



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:54 PM GMT

PDB ID : 1R5O
Title : crystal structure analysis of sup35 complexed with GMPPNP
Authors : Kong, C.; Song, H.
Deposited on : 2003-10-11
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

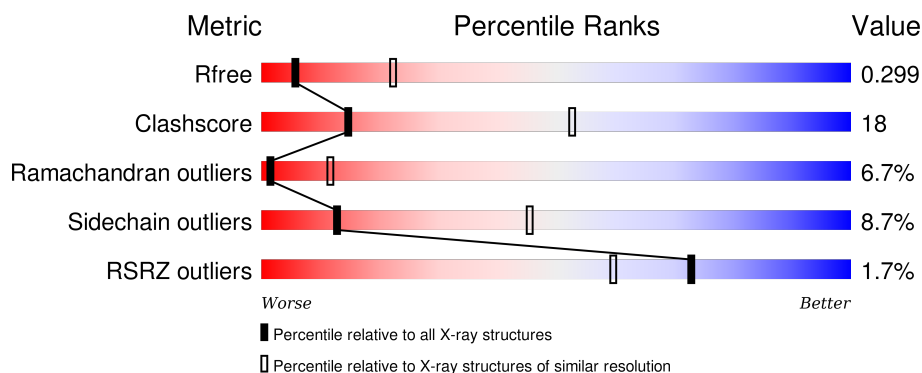
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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. 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	467	<div> <div></div> <div>52%</div> <div>29%</div> <div>6%</div> <div>12%</div> </div>

2 Entry composition [i](#)

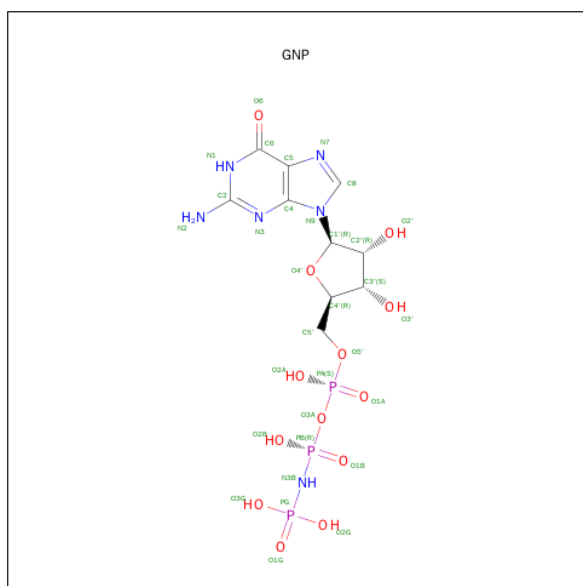
There are 3 unique types of molecules in this entry. The entry contains 3310 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 peptide chain release factor GTP-binding subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	409	Total	C	N	O	S	0	0	0
			3222	2024	557	622	19			

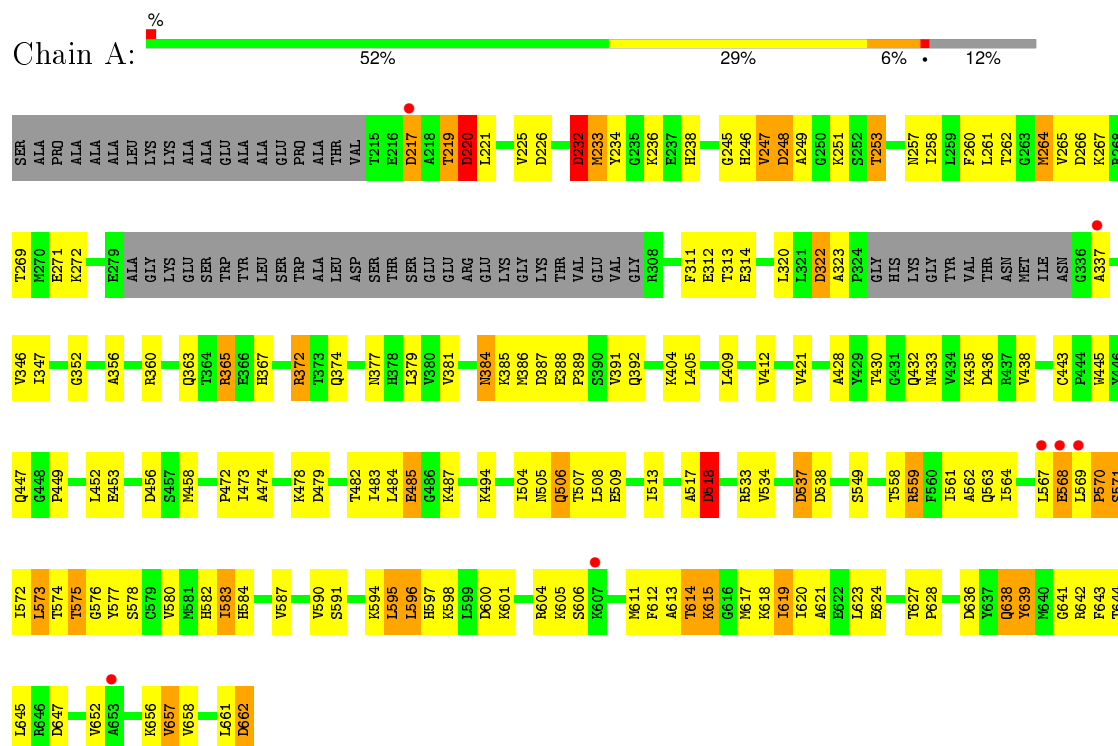
- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



