

Full wwPDB X-ray Structure Validation Report (i)

Aug 16, 2023 – 10:01 PM EDT

PDB ID	:	2B92
Title	:	Crystal-structure of the N-terminal Large GTPase Domain of human Guany-
		late Binding protein 1 (hGBP1) in complex with $GDP/AlF3$
Authors	:	Ghosh, A.; Praefcke, G.J.K.; Renault, L.; Wittinghofer, A.; Herrmann, C.
Deposited on	:	2005-10-10
Resolution	:	3.20 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 (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	:	2.35
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)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 3.20 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	А	328	^{2%} 56%	25%	6% • 12%		
1	В	328	^{2%} 54%	26%	6% • 12%		



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4666 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	А	288	Total	C	N	0	S	0	0	0
			2284	1466	385	421	12			
1	В	200	Total	\mathbf{C}	Ν	Ο	\mathbf{S}	0	0	0
		290	2301	1478	387	424	12	0		0

• Molecule 1 is a protein called Interferon-induced guarylate-binding protein 1.

Chain	Residue	Modelled	Actual	Comment	Reference
А	-10	MET	-	cloning artifact	UNP P32455
А	-9	HIS	-	expression tag	UNP P32455
А	-8	HIS	-	expression tag	UNP P32455
А	-7	HIS	-	expression tag	UNP P32455
А	-6	HIS	-	expression tag	UNP P32455
А	-5	HIS	-	expression tag	UNP P32455
А	-4	HIS	-	expression tag	UNP P32455
А	-3	MET	-	cloning artifact	UNP P32455
А	-2	ARG	-	cloning artifact	UNP P32455
А	-1	GLY	-	cloning artifact	UNP P32455
А	0	SER	-	cloning artifact	UNP P32455
В	-10	MET	-	cloning artifact	UNP P32455
В	-9	HIS	-	expression tag	UNP P32455
В	-8	HIS	-	expression tag	UNP P32455
В	-7	HIS	-	expression tag	UNP P32455
В	-6	HIS	-	expression tag	UNP P32455
В	-5	HIS	-	expression tag	UNP P32455
В	-4	HIS	-	expression tag	UNP P32455
В	-3	MET	-	cloning artifact	UNP P32455
В	-2	ARG	-	cloning artifact	UNP P32455
В	-1	GLY	-	cloning artifact	UNP P32455
В	0	SER	-	cloning artifact	UNP P32455

There are 22 discrepancies between the modelled and reference sequences:

• Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total Mg 1 1	0	0
2	В	1	Total Mg 1 1	0	0

• Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	Λ	1	Total	С	Ν	Ο	Р	0	0
J A	1	28	10	5	11	2	0	0	
3	В	1	Total	С	Ν	Ο	Р	0	0
J	3 B		28	10	5	11	2	0	

• Molecule 4 is ALUMINUM FLUORIDE (three-letter code: AF3) (formula: AlF_3).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	TotalAlF413	0	0
4	В	1	TotalAlF413	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	9	Total O 9 9	0	0
5	В	6	Total O 6 6	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: Interferon-induced guanylate-binding protein 1



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	148.82Å 103.92Å 55.48Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
$\mathbf{B}_{\mathrm{ascolution}}(\hat{\boldsymbol{\lambda}})$	30.00 - 3.20	Depositor
Resolution (A)	29.62 - 3.20	EDS
% Data completeness	99.3 (30.00-3.20)	Depositor
(in resolution range)	99.3 (29.62-3.20)	EDS
R_{merge}	(Not available)	Depositor
R _{sym}	0.09	Depositor
$< I/\sigma(I) > 1$	$6.18 (at 3.18 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
P. P.	0.204 , 0.250	Depositor
n, n_{free}	0.198 , 0.248	DCC
R_{free} test set	989 reflections (6.73%)	wwPDB-VP
Wilson B-factor $(Å^2)$	79.0	Xtriage
Anisotropy	0.289	Xtriage
Bulk solvent $k_{sol}(e/A^3), B_{sol}(A^2)$	0.30 , 48.6	EDS
L-test for $twinning^2$	$ < L >=0.48, < L^2>=0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4666	wwPDB-VP
Average B, all atoms $(Å^2)$	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 65.95 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.5306e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities 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: AF3, MG, GDP

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).

