



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 07:16 PM EDT

PDB ID : 4NCL / pdb_00004ncl
Title : Crystal structure of eukaryotic translation initiation factor eIF5B (517-970)
from *Chaetomium thermophilum* in complex with GDP
Authors : Kuhle, B.; Ficner, R.
Deposited on : 2013-10-24
Resolution : 2.12 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

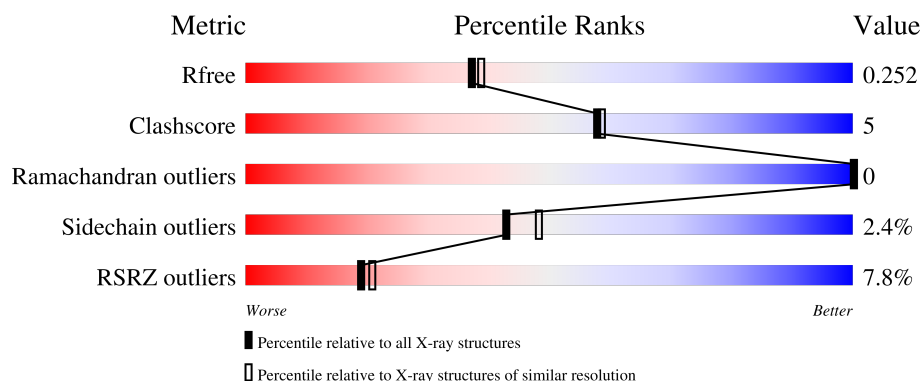
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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}	180053	8290 (2.14-2.10)
Clashscore	190562	8817 (2.14-2.10)
Ramachandran outliers	187476	8738 (2.14-2.10)
Sidechain outliers	187428	8739 (2.14-2.10)
RSRZ outliers	180081	8294 (2.14-2.10)

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 $\leq 5\%$. 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	457	9% 83% 10% 6%
1	B	457	6% 80% 14% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7106 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 Eukaryotic translation initiation factor 5B-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	428	Total	C	N	O	S	0	6	0
			3384	2144	586	637	17			
1	B	435	Total	C	N	O	S	0	9	0
			3471	2200	599	653	19			

There are 54 discrepancies between the modelled and reference sequences:

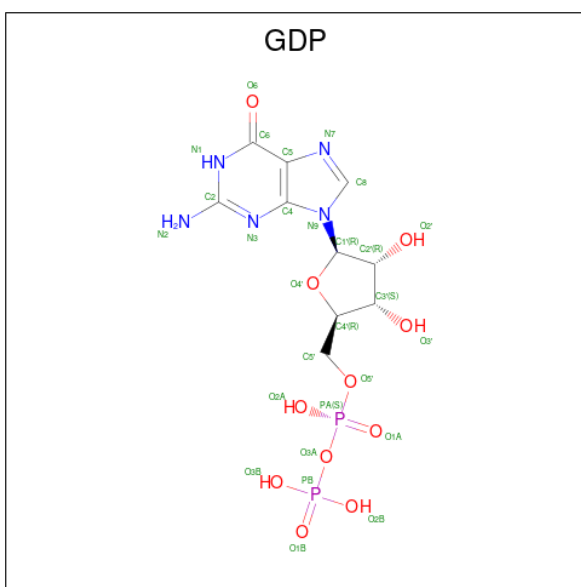
Chain	Residue	Modelled	Actual	Comment	Reference
A	514	SER	-	expression tag	UNP G0S8G9
A	515	HIS	-	expression tag	UNP G0S8G9
A	516	MET	-	expression tag	UNP G0S8G9
A	576	VAL	-	SEE REMARK 999	UNP G0S8G9
A	577	VAL	-	SEE REMARK 999	UNP G0S8G9
A	578	ASN	-	SEE REMARK 999	UNP G0S8G9
A	579	LYS	-	SEE REMARK 999	UNP G0S8G9
A	580	ASP	-	SEE REMARK 999	UNP G0S8G9
A	581	GLY	-	SEE REMARK 999	UNP G0S8G9
A	582	LYS	-	SEE REMARK 999	UNP G0S8G9
A	583	PHE	-	SEE REMARK 999	UNP G0S8G9
A	584	GLU	-	SEE REMARK 999	UNP G0S8G9
A	585	PHE	-	SEE REMARK 999	UNP G0S8G9
A	586	LYS	-	SEE REMARK 999	UNP G0S8G9
A	587	VAL	-	SEE REMARK 999	UNP G0S8G9
A	588	PRO	-	SEE REMARK 999	UNP G0S8G9
A	589	GLY	-	SEE REMARK 999	UNP G0S8G9
A	590	LEU	-	SEE REMARK 999	UNP G0S8G9
A	591	LEU	-	SEE REMARK 999	UNP G0S8G9
A	592	ILE	-	SEE REMARK 999	UNP G0S8G9
A	593	ILE	-	SEE REMARK 999	UNP G0S8G9
A	594	ASP	-	SEE REMARK 999	UNP G0S8G9
A	595	THR	-	SEE REMARK 999	UNP G0S8G9
A	596	PRO	-	SEE REMARK 999	UNP G0S8G9
A	597	GLY	-	SEE REMARK 999	UNP G0S8G9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	598	HIS	-	SEE REMARK 999	UNP G0S8G9
A	599	GLU	-	SEE REMARK 999	UNP G0S8G9
B	514	SER	-	expression tag	UNP G0S8G9
B	515	HIS	-	expression tag	UNP G0S8G9
B	516	MET	-	expression tag	UNP G0S8G9
B	576	VAL	-	SEE REMARK 999	UNP G0S8G9
B	577	VAL	-	SEE REMARK 999	UNP G0S8G9
B	578	ASN	-	SEE REMARK 999	UNP G0S8G9
B	579	LYS	-	SEE REMARK 999	UNP G0S8G9
B	580	ASP	-	SEE REMARK 999	UNP G0S8G9
B	581	GLY	-	SEE REMARK 999	UNP G0S8G9
B	582	LYS	-	SEE REMARK 999	UNP G0S8G9
B	583	PHE	-	SEE REMARK 999	UNP G0S8G9
B	584	GLU	-	SEE REMARK 999	UNP G0S8G9
B	585	PHE	-	SEE REMARK 999	UNP G0S8G9
B	586	LYS	-	SEE REMARK 999	UNP G0S8G9
B	587	VAL	-	SEE REMARK 999	UNP G0S8G9
B	588	PRO	-	SEE REMARK 999	UNP G0S8G9
B	589	GLY	-	SEE REMARK 999	UNP G0S8G9
B	590	LEU	-	SEE REMARK 999	UNP G0S8G9
B	591	LEU	-	SEE REMARK 999	UNP G0S8G9
B	592	ILE	-	SEE REMARK 999	UNP G0S8G9
B	593	ILE	-	SEE REMARK 999	UNP G0S8G9
B	594	ASP	-	SEE REMARK 999	UNP G0S8G9
B	595	THR	-	SEE REMARK 999	UNP G0S8G9
B	596	PRO	-	SEE REMARK 999	UNP G0S8G9
B	597	GLY	-	SEE REMARK 999	UNP G0S8G9
B	598	HIS	-	SEE REMARK 999	UNP G0S8G9
B	599	GLU	-	SEE REMARK 999	UNP G0S8G9