3 Residue-property plots

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 ($\text{RSRZ} > 2$). 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 peptide chain release factor GTP-binding subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	82.52Å 82.52Å 168.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.20 46.35 – 3.00	Depositor EDS
% Data completeness (in resolution range)	97.7 (20.00-3.20) 97.7 (46.35-3.00)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.266 , 0.320 0.242 , 0.299	Depositor DCC
R_{free} test set	452 reflections (4.80%)	DCC
Wilson B-factor (Å ²)	68.2	Xtriage
Anisotropy	0.235	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 53.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 11972 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3310	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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 ⓘ

5.1 Standard geometry ⓘ

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

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	0.57	0/3273	0.83	12/4412 (0.3%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	662	ASP	CB-CG-OD2	6.70	124.33	118.30
1	A	220	ASP	CB-CG-OD2	6.40	124.06	118.30
1	A	436	ASP	CB-CG-OD2	6.34	124.01	118.30
1	A	600	ASP	CB-CG-OD2	6.19	123.87	118.30
1	A	537	ASP	CB-CG-OD2	6.13	123.82	118.30
1	A	232	ASP	CB-CG-OD2	5.95	123.65	118.30
1	A	217	ASP	CB-CG-OD2	5.88	123.59	118.30
1	A	636	ASP	CB-CG-OD2	5.82	123.53	118.30
1	A	387	ASP	CB-CG-OD2	5.63	123.37	118.30
1	A	518	ASP	CB-CG-OD2	5.45	123.21	118.30
1	A	322	ASP	CB-CG-OD2	5.04	122.84	118.30
1	A	226	ASP	CB-CG-OD2	5.02	122.82	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	3222	0	3234	116	0
2	A	32	0	13	3	0
3	A	56	0	0	12	0
All	All	3310	0	3247	116	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 18.