Mal	Chain	Bo	nd lengths	Bond angles		
		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	1.26	13/2334~(0.6%)	0.40	0/3156	
1	В	1.31	19/2352~(0.8%)	0.44	2/3180~(0.1%)	
All	All	1.28	32/4686~(0.7%)	0.42	2/6336~(0.0%)	

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	А	0	3
1	В	0	5
All	All	0	8

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
1	В	85	HIS	N-CA	-10.08	1.26	1.46
1	В	84	PRO	N-CA	-8.45	1.32	1.47
1	А	26	GLU	CB-CG	8.39	1.68	1.52
1	В	147	GLU	CB-CG	8.05	1.67	1.52
1	А	251	GLU	CG-CD	7.92	1.63	1.51
1	А	251	GLU	CB-CG	7.42	1.66	1.52
1	А	26	GLU	CG-CD	7.27	1.62	1.51
1	В	147	GLU	CG-CD	7.07	1.62	1.51
1	А	214	GLN	CG-CD	6.67	1.66	1.51
1	В	84	PRO	CA-C	-6.64	1.39	1.52
1	В	15	GLU	CG-CD	6.56	1.61	1.51
1	В	306	SER	N-CA	6.29	1.58	1.46
1	В	128	TYR	CB-CG	-6.14	1.42	1.51
1	В	211	GLY	N-CA	6.07	1.55	1.46



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	В	15	GLU	CB-CG	5.97	1.63	1.52
1	А	135	ASN	CB-CG	-5.89	1.37	1.51
1	А	243	HIS	CA-C	5.88	1.68	1.52
1	А	105	GLU	CG-CD	5.74	1.60	1.51
1	В	213	SER	N-CA	5.74	1.57	1.46
1	А	252	LYS	CE-NZ	5.69	1.63	1.49
1	В	84	PRO	N-CD	5.63	1.55	1.47
1	В	135	ASN	CB-CG	-5.62	1.38	1.51
1	В	110	GLN	CG-CD	5.59	1.64	1.51
1	А	251	GLU	N-CA	5.40	1.57	1.46
1	В	20	ARG	CB-CG	5.33	1.67	1.52
1	В	308	ASP	CB-CG	5.30	1.62	1.51
1	В	20	ARG	CG-CD	5.28	1.65	1.51
1	В	49	THR	N-CA	-5.25	1.35	1.46
1	А	297	VAL	N-CA	-5.19	1.35	1.46
1	В	210	LYS	C-O	5.16	1.33	1.23
1	А	227	ARG	CG-CD	5.14	1.64	1.51
1	А	216	ASP	CB-CG	5.01	1.62	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	210	LYS	C-N-CA	-6.33	109.02	122.30
1	В	219	PHE	O-C-N	-5.59	113.75	122.70

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	212	THR	Peptide
1	А	243	HIS	Peptide
1	А	245	ARG	Peptide
1	В	154	SER	Mainchain
1	В	156	SER	Peptide
1	В	219	PHE	Mainchain
1	В	248	ALA	Peptide
1	В	66	SER	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	А	2284	0	2308	69	0
1	В	2301	0	2323	77	0
2	А	1	0	0	0	0
2	В	1	0	0	0	0
3	А	28	0	12	1	0
3	В	28	0	12	1	0
4	А	4	0	0	0	0
4	В	4	0	0	0	0
5	А	9	0	0	1	0
5	В	6	0	0	1	0
All	All	4666	0	4655	144	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 15.