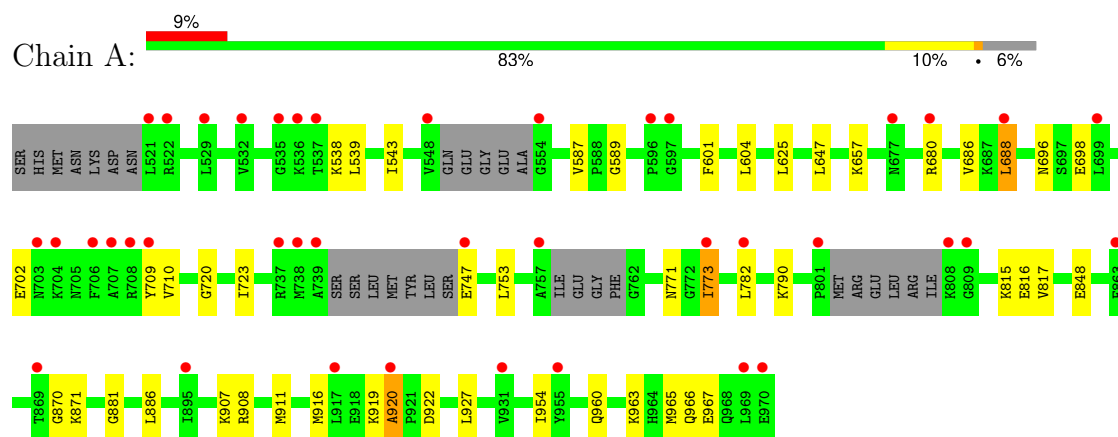
- Molecule 2 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



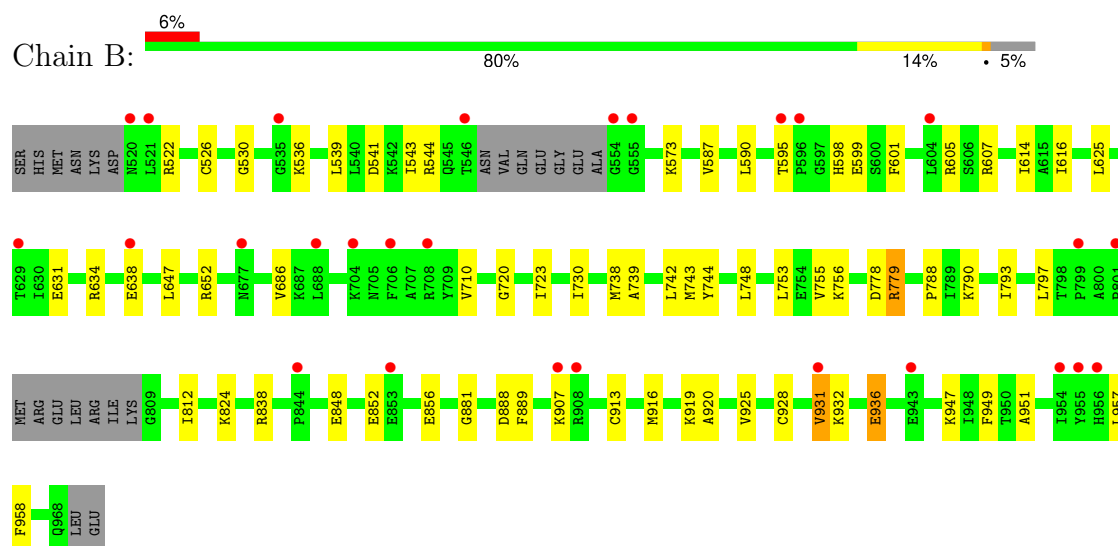
3 Residue-property plots [i](#)

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: Eukaryotic translation initiation factor 5B-like protein



- Molecule 1: Eukaryotic translation initiation factor 5B-like protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	66.90Å 72.96Å 199.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.87 – 2.12 47.87 – 2.12	Depositor EDS
% Data completeness (in resolution range)	99.6 (47.87-2.12) 99.7 (47.87-2.12)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.214 , 0.248 0.216 , 0.252	Depositor DCC
R_{free} test set	2829 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	(Not available)	Xtriage
Anisotropy	(Not available)	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 51.6	EDS
L-test for twinning ¹	$\langle L \rangle =$ (Not available), $\langle L^2 \rangle =$ (Not available)	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7106	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *(Not available)*

¹Theoretical 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.