All (116) 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:384:ASN:HD21	1:A:428:ALA:H	1.23	0.86
1:A:246:HIS:HE2	1:A:347:ILE:HA	1.47	0.80
1:A:570:PRO:HA	3:A:31:HOH:O	1.82	0.79
1:A:389:PRO:HA	1:A:392:GLN:HE21	1.48	0.79
1:A:389:PRO:HA	1:A:392:GLN:NE2	2.04	0.72
1:A:583:ILE:HG23	1:A:643:PHE:HB3	1.74	0.69
1:A:313:THR:HG21	1:A:456:ASP:HB2	1.74	0.69
1:A:257:ASN:ND2	1:A:261:LEU:HD12	2.08	0.68
1:A:563:GLN:HA	1:A:619:ILE:O	1.95	0.67
1:A:613:ALA:O	1:A:614:THR:HB	1.94	0.67
1:A:563:GLN:HG2	1:A:620:ILE:HG22	1.79	0.65
1:A:595:LEU:HG	1:A:619:ILE:HD11	1.77	0.65
1:A:656:LYS:HG3	3:A:28:HOH:O	1.97	0.64
1:A:262:THR:HG21	1:A:311:PHE:HB2	1.81	0.62
1:A:236:LYS:NZ	1:A:312:GLU:OE1	2.25	0.60
1:A:620:ILE:O	1:A:620:ILE:HG13	1.99	0.60
1:A:597:HIS:HB2	1:A:620:ILE:HG12	1.84	0.60
1:A:246:HIS:NE2	1:A:347:ILE:HA	2.15	0.59
1:A:573:LEU:HA	1:A:612:PHE:HB2	1.84	0.59
1:A:430:THR:OG1	1:A:432:GLN:HG3	2.03	0.58
1:A:374:GLN:HG2	3:A:44:HOH:O	2.03	0.58
1:A:573:LEU:HD13	1:A:573:LEU:H	1.69	0.58
1:A:580:VAL:O	1:A:645:LEU:HA	2.05	0.57
1:A:365:ARG:HG3	1:A:412:VAL:HG11	1.87	0.57
1:A:221:LEU:HD12	1:A:644:THR:HG23	1.86	0.57
1:A:267:LYS:O	1:A:271:GLU:HG3	2.05	0.57
1:A:313:THR:HB	1:A:456:ASP:OD1	2.05	0.56
1:A:596:LEU:HD22	1:A:597:HIS:CE1	2.40	0.56
1:A:221:LEU:HD12	1:A:644:THR:CG2	2.37	0.55
1:A:246:HIS:CE1	1:A:347:ILE:HD13	2.42	0.55
1:A:647:ASP:HB2	1:A:652:VAL:HG21	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:558:THR:O	1:A:624:GLU:HA	2.09	0.53
1:A:572:ILE:HG21	1:A:577:TYR:CG	2.43	0.53
1:A:253:THR:HG21	2:A:1986:GNP:N7	2.24	0.53
1:A:221:LEU:HD11	1:A:582:HIS:HB2	1.90	0.52
1:A:483:ILE:HD11	1:A:533:ARG:HE	1.74	0.52
1:A:538:ASP:O	3:A:25:HOH:O	2.19	0.52
1:A:363:GLN:HB2	1:A:367:HIS:CE1	2.43	0.52
1:A:435:LYS:HA	1:A:452:LEU:HD12	1.90	0.52
1:A:474:ALA:HB3	1:A:485:GLU:HG3	1.90	0.52
1:A:360:ARG:HD2	3:A:52:HOH:O	2.09	0.51
1:A:220:ASP:CG	1:A:221:LEU:H	2.14	0.51
1:A:379:LEU:O	1:A:421:VAL:HA	2.10	0.51
1:A:432:GLN:HB3	1:A:438:VAL:HG12	1.91	0.51
1:A:647:ASP:CB	1:A:652:VAL:HG21	2.41	0.51
1:A:573:LEU:HD22	1:A:574:THR:N	2.27	0.50
1:A:236:LYS:HE2	1:A:314:GLU:O	2.12	0.50
1:A:221:LEU:HD22	1:A:221:LEU:N	2.27	0.50
1:A:619:ILE:HD11	1:A:621:ALA:HB2	1.94	0.50
1:A:257:ASN:O	1:A:261:LEU:HB2	2.11	0.49
1:A:574:THR:OG1	1:A:575:THR:N	2.43	0.49
1:A:269:THR:O	1:A:272:LYS:HB3	2.12	0.49
1:A:247:VAL:HG13	1:A:363:GLN:HE22	1.76	0.49
1:A:246:HIS:NE2	1:A:347:ILE:HD13	2.26	0.48
1:A:590:VAL:HG21	1:A:623:LEU:HD23	1.94	0.48
1:A:245:GLY:C	1:A:251:LYS:HZ1	2.17	0.48
1:A:494:LYS:O	1:A:513:ILE:HD11	2.12	0.48
1:A:388:GLU:OE1	1:A:389:PRO:HD2	2.14	0.48