All (144) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:219:PHE:O	1:A:222:PRO:HD2	1.39	1.19
1:B:171:PHE:O	1:B:172:VAL:HG12	1.42	1.16
1:A:49:THR:HG23	1:A:129:ASN:ND2	1.63	1.12
1:B:244:ARG:HH11	1:B:244:ARG:HG3	1.11	1.11
1:B:49:THR:HG23	1:B:129:ASN:ND2	1.76	1.01
1:B:244:ARG:HH11	1:B:244:ARG:CG	1.76	0.98
1:A:242:VAL:HG23	1:A:244:ARG:O	1.65	0.95
1:B:154:SER:C	1:B:156:SER:H	1.69	0.95
1:B:49:THR:CG2	1:B:129:ASN:HD22	1.79	0.95
1:A:49:THR:CG2	1:A:129:ASN:ND2	2.29	0.94
1:A:242:VAL:HG22	1:A:247:LEU:HD13	1.45	0.94
1:A:16:ASN:HD21	1:A:111:ASN:HD21	1.12	0.94
1:B:171:PHE:O	1:B:172:VAL:CG1	2.17	0.93
1:A:49:THR:CG2	1:A:129:ASN:HD22	1.82	0.92
1:A:62:LYS:NZ	1:A:254:GLN:HA	1.85	0.92
1:B:244:ARG:HG3	1:B:244:ARG:NH1	1.74	0.91
1:B:16:ASN:HD21	1:B:111:ASN:HD21	1.15	0.90



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:B:197:THR:OG1	1:B:200:GLU:HG3	1.80	0.81	
1:B:49:THR:CG2	1:B:129:ASN:ND2	2.38	0.81	
1:A:174:PHE:HB2	1:A:281:THR:HG22	1.64	0.79	
1:B:154:SER:C	1:B:156:SER:N	2.34	0.78	
1:A:49:THR:HG21	1:A:129:ASN:HD22	1.48	0.77	
1:B:213:SER:OG	1:B:214:GLN:N	2.16	0.76	
1:A:49:THR:HG23	1:A:129:ASN:HD21	1.48	0.76	
1:B:154:SER:O	1:B:156:SER:N	2.19	0.75	
1:A:73:SER:OG	1:A:76:LYS:HE2	1.90	0.72	
1:B:82:CYS:O	1:B:83:VAL:CG1	2.37	0.72	
1:A:219:PHE:O	1:A:221:LEU:N	2.24	0.70	
1:A:281:THR:HG23	1:A:282:LEU:O	1.92	0.70	
1:B:82:CYS:O	1:B:83:VAL:HG13	1.92	0.70	
1:B:49:THR:HG23	1:B:129:ASN:HD21	1.53	0.69	
1:A:155:LYS:O	1:A:156:SER:CB	2.41	0.69	
1:A:62:LYS:HZ2	1:A:254:GLN:HA	1.58	0.68	
1:A:155:LYS:O	1:A:156:SER:HB3	1.93	0.68	
1:A:31:LEU:HA	1:A:34:ILE:HD12	1.74	0.68	
1:B:49:THR:HG21	1:B:129:ASN:HD22	1.55	0.68	
1:A:151:ARG:O	1:A:154:SER:HB2	1.94	0.67	
1:A:6:HIS:HB2	1:A:84:PRO:HD3	1.77	0.67	
1:A:218:THR:O	1:A:219:PHE:O	2.13	0.66	
1:B:49:THR:HG22	1:B:51:LYS:HG3	1.77	0.66	
1:A:197:THR:OG1	1:A:200:GLU:HG3	1.95	0.66	
1:B:261:GLU:O	1:B:265:GLN:HG3	1.97	0.65	
1:A:49:THR:HG22	1:A:51:LYS:HG3	1.77	0.64	
1:B:296:LEU:HD22	1:B:300:TYR:CE1	2.32	0.64	
1:B:245:ARG:C	1:B:247:LEU:H	2.01	0.64	
1:B:171:PHE:C	1:B:172:VAL:HG12	2.18	0.63	
1:B:82:CYS:C	1:B:83:VAL:HG13	2.19	0.63	
1:A:62:LYS:O	1:A:63:LYS:HB3	1.99	0.63	
1:A:213:SER:H	1:A:216:ASP:HB2	1.64	0.63	
1:A:219:PHE:O	1:A:222:PRO:CD	2.33	0.62	
1:B:297:VAL:O	1:B:301:VAL:HG23	2.00	0.62	
1:B:239:ASP:O	1:B:240:ARG:C	2.38	0.61	
1:B:262:PHE:O	1:B:266:VAL:HG23	2.02	0.60	
1:B:16:ASN:ND2	1:B:111:ASN:HD21	1.93	0.60	
1:B:234:LYS:HD3	1:B:272:TYR:CE1	2.37	0.60	
1:B:44:VAL:HG23	1:B:45:GLY:N	2.15	0.59	
1:A:146:THR:HG22	1:A:147:GLU:N	2.17	0.59	
1:B:134:ILE:HD12	1:B:201:TYR:CE2	2.38	0.59	