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: 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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.37	0/3432	0.74	2/4623 (0.0%)
1	B	0.37	0/3524	0.74	0/4748
All	All	0.37	0/6956	0.74	2/9371 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	920	ALA	CA-C-N	5.60	125.97	119.47
1	A	920	ALA	C-N-CA	5.60	125.97	119.47

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	3384	0	3433	25	0
1	B	3471	0	3518	39	0
2	A	28	0	12	1	0
2	B	28	0	12	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	92	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	101	0	0	1	0
All	All	7106	0	6975	63	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 (63) 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:886:LEU:HA	1:A:954:ILE:HD11	1.72	0.69
1:A:773:ILE:HD11	1:A:816:GLU:HB2	1.75	0.68
1:B:526[B]:CYS:SG	1:B:590:LEU:HD11	2.36	0.65
1:B:925:VAL:HG12	1:B:947:LYS:HB2	1.80	0.63
1:B:530:GLY:N	1:B:536:LYS:HD3	2.15	0.60
1:B:605:ARG:NH1	1:B:888:ASP:OD2	2.33	0.60
1:A:916:MET:O	1:A:920:ALA:N	2.32	0.59
1:B:634:ARG:NH1	1:B:638:GLU:OE2	2.35	0.58
1:B:541:ASP:OD2	1:B:544:ARG:NH1	2.38	0.57
1:A:963:LYS:NZ	1:A:967:GLU:OE2	2.31	0.56
1:B:647:LEU:HD21	1:B:686:VAL:HG11	1.89	0.55
1:A:696:ASN:HB3	1:A:709:TYR:CE1	2.43	0.54
1:B:779:ARG:HD3	1:B:848:GLU:OE1	2.07	0.54
1:A:601:PHE:O	1:A:881:GLY:HA3	2.08	0.54
1:A:698:GLU:HG2	1:A:709:TYR:CD1	2.44	0.53
1:A:747:GLU:O	1:A:771:ASN:ND2	2.39	0.53
1:B:598:HIS:NE2	1:B:631[A]:GLU:OE1	2.41	0.52
1:A:657:LYS:HD3	1:B:744:TYR:CE2	2.45	0.52
1:B:907:LYS:HD3	1:B:936[B]:GLU:OE1	2.11	0.50
1:A:647:LEU:HD21	1:A:686:VAL:HG11	1.93	0.49
1:B:947:LYS:HD3	1:B:949:PHE:CZ	2.47	0.49
1:B:916:MET:O	1:B:920:ALA:N	2.42	0.49
1:B:614:ILE:HB	1:B:738:MET:HE1	1.95	0.48
1:B:889:PHE:HE1	1:B:958:PHE:HB2	1.78	0.48
1:B:790:LYS:HD3	1:B:852:GLU:OE1	2.14	0.48
1:B:916:MET:HE1	1:B:919:LYS:HD3	1.95	0.48
1:A:790:LYS:HD2	1:A:848:GLU:OE2	2.13	0.48
1:B:539:LEU:O	1:B:543:ILE:HG13	2.14	0.48
1:A:773:ILE:HD12	1:A:817:VAL:O	2.14	0.47
1:A:963:LYS:O	1:A:966:GLN:HG2	2.14	0.47
1:B:607:ARG:HD3	1:B:838:ARG:HD3	1.97	0.47
1:A:538:LYS:HE3	2:A:1001:GDP:H2'	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:522:ARG:HG2	1:B:742:LEU:O	2.15	0.46
1:B:951:ALA:HB3	1:B:957:LEU:HG	1.98	0.46
1:B:616:ILE:HD11	1:B:730:ILE:HD11	1.97	0.46
1:B:788:PRO:HG3	1:B:856:GLU:HB2	1.98	0.45
1:B:907:LYS:HG3	4:B:1175:HOH:O	2.14	0.45
1:B:932:LYS:HE2	1:B:932:LYS:H	1.81	0.45
1:B:755:VAL:O	1:B:756:LYS:HD2	2.17	0.45
1:A:922:ASP:HB3	1:A:965:MET:HE1	1.97	0.45
1:B:720:GLY:HA2	1:B:723:ILE:HD12	1.99	0.45
1:A:871:LYS:NZ	1:A:919:LYS:HG2	2.32	0.44
1:A:680[A]:ARG:NH2	1:A:702:GLU:OE1	2.51	0.44
1:B:739:ALA:O	1:B:743:MET:HG2	2.17	0.44
1:B:932:LYS:HE2	1:B:932:LYS:HB2	1.78	0.44
1:A:907:LYS:HB3	1:A:911:MET:HE3	2.00	0.44
1:A:587:VAL:HG22	1:A:589:GLY:H	1.83	0.43
1:A:815:LYS:HB3	1:A:815:LYS:HE3	1.60	0.43
1:A:539:LEU:O	1:A:543:ILE:HG13	2.18	0.43
1:B:907:LYS:HD3	1:B:936[B]:GLU:CD	2.43	0.43
1:B:913:CYS:O	1:B:916:MET:HB2	2.18	0.43
1:B:778:ASP:HB2	1:B:793:ILE:HD12	2.01	0.42
1:A:870:GLY:O	1:A:916:MET:HE1	2.20	0.42
1:B:543:ILE:O	1:B:573:LYS:NZ	2.41	0.42
1:B:753:LEU:HD12	1:B:753:LEU:HA	1.81	0.42
1:B:928:CYS:HB3	1:B:931:VAL:CG2	2.50	0.42
1:A:688:LEU:HA	1:A:688:LEU:HD12	1.78	0.41
1:A:960:GLN:NE2	4:A:1180:HOH:O	2.30	0.41
1:B:595:THR:HG23	1:B:599:GLU:HB2	2.02	0.41
1:B:536:LYS:HB2	1:B:536:LYS:HE2	1.89	0.41
1:B:797:LEU:HB2	1:B:824:LYS:HB3	2.02	0.41
1:A:720:GLY:HA2	1:A:723:ILE:HD12	2.02	0.41
1:B:601:PHE:O	1:B:881:GLY:HA3	2.21	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	424/457 (93%)	420 (99%)	4 (1%)	0	100	100
1	B	438/457 (96%)	435 (99%)	3 (1%)	0	100	100
All	All	862/914 (94%)	855 (99%)	7 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	370/393 (94%)	361 (98%)	9 (2%)	43	48
1	B	381/393 (97%)	371 (97%)	10 (3%)	40	45
All	All	751/786 (96%)	732 (98%)	19 (2%)	43	47

