P50743
A	328	MSE	MET	MODIFIED RESIDUE	UNP P50743
A	340	MSE	MET	MODIFIED RESIDUE	UNP P50743
A	364	MSE	MET	MODIFIED RESIDUE	UNP P50743
A	369	MSE	MET	MODIFIED RESIDUE	UNP P50743
A	405	MSE	MET	MODIFIED RESIDUE	UNP P50743

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>11</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 28	C 10	N 5	O 11	P 2	0	0
3	A	1	Total 28	C 10	N 5	O 11	P 2	0	0

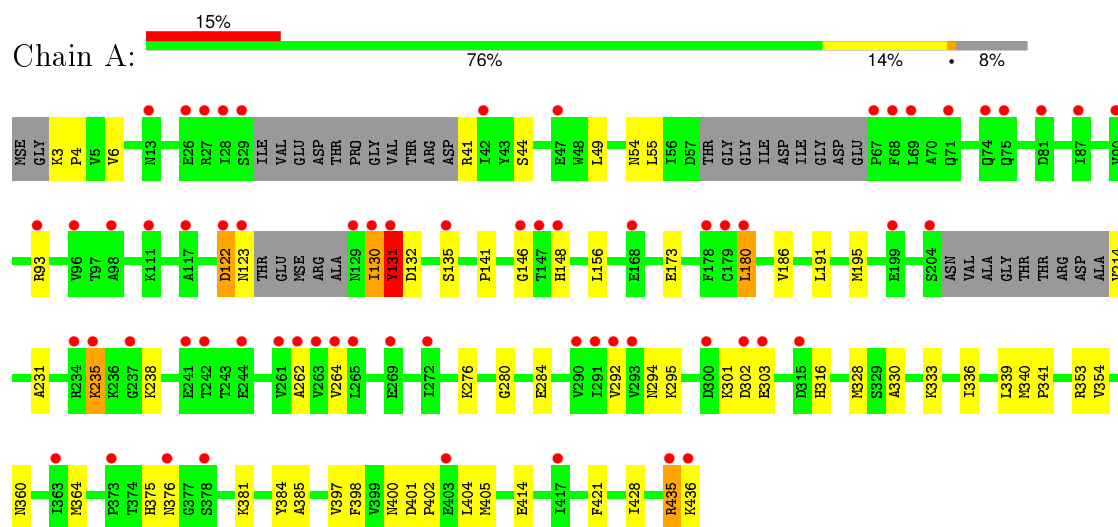
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	31	Total O 31 31	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: GTP-binding protein engA



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	62.71Å 65.05Å 110.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.96 – 2.50 19.90 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.96-2.50) 100.0 (19.90-2.50)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.15 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.215 , 0.274 0.243 , 0.286	Depositor DCC
$R_{free}$ test set	813 reflections (5.03%)	DCC
Wilson B-factor (Å <sup>2</sup> )	39.7	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 34.6	EDS
Estimated twinning fraction	0.032 for k,h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 16178 reflections (0.006%)	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	3235	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.44% 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.52	0/3196	0.69	3/4305 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	131	TYR	O-C-N	7.49	134.68	122.70
1	A	131	TYR	CA-C-N	-5.79	104.45	117.20
1	A	402	PRO	O-C-N	-5.40	114.06	122.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	122	ASP	Peptide
1	A	435	ARG	Peptide