1:A:433:ASN:HB2	1:A:438:VAL:HG13	1.95	0.48
1:A:614:THR:O	1:A:615:LYS:C	2.52	0.48
1:A:652:VAL:HG13	3:A:35:HOH:O	2.14	0.47
1:A:389:PRO:CA	1:A:392:GLN:HE21	2.24	0.47
1:A:573:LEU:CD2	1:A:574:THR:N	2.77	0.47
1:A:508:LEU:C	1:A:508:LEU:HD23	2.36	0.47
1:A:248:ASP:HA	2:A:1986:GNP:H5'2	1.97	0.46
1:A:570:PRO:O	1:A:571:SER:CB	2.64	0.46
1:A:598:LYS:HG3	1:A:617:MET:HE3	1.97	0.46
1:A:638:GLN:O	1:A:639:TYR:C	2.53	0.46
1:A:405:LEU:O	1:A:409:LEU:HG	2.15	0.46
1:A:508:LEU:CD2	1:A:534:VAL:HB	2.45	0.45
1:A:384:ASN:ND2	1:A:385:LYS:H	2.15	0.45
1:A:613:ALA:O	1:A:614:THR:CB	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:508:LEU:HD21	1:A:534:VAL:HB	1.98	0.45
1:A:249:ALA:HB1	1:A:346:VAL:HG12	1.99	0.45
1:A:573:LEU:CD1	1:A:573:LEU:H	2.30	0.45
1:A:590:VAL:HG13	1:A:590:VAL:O	2.17	0.45
1:A:245:GLY:C	1:A:251:LYS:NZ	2.71	0.45
1:A:504:ILE:HG13	1:A:506:GLN:HB3	2.00	0.44
1:A:246:HIS:HE2	1:A:347:ILE:HD13	1.81	0.44
1:A:487:LYS:HD3	3:A:24:HOH:O	2.18	0.44
1:A:433:ASN:ND2	1:A:438:VAL:HG22	2.32	0.44
1:A:559:ARG:O	1:A:661:LEU:HB2	2.18	0.44
1:A:384:ASN:HD21	1:A:428:ALA:N	2.04	0.44
1:A:258:ILE:O	1:A:262:THR:HB	2.18	0.44
1:A:573:LEU:HA	1:A:612:PHE:CB	2.48	0.43
1:A:372:ARG:NH1	1:A:377:ASN:HA	2.34	0.43
1:A:567:LEU:O	3:A:57:HOH:O	2.21	0.43
1:A:590:VAL:CG2	1:A:623:LEU:HD23	2.49	0.43
1:A:473:ILE:HG23	1:A:484:LEU:HD22	2.01	0.43
1:A:582:HIS:O	1:A:643:PHE:HA	2.18	0.43
1:A:236:LYS:HA	3:A:20:HOH:O	2.19	0.43
1:A:517:ALA:O	1:A:518:ASP:C	2.57	0.43
1:A:449:PRO:HB2	1:A:453:GLU:HB3	2.00	0.43
1:A:568:GLU:HB3	1:A:569:LEU:H	1.69	0.43
1:A:573:LEU:CD2	1:A:574:THR:H	2.33	0.42
1:A:253:THR:HG21	2:A:1986:GNP:C8	2.49	0.42
1:A:320:LEU:HD12	1:A:320:LEU:N	2.34	0.42
1:A:262:THR:HG23	1:A:264:MET:HE2	2.01	0.42
1:A:658:VAL:HB	3:A:28:HOH:O	2.20	0.42
1:A:478:LYS:HD2	3:A:46:HOH:O	2.19	0.41
1:A:233:MET:HG3	1:A:563:GLN:HE21	1.85	0.41
1:A:561:ILE:HG22	1:A:562:ALA:N	2.35	0.41
1:A:472:PRO:HB3	1:A:584:HIS:HD2	1.84	0.41
1:A:266:ASP:C	1:A:266:ASP:OD2	2.59	0.41
1:A:570:PRO:HD3	3:A:35:HOH:O	2.19	0.41
1:A:262:THR:HG23	1:A:264:MET:CE	2.50	0.41
1:A:443:CYS:SG	1:A:445:TRP:CE2	3.14	0.41
1:A:386:MET:HA	1:A:391:VAL:HG11	2.02	0.41
1:A:381:VAL:HG23	1:A:421:VAL:HG13	2.03	0.41
1:A:627:THR:HA	1:A:628:PRO:HD3	1.97	0.41
1:A:234:TYR:CZ	1:A:642:ARG:HG3	2.55	0.41
1:A:260:PHE:HA	1:A:265:VAL:O	2.21	0.41
1:A:221:LEU:HD13	1:A:221:LEU:HA	1.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:564:ILE:O	1:A:618:LYS:HA	2.22	0.40
1:A:641:GLY:HA2	1:A:657:VAL:CG1	2.51	0.40
1:A:352:GLY:O	1:A:356:ALA:HB2	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	403/467 (86%)	310 (77%)	66 (16%)	27 (7%)	1	12