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	604	LEU
1	A	625	LEU
1	A	688	LEU
1	A	710	VAL
1	A	753	LEU
1	A	773	ILE
1	A	782	LEU
1	A	908	ARG
1	A	927	LEU
1	B	587	VAL
1	B	625	LEU
1	B	652	ARG
1	B	710	VAL
1	B	748	LEU
1	B	779	ARG

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Mol	Chain	Res	Type
1	B	812	ILE
1	B	931	VAL
1	B	936[A]	GLU
1	B	936[B]	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	628	GLN
1	A	938	GLN
1	A	960	GLN
1	A	968	GLN
1	B	661	ASN
1	B	718	HIS
1	B	771	ASN
1	B	938	GLN
1	B	944	ASN
1	B	960	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are 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
2	GDP	B	1001	3	29,30,30	1.16	2 (6%)	45,47,47	1.72	5 (11%)
2	GDP	A	1001	3	29,30,30	1.13	2 (6%)	45,47,47	1.76	6 (13%)

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
2	GDP	B	1001	3	-	2/16/32/32	0/3/3/3
2	GDP	A	1001	3	-	5/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	GDP	C5-C4	3.12	1.47	1.38
2	B	1001	GDP	C5-C4	3.11	1.47	1.38
2	B	1001	GDP	C6-N1	-2.45	1.34	1.38
2	A	1001	GDP	C6-N1	-2.36	1.34	1.38