	lo ao pagom	Interatomic	Clash		
Atom-1	Atom-2	distance (Å)	overlap (Å)		
1:B:219:PHE:O	1:B:221:LEU:N	2.31	0.59		
1:A:221:LEU:N	1:A:222:PRO:HD2	2.18	0.58		
1:B:16:ASN:HD21	1:B:111:ASN:ND2	1.96	0.58		
1:B:106:LYS:NZ	1:B:111:ASN:HD22	2.01	0.58		
1:B:219:PHE:O	1:B:220:ASN:HB2	2.05	0.57		
1:A:149:THR:HG22	1:A:150:HIS:N	2.19	0.57		
1:A:149:THR:CG2	1:A:153:ARG:NH2	2.68	0.57		
1:A:62:LYS:HZ3	1:A:254:GLN:HA	1.67	0.56		
1:B:244:ARG:CG	1:B:244:ARG:NH1	2.46	0.56		
1:B:221:LEU:N	1:B:222:PRO:HD2	2.21	0.55		
1:B:171:PHE:N	1:B:171:PHE:CD2	2.74	0.55		
1:A:172:VAL:O	1:A:172:VAL:HG12	2.08	0.54		
1:A:262:PHE:O	1:A:266:VAL:HG23	2.08	0.53		
1:B:149:THR:HG22	1:B:150:HIS:N	2.22	0.53		
1:B:239:ASP:O	1:B:240:ARG:O	2.27	0.53		
1:A:24:ASN:OD1	1:A:24:ASN:C	2.47	0.52		
1:B:49:THR:HG23	1:B:49:THR:O	2.09	0.52		
1:B:31:LEU:HA	1:B:34:ILE:HD12	1.91	0.51		
1:A:296:LEU:HD22	1:A:300:TYR:CE1	2.45	0.51		
1:A:239:ASP:OD2	1:B:245:ARG:CZ	2.59	0.51		
1:A:242:VAL:CG2	1:A:247:LEU:HD13	2.31	0.51		
1:B:209:LYS:O	1:B:211:GLY:N	2.44	0.51		
1:A:297:VAL:O	1:A:301:VAL:HG23	2.12	0.50		
1:B:221:LEU:N	1:B:222:PRO:CD	2.75	0.49		
1:A:44:VAL:HG23	1:A:45:GLY:N	2.26	0.49		
1:A:49:THR:HG23	1:A:49:THR:O	2.11	0.49		
1:B:46:LEU:O	1:B:49:THR:HB	2.13	0.49		
1:B:36:GLN:HB3	1:B:37:PRO:HD2	1.95	0.48		
1:B:172:VAL:O	1:B:172:VAL:HG13	2.13	0.48		
1:A:67:LEU:O	3:A:593:GDP:O2A	2.31	0.48		
1:B:244:ARG:HH11	1:B:244:ARG:CB	2.24	0.48		
1:A:46:LEU:O	1:A:49:THR:HB	2.13	0.48		
1:B:34:ILE:O	1:B:290:GLY:HA3	2.13	0.48		
1:B:82:CYS:C	1:B:83:VAL:CG1	2.80	0.48		
1:B:281:THR:CG2	1:B:282:LEU:O	2.62	0.48		
1:B:24:ASN:OD1	1:B:24:ASN:C	2.51	0.48		
1:A:116:PHE:CG	1:A:145:VAL:HG21	2.49	0.47		
1:B:289:ASN:OD1	1:B:291:PRO:HD2	2.14	0.47		
1:B:82:CYS:O	1:B:83:VAL:HG12	2.14	0.47		
1:A:245:ARG:HB2	1:A:247:LEU:HB2	1.97	0.47		
1:A:261:GLU:O	1:A:265:GLN:HG3	2.14	0.47		