### 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	3147	0	3124	50	0
2	A	1	0	0	0	0
3	A	56	0	24	2	0
4	A	31	0	0	0	0
All	All	3235	0	3148	50	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 (50) 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:131:TYR:CD1	1:A:131:TYR:N	2.16	1.06
1:A:130:ILE:HD11	1:A:141:PRO:CB	1.87	1.04
1:A:131:TYR:N	1:A:131:TYR:HD1	1.53	1.01
1:A:130:ILE:HD11	1:A:141:PRO:HB2	1.01	0.99
1:A:130:ILE:CD1	1:A:141:PRO:HB2	1.92	0.98
1:A:131:TYR:H	1:A:131:TYR:HD1	0.94	0.92
1:A:328:MSE:HE1	1:A:339:LEU:HD22	1.54	0.88
1:A:195:MSE:CE	1:A:339:LEU:HD23	2.08	0.82
1:A:191:LEU:HD22	1:A:328:MSE:HE3	1.66	0.77
1:A:191:LEU:CD2	1:A:328:MSE:HE3	2.15	0.75
1:A:292:VAL:CG1	1:A:328:MSE:HE2	2.20	0.72
1:A:292:VAL:HG11	1:A:328:MSE:HE2	1.72	0.71
1:A:435:ARG:HH11	1:A:435:ARG:HG2	1.58	0.67
1:A:294:ASN:HD21	1:A:330:ALA:H	1.43	0.67
1:A:195:MSE:HE2	1:A:339:LEU:HD23	1.80	0.63
1:A:360:ASN:HD21	1:A:385:ALA:H	1.48	0.60
1:A:375:HIS:CD2	1:A:376:ASN:ND2	2.74	0.56
1:A:180:LEU:HD13	1:A:262:ALA:HB3	1.87	0.56
1:A:397:VAL:HG21	1:A:405:MSE:HE1	1.87	0.55
1:A:231:ALA:O	1:A:235:LYS:HD3	2.06	0.55
1:A:3:LYS:HB3	1:A:4:PRO:HD3	1.87	0.55
1:A:195:MSE:CE	1:A:339:LEU:CD2	2.83	0.54
1:A:360:ASN:O	1:A:364:MSE:HG2	2.08	0.54
1:A:360:ASN:HD21	1:A:385:ALA:N	2.07	0.53
1:A:295:LYS:NZ	3:A:500:GDP:O4'	2.42	0.52
1:A:44:SER:HA	1:A:54:ASN:HD22	1.74	0.52
1:A:292:VAL:HG13	1:A:328:MSE:HE2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:302:ASP:OD1	1:A:303:GLU:N	2.44	0.49
1:A:330:ALA:HA	1:A:336:ILE:HD11	1.95	0.49
1:A:122:ASP:O	1:A:123:ASN:HB2	2.15	0.46
1:A:340:MSE:HB2	1:A:341:PRO:HD3	1.98	0.46
1:A:131:TYR:HB2	1:A:132:ASP:H	1.29	0.46
1:A:146:GLY:N	3:A:800:GDP:O6	2.49	0.46
1:A:435:ARG:CG	1:A:435:ARG:HH11	2.28	0.45
1:A:235:LYS:HD2	1:A:238:LYS:HZ2	1.82	0.45
1:A:401:ASP:HB3	1:A:404:LEU:HG	1.99	0.44
1:A:191:LEU:HD21	1:A:328:MSE:HE3	1.97	0.44
1:A:49:LEU:HD21	1:A:156:LEU:HD13	2.00	0.44
1:A:354:VAL:HG13	1:A:421:PHE:CE2	2.53	0.44
1:A:130:ILE:HG23	1:A:130:ILE:O	2.18	0.43
1:A:49:LEU:CD2	1:A:156:LEU:HD13	2.48	0.43
1:A:328:MSE:HE1	1:A:339:LEU:CD2	2.38	0.42
1:A:280:GLY:O	1:A:284:GLU:HG2	2.19	0.42
1:A:195:MSE:HE2	1:A:339:LEU:CD2	2.48	0.42
1:A:276:LYS:HE2	1:A:316:HIS:HB3	2.02	0.42
1:A:381:LYS:HB2	1:A:400:ASN:HB2	2.03	0.41
1:A:6:VAL:HB	1:A:55:LEU:HD13	2.02	0.41
1:A:186:VAL:HG21	1:A:264:VAL:CG2	2.51	0.40
1:A:384:TYR:HD2	1:A:398:PHE:CD1	2.39	0.40
1:A:414:GLU:HG2	1:A:428:ILE:HD11	2.03	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	390/436 (89%)	376 (96%)	13 (3%)	1 (0%)	46 68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	135	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	336/359 (94%)	323 (96%)	13 (4%)	39 66

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	ARG
1	A	93	ARG
1	A	130	ILE
1	A	131	TYR
1	A	148	HIS
1	A	173	GLU
1	A	180	LEU
1	A	214	VAL
1	A	235	LYS
1	A	301	LYS
1	A	333	LYS
1	A	353	ARG
1	A	436	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	75	GLN
1	A	172	ASN
1	A	294	ASN
1	A	360	ASN
1	A	376	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 1 is 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	GDP	A	500	-	23,30,30	1.13	2 (8%)	30,47,47	1.87	8 (26%)
3	GDP	A	800	-	23,30,30	1.13	2 (8%)	30,47,47	1.67	6 (20%)