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1001	GDP	C5-C4-N3	-5.96	118.90	128.39
2	A	1001	GDP	C5-C4-N3	-5.79	119.18	128.39
2	A	1001	GDP	C2-N3-C4	4.98	120.87	112.30
2	B	1001	GDP	C2-N3-C4	4.91	120.76	112.30
2	B	1001	GDP	N9-C4-N3	4.19	134.32	125.95
2	A	1001	GDP	N9-C4-N3	3.92	133.79	125.95
2	A	1001	GDP	C6-C5-N7	3.68	136.98	130.29
2	B	1001	GDP	C6-C5-N7	3.48	136.62	130.29
2	A	1001	GDP	C4-C5-N7	-2.80	106.23	110.67
2	B	1001	GDP	C4-C5-N7	-2.75	106.31	110.67
2	A	1001	GDP	C3'-C2'-C1'	2.35	105.91	101.46

There are no chirality outliers.

All (7) torsion outliers are listed below:

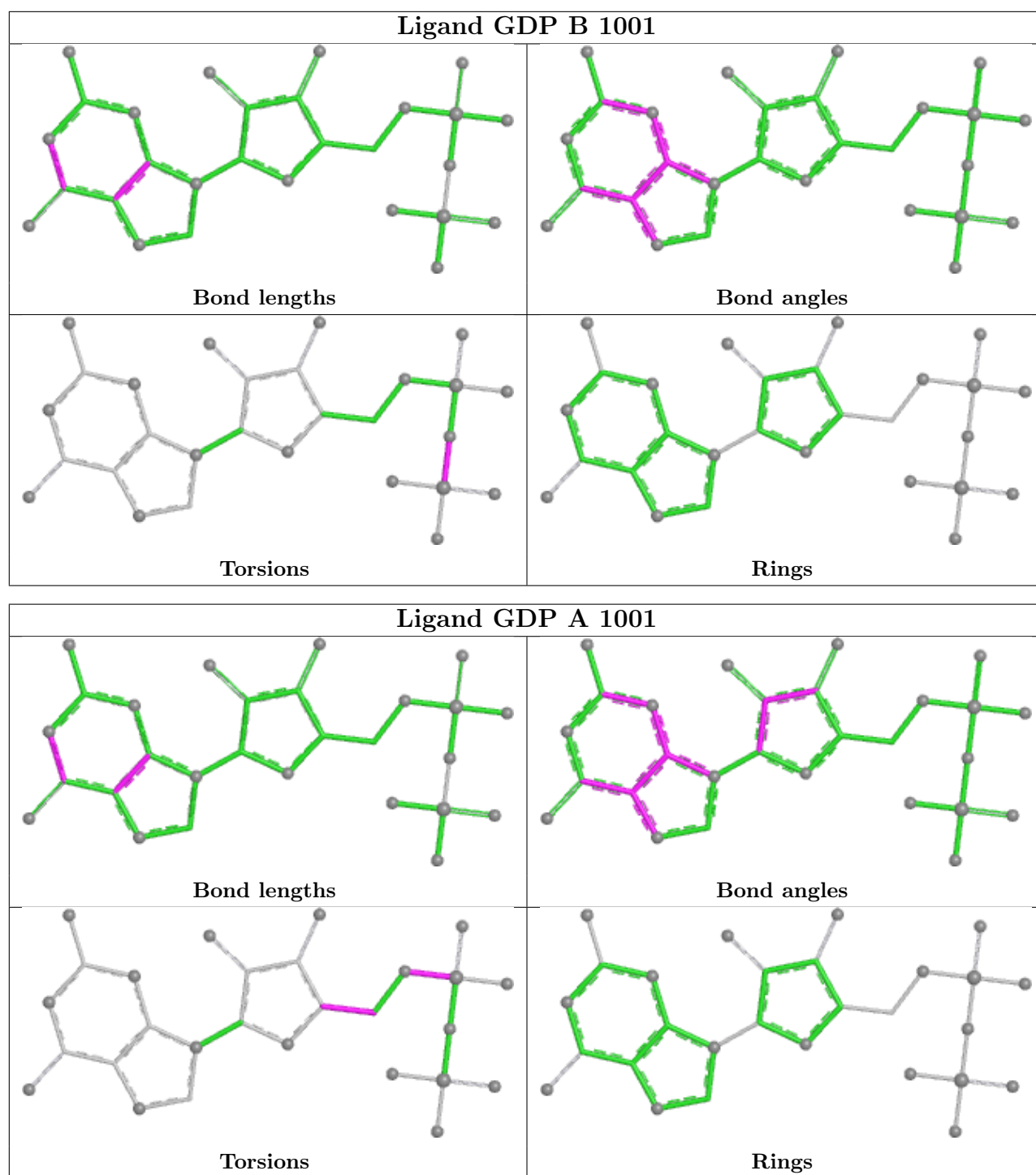
Mol	Chain	Res	Type	Atoms
2	B	1001	GDP	PA-O3A-PB-O3B
2	A	1001	GDP	O4'-C4'-C5'-O5'
2	A	1001	GDP	C3'-C4'-C5'-O5'
2	A	1001	GDP	C5'-O5'-PA-O3A
2	A	1001	GDP	C5'-O5'-PA-O1A
2	A	1001	GDP	C5'-O5'-PA-O2A
2	B	1001	GDP	PA-O3A-PB-O1B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	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 than 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