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:209:LYS:O	1:A:210:LYS:C	2.53	0.47	
1:B:146:THR:O	1:B:149:THR:HB	2.14	0.47	
1:B:210:LYS:HB2	1:B:210:LYS:HE2	1.71	0.47	
1:A:134:ILE:HG22	1:B:104:VAL:HG11	1.96	0.46	
1:B:67:LEU:HG	1:B:251:GLU:CG	2.45	0.46	
1:B:134:ILE:HD12	1:B:201:TYR:CZ	2.51	0.46	
1:B:29:LYS:HB2	1:B:29:LYS:HE2	1.51	0.46	
1:B:245:ARG:C	1:B:247:LEU:N	2.68	0.46	
1:A:250:LEU:C	1:A:252:LYS:H	2.20	0.45	
1:B:95:LEU:O	1:B:96:LEU:HD23	2.17	0.45	
1:B:128:TYR:CD2	1:B:128:TYR:C	2.89	0.45	
1:B:83:VAL:O	1:B:93:LEU:N	2.47	0.44	
1:A:80:MET:HA	1:A:95:LEU:O	2.17	0.44	
1:A:242:VAL:HG23	1:A:242:VAL:O	2.16	0.44	
1:A:289:ASN:O	1:A:290:GLY:C	2.56	0.44	
1:B:80:MET:HA	1:B:95:LEU:O	2.18	0.44	
1:B:289:ASN:O	1:B:290:GLY:C	2.56	0.44	
1:A:149:THR:HG21	1:A:153:ARG:NH2	2.33	0.44	
1:B:11:MET:SD	1:B:30:ILE:HD12	2.57	0.44	
1:A:121:LEU:HD22	1:A:300:TYR:CZ	2.53	0.43	
1:A:87:LYS:HE2	1:A:87:LYS:HB3	1.75	0.43	
1:A:6:HIS:HB3	1:A:7:MET:H	1.53	0.43	
1:A:69:SER:OG	1:A:248:ALA:HB1	2.19	0.43	
1:A:116:PHE:CD2	1:A:145:VAL:HG11	2.53	0.43	
1:B:281:THR:HG23	1:B:282:LEU:O	2.18	0.43	
1:A:31:LEU:O	1:A:290:GLY:HA3	2.19	0.43	
1:A:242:VAL:CG2	1:A:242:VAL:O	2.66	0.43	
1:A:106:LYS:NZ	1:A:111:ASN:HD22	2.17	0.42	
1:A:279:THR:HG21	1:A:287:GLN:HG2	2.01	0.42	
1:B:218:THR:C	1:B:219:PHE:O	2.57	0.42	
1:B:24:ASN:HA	1:B:25:PRO:HD2	1.77	0.42	
1:A:24:ASN:HA	1:A:25:PRO:HD3	1.88	0.42	
1:B:177:ASP:OD1	1:B:232:LYS:HB2	2.20	0.42	
1:B:106:LYS:HZ1	1:B:111:ASN:HD22	1.67	0.42	
1:A:183:ARG:HA	1:A:183:ARG:HD2	1.86	0.42	
1:A:23:ALA:HB1	1:A:28:LEU:HD11	2.02	0.41	
1:A:20:ARG:HA	1:A:20:ARG:HD3	1.92	0.41	
1:A:198:PRO:O	1:A:201:TYR:HB3	2.19	0.41	
1:B:67:LEU:O	3:B:593:GDP:O2A	2.39	0.41	
1:A:67:LEU:HG	1:A:251:GLU:HG2	2.03	0.40	
1:B:6:HIS:N	5:B:596:HOH:O	2.53	0.40	