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	225	VAL
1	A	232	ASP
1	A	248	ASP
1	A	568	GLU
1	A	570	PRO
1	A	571	SER
1	A	575	THR
1	A	594	LYS
1	A	604	ARG
1	A	605	LYS
1	A	479	ASP
1	A	518	ASP
1	A	614	THR
1	A	615	LYS
1	A	323	ALA
1	A	537	ASP
1	A	601	LYS
1	A	220	ASP

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Mol	Chain	Res	Type
1	A	337	ALA
1	A	505	ASN
1	A	595	LEU
1	A	638	GLN
1	A	219	THR
1	A	576	GLY
1	A	606	SER
1	A	587	VAL
1	A	247	VAL

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	356/398 (89%)	325 (91%)	31 (9%)	13 45

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

Mol	Chain	Res	Type
1	A	217	ASP
1	A	219	THR
1	A	232	ASP
1	A	233	MET
1	A	238	HIS
1	A	253	THR
1	A	264	MET
1	A	322	ASP
1	A	365	ARG
1	A	372	ARG
1	A	384	ASN
1	A	404	LYS
1	A	447	GLN
1	A	458	MET
1	A	482	THR
1	A	485	GLU
1	A	506	GLN

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Mol	Chain	Res	Type
1	A	507	THR
1	A	509	GLU
1	A	549	SER
1	A	559	ARG
1	A	573	LEU
1	A	578	SER
1	A	583	ILE
1	A	591	SER
1	A	596	LEU
1	A	611	MET
1	A	619	ILE
1	A	639	TYR
1	A	657	VAL
1	A	662	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	257	ASN
1	A	315	HIS
1	A	363	GLN
1	A	367	HIS
1	A	377	ASN
1	A	384	ASN
1	A	392	GLN
1	A	506	GLN
1	A	542	GLN
1	A	563	GLN
1	A	584	HIS

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

1 ligand is modelled in this entry.

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	GNP	A	1986	-	28,34,34	1.71	6 (21%)	33,54,54	2.26	7 (21%)

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	GNP	A	1986	-	-	0/12/38/38	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1986	GNP	PB-O3A	-4.20	1.53	1.59
2	A	1986	GNP	PB-O2B	-3.04	1.48	1.56
2	A	1986	GNP	PG-O2G	-2.94	1.48	1.56
2	A	1986	GNP	PB-O1B	2.11	1.48	1.46
2	A	1986	GNP	PG-O1G	2.93	1.49	1.46
2	A	1986	GNP	C6-N1	3.76	1.40	1.33

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1986	GNP	C5-C6-N1	-8.45	112.03	123.59
2	A	1986	GNP	O3G-PG-O1G	-2.92	105.73	113.49
2	A	1986	GNP	O1G-PG-N3B	-2.59	107.92	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1986	GNP	PA-O3A-PB	-2.33	124.86	132.67
2	A	1986	GNP	O3G-PG-O2G	3.07	116.69	107.58
2	A	1986	GNP	O2B-PB-O1B	3.50	117.31	110.00
2	A	1986	GNP	C6-N1-C2	5.80	123.99	115.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1986	GNP	3	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, 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	409/467 (87%)	-0.17	7 (1%)	73 60	15, 47, 90, 100	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	568	GLU	3.3
1	A	567	LEU	3.0
1	A	607	LYS	2.9
1	A	337	ALA	2.8
1	A	569	LEU	2.6
1	A	217	ASP	2.4
1	A	653	ALA	2.2

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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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, 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	LLDF	B-factors(\AA^2)	Q<0.9
2	GNP	A	1986	32/32	0.86	0.23	1.37	115,116,123,123	0

6.5 Other polymers [i](#)

There are no such residues in this entry.