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, 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	428/457 (93%)	0.84	40 (9%) 14 15	21, 58, 93, 143	7 (1%)
1	B	435/457 (95%)	0.76	27 (6%) 26 29	21, 58, 90, 109	9 (2%)
All	All	863/914 (94%)	0.80	67 (7%) 19 21	21, 58, 92, 143	16 (1%)

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	739	ALA	4.5
1	B	520	ASN	4.5
1	A	706	PHE	4.4
1	B	554	GLY	4.4
1	B	706	PHE	4.4
1	A	537	THR	4.3
1	B	955	TYR	3.9
1	A	709	TYR	3.7
1	A	738	MET	3.6
1	A	808	LYS	3.5
1	A	809	GLY	3.4
1	A	917	LEU	3.4
1	B	801	PRO	3.4
1	B	956[A]	HIS	3.1
1	A	955	TYR	3.1
1	A	596	PRO	3.1
1	A	801	PRO	3.0
1	A	521	LEU	3.0
1	B	535	GLY	3.0
1	A	532	VAL	3.0
1	A	554	GLY	3.0
1	A	969	LEU	2.9
1	A	747	GLU	2.9
1	A	688	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	757	ALA	2.8
1	B	596	PRO	2.8
1	B	844	PRO	2.8
1	A	704	LYS	2.7
1	B	708	ARG	2.7
1	B	954	ILE	2.7
1	B	704	LYS	2.7
1	B	638	GLU	2.7
1	A	703	ASN	2.6
1	A	536	LYS	2.5
1	A	699	LEU	2.5
1	B	629	THR	2.4
1	B	521	LEU	2.4
1	A	597	GLY	2.4
1	A	680[A]	ARG	2.4
1	A	548	VAL	2.4
1	B	546	THR	2.4
1	B	555	GLY	2.3
1	A	782	LEU	2.3
1	B	907	LYS	2.3
1	B	853	GLU	2.3
1	B	604	LEU	2.3
1	A	737	ARG	2.2
1	A	773	ILE	2.2
1	A	707	ALA	2.2
1	B	943	GLU	2.2
1	A	522	ARG	2.2
1	A	931	VAL	2.2
1	B	931	VAL	2.2
1	A	529	LEU	2.1
1	B	688	LEU	2.1
1	B	908[A]	ARG	2.1
1	B	595	THR	2.1
1	A	863	PHE	2.1
1	B	799	PRO	2.1
1	A	895	ILE	2.1
1	A	708	ARG	2.1
1	A	920	ALA	2.1
1	A	970	GLU	2.0
1	B	677	ASN	2.0
1	A	869	THR	2.0
1	A	535	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	677	ASN	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