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)	
1:B:146:THR:HG22	1:B:147:GLU:N	2.36	0.40	
1:B:229:PHE:CD2	1:B:229:PHE:C	2.95	0.40	
1:A:110:GLN:HB2	5:A:601:HOH:O	2.21	0.40	
1:A:149:THR:O	1:A:150:HIS:C	2.60	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	Perc	centiles
1	А	284/328 (87%)	252~(89%)	27 (10%)	5(2%)	8	41
1	В	286/328 (87%)	250 (87%)	24 (8%)	12 (4%)	3	20
All	All	570/656~(87%)	502~(88%)	51 (9%)	17 (3%)	4	28

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	210	LYS
1	А	219	PHE
1	А	220	ASN
1	В	155	LYS
1	В	219	PHE
1	В	63	LYS
1	В	210	LYS
1	В	240	ARG
1	В	231	PRO
1	В	307	GLY
1	В	195	PRO
1	В	220	ASN
1	А	290	GLY
1	В	172	VAL



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Mol	Chain	Res	Type
1	В	212	THR
1	В	290	GLY
1	А	307	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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Perce	entiles
1	А	257/293~(88%)	229~(89%)	28 (11%)	6	26
1	В	259/293~(88%)	219~(85%)	40 (15%)	2	13
All	All	516/586~(88%)	448 (87%)	68 (13%)	4	19

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	6	HIS
1	А	7	MET
1	А	29	LYS
1	А	47	TYR
1	А	48	ARG
1	А	49	THR
1	А	63	LYS
1	А	69	SER
1	А	70	THR
1	А	116	PHE
1	А	137	GLN
1	А	139	MET
1	А	146	THR
1	А	149	THR
1	А	174	PHE
1	А	186	SER
1	A	208	LEU
1	А	210	LYS
1	A	212	THR
1	А	214	GLN



Mol	Chain	Res	Type
1	А	217	GLU
1	А	233	LYS
1	А	245	ARG
1	А	246	LYS
1	А	281	THR
1	А	283	SER
1	А	305	SER
1	А	306	SER
1	В	7	MET
1	В	8	THR
1	В	14	ILE
1	В	17	THR
1	В	20	ARG
1	В	29	LYS
1	В	47	TYR
1	В	49	THR
1	В	55	MET
1	В	61	LYS
1	В	66	SER
1	В	67	LEU
1	В	84	PRO
1	В	116	PHE
1	В	137	GLN
1	В	139	MET
1	В	146	THR
1	В	149	THR
1	В	153	ARG
1	В	154	SER
1	В	171	PHE
1	В	194	GLN
1	В	205	SER
1	В	207	LYS
1	В	209	LYS
1	В	210	LYS
1	В	213	SER
1	В	215	LYS
1	В	228	LYS
1	В	240	ARG
1	В	244	ARG
1	В	245	ARG
1	В	246	LYS
1	В	249	GLN



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Mol	Chain	Res	Type
1	В	252	LYS
1	В	254	GLN
1	В	256	GLU
1	В	281	THR
1	В	295	SER
1	В	306	SER

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

Mol	Chain	Res	Type
1	А	111	ASN
1	В	18	ASN
1	В	111	ASN
1	В	129	ASN
1	В	194	GLN
1	В	214	GLN

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 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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).