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	GDP	A	500	-	-	0/12/32/32	0/3/3/3
3	GDP	A	800	-	-	0/12/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	800	GDP	C5-C4	2.79	1.46	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	500	GDP	C5-C4	2.96	1.47	1.40
3	A	500	GDP	C6-C5	3.46	1.48	1.41
3	A	800	GDP	C6-C5	3.53	1.48	1.41

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	500	GDP	C5-C6-N1	-4.01	118.10	123.59
3	A	800	GDP	C5-C6-N1	-3.80	118.39	123.59
3	A	500	GDP	C6-C5-C4	-3.73	116.44	120.90
3	A	500	GDP	PA-O3A-PB	-3.42	121.19	132.67
3	A	800	GDP	C6-C5-C4	-3.33	116.92	120.90
3	A	500	GDP	N3-C2-N1	-3.21	122.55	127.44
3	A	800	GDP	N3-C2-N1	-3.09	122.73	127.44
3	A	800	GDP	C4-C5-N7	-2.93	106.79	109.48
3	A	800	GDP	PA-O3A-PB	-2.78	123.34	132.67
3	A	500	GDP	C2'-C1'-N9	-2.71	110.16	114.29
3	A	500	GDP	C1'-N9-C4	-2.43	123.27	126.94
3	A	500	GDP	C4-C5-N7	-2.11	107.54	109.48
3	A	800	GDP	C6-N1-C2	4.42	122.07	115.94
3	A	500	GDP	C6-N1-C2	5.14	123.07	115.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	500	GDP	1	0
3	A	800	GDP	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 ⓘ

### 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	390/436 (89%)	0.92	65 (16%) 2 2	31, 42, 51, 61	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	123	ASN	6.5
1	A	68	PHE	6.2
1	A	29	SER	6.1
1	A	130	ILE	5.5
1	A	28	ILE	4.7
1	A	122	ASP	4.6
1	A	264	VAL	4.5
1	A	148	HIS	4.4
1	A	71	GLN	4.3
1	A	291	ILE	4.0
1	A	265	LEU	3.7
1	A	300	ASP	3.7
1	A	67	PRO	3.6
1	A	436	LYS	3.5
1	A	234	ARG	3.5
1	A	302	ASP	3.4
1	A	93	ARG	3.4
1	A	292	VAL	3.3
1	A	129	ASN	3.3
1	A	293	VAL	3.2
1	A	117	ALA	3.2
1	A	131	TYR	3.2
1	A	168	GLU	3.2
1	A	237	GLY	3.2
1	A	199	GLU	3.1
1	A	96	VAL	2.9
1	A	303	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	81	ASP	2.8
1	A	13	ASN	2.7
1	A	135	SER	2.7
1	A	75	GLN	2.7
1	A	69	LEU	2.6
1	A	242	THR	2.6
1	A	435	ARG	2.5
1	A	111	LYS	2.5
1	A	262	ALA	2.5
1	A	263	VAL	2.5
1	A	315	ASP	2.5
1	A	146	GLY	2.5
1	A	204	SER	2.5
1	A	244	GLU	2.4
1	A	363	ILE	2.4
1	A	417	ILE	2.4
1	A	241	GLU	2.4
1	A	272	ILE	2.4
1	A	42	ILE	2.3
1	A	98	ALA	2.3
1	A	27	ARG	2.3
1	A	378	SER	2.3
1	A	90	VAL	2.3
1	A	147	THR	2.2
1	A	376	ASN	2.2
1	A	178	PHE	2.2
1	A	179	CYS	2.2
1	A	87	ILE	2.1
1	A	235	LYS	2.1
1	A	261	VAL	2.1
1	A	47	GLU	2.1
1	A	269	GLU	2.1
1	A	26	GLU	2.1
1	A	74	GLN	2.0
1	A	373	PRO	2.0
1	A	290	VAL	2.0
1	A	403	GLU	2.0
1	A	180	LEU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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
3	GDP	A	800	28/28	0.88	0.21	-0.24	41,48,51,52	0
3	GDP	A	500	28/28	0.95	0.13	-1.01	32,34,42,42	0
2	ZN	A	900	1/1	0.96	0.06	-3.27	54,54,54,54	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.