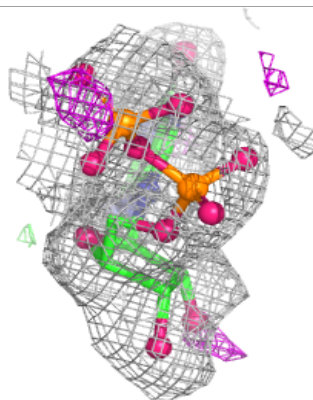
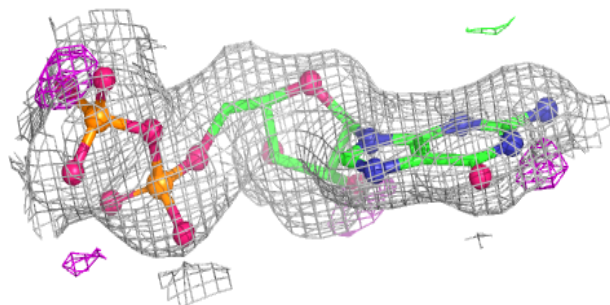
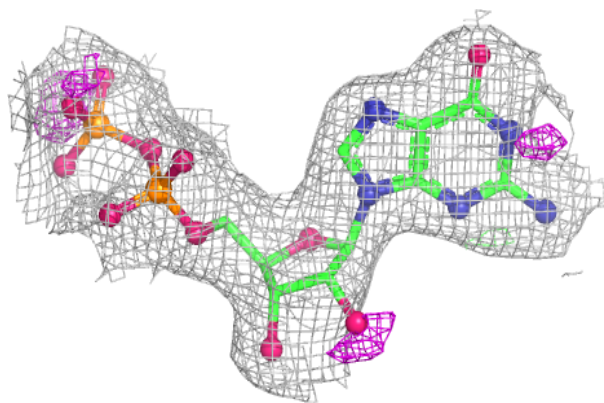
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GDP	A	1001	28/28	0.86	0.11	61,77,106,192	0
3	MG	A	1002	1/1	0.86	0.11	75,75,75,75	0
3	MG	B	1002	1/1	0.91	0.12	70,70,70,70	0
2	GDP	B	1001	28/28	0.92	0.09	57,72,80,122	0

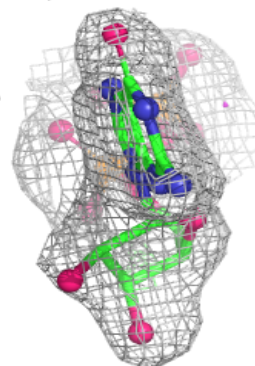
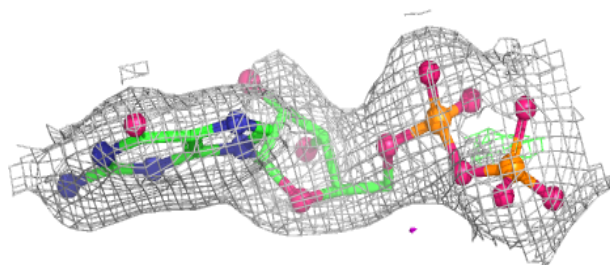
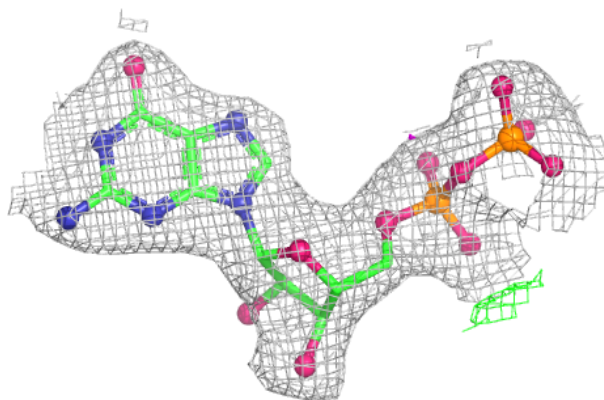
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around GDP A 1001:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around GDP B 1001:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.