Mal	al Trme Chain		Dec	Bond lengths			Bond angles			
NIOI	туре	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
3	GDP	А	593	2,4	24,30,30	2.21	7 (29%)	30,47,47	1.42	5 (16%)
4	AF3	В	594	2,5,3	0,3,3	-	-	-		
3	GDP	В	593	2,4	24,30,30	2.29	7 (29%)	30,47,47	1.39	5 (16%)
4	AF3	А	594	2,5,3	0,3,3	-	-	-		

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	GDP	А	593	2,4	-	2/12/32/32	0/3/3/3
3	GDP	В	593	2,4	-	2/12/32/32	0/3/3/3

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	А	593	GDP	O4'-C1'	5.97	1.49	1.41
3	В	593	GDP	O4'-C1'	5.72	1.49	1.41
3	В	593	GDP	C5-C6	-4.87	1.37	1.47
3	А	593	GDP	C5-C6	-4.16	1.39	1.47
3	В	593	GDP	PB-O2B	-3.95	1.39	1.54
3	А	593	GDP	PB-O2B	-3.94	1.39	1.54
3	В	593	GDP	PB-O3B	-3.83	1.40	1.54
3	А	593	GDP	O4'-C4'	3.64	1.53	1.45
3	В	593	GDP	O4'-C4'	3.37	1.52	1.45
3	А	593	GDP	PB-O1B	-3.20	1.40	1.50
3	В	593	GDP	C2'-C1'	-2.84	1.49	1.53
3	В	593	GDP	PB-O1B	-2.76	1.41	1.50
3	А	593	GDP	PB-O3B	-2.49	1.45	1.54
3	А	593	GDP	C2'-C1'	-2.15	1.50	1.53

All (14) bond length outliers are listed below:

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
3	А	593	GDP	PA-O3A-PB	-3.66	120.26	132.83
3	В	593	GDP	PA-O3A-PB	-3.50	120.81	132.83
3	А	593	GDP	C2-N1-C6	-3.16	119.28	125.10
3	А	593	GDP	C5-C6-N1	3.12	119.47	113.95
3	В	593	GDP	C2-N1-C6	-3.06	119.47	125.10
3	В	593	GDP	C5-C6-N1	2.97	119.19	113.95



2B92	
2B92	

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	593	GDP	C8-N7-C5	2.58	107.91	102.99
3	В	593	GDP	C8-N7-C5	2.54	107.83	102.99
3	В	593	GDP	O6-C6-C5	-2.09	120.29	124.37
3	А	593	GDP	O6-C6-C5	-2.02	120.42	124.37

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	593	GDP	PA-O3A-PB-O2B
3	В	593	GDP	PA-O3A-PB-O2B
3	А	593	GDP	PA-O3A-PB-O1B
3	В	593	GDP	PA-O3A-PB-O3B

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	А	593	GDP	1	0
3	В	593	GDP	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.





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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	288/328~(87%)	-0.26	6 (2%) 63 49	33, 58, 90, 98	0
1	В	290/328~(88%)	-0.26	7 (2%) 59 44	32, 58, 90, 99	0
All	All	578/656~(88%)	-0.26	13 (2%) 62 48	32, 58, 90, 99	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	243	HIS	3.6
1	А	243	HIS	3.6
1	В	307	GLY	3.4
1	В	157	SER	3.4
1	А	306	SER	2.7
1	В	215	LYS	2.6
1	А	307	GLY	2.6
1	В	308	ASP	2.6
1	А	215	LYS	2.5
1	А	256	GLU	2.4
1	А	69	SER	2.1
1	В	306	SER	2.0
1	В	210	LYS	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 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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
2	MG	В	595	1/1	0.93	0.24	43,43,43,43	0
2	MG	А	595	1/1	0.96	0.19	40,40,40,40	0
4	AF3	А	594	4/4	0.96	0.20	32,37,38,38	0
3	GDP	В	593	28/28	0.97	0.15	$47,\!51,\!55,\!56$	0
3	GDP	А	593	28/28	0.97	0.17	46,49,55,59	0
4	AF3	В	594	4/4	0.97	0.20	30,34,36,37	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.







6.5 Other polymers (i)

There are no such residues in this entry.

