Full wwPDB X-ray Structure Validation Report (i)

Sep 10, 2023 – 02:14 PM EDT

PDB ID	:	4JU1
Title	:	Crystal structure of hcv ns5b polymerase in complex with compound 6
Authors	:	Coulombe, R.
Deposited on	:	2013-03-24
Resolution	:	2.90 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:

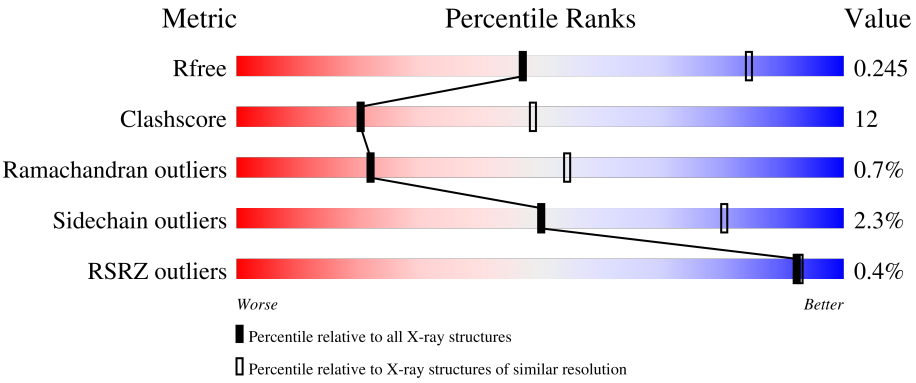
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	576	73% 22%
1	B	576	% 70% 26%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MG	A	3004	-	-	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 9146 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.

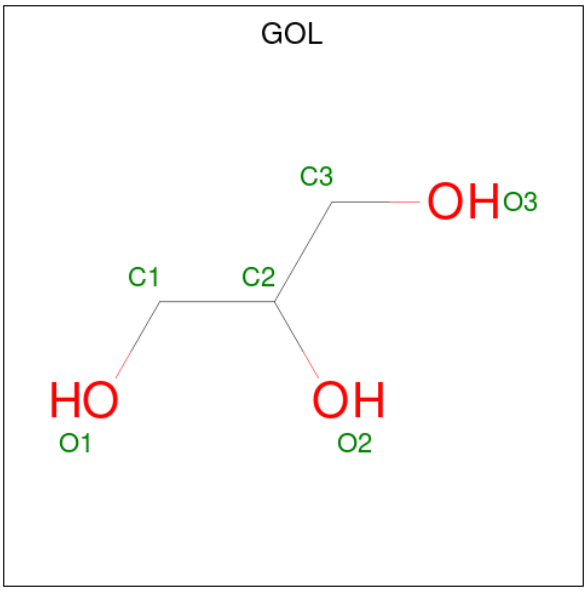
- Molecule 1 is a protein called Genome polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	560	Total	C	N	O	S	0	0	0
			4362	2747	771	812	32			
1	B	560	Total	C	N	O	S	0	0	0
			4362	2747	771	812	32			

There are 12 discrepancies between the modelled and reference sequences:

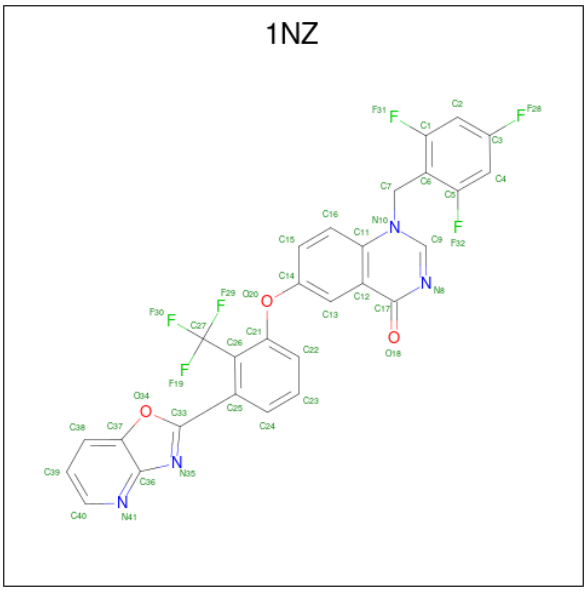
Chain	Residue	Modelled	Actual	Comment	Reference
A	571	HIS	-	expression tag	UNP O92972
A	572	HIS	-	expression tag	UNP O92972
A	573	HIS	-	expression tag	UNP O92972
A	574	HIS	-	expression tag	UNP O92972
A	575	HIS	-	expression tag	UNP O92972
A	576	HIS	-	expression tag	UNP O92972
B	571	HIS	-	expression tag	UNP O92972
B	572	HIS	-	expression tag	UNP O92972
B	573	HIS	-	expression tag	UNP O92972
B	574	HIS	-	expression tag	UNP O92972
B	575	HIS	-	expression tag	UNP O92972
B	576	HIS	-	expression tag	UNP O92972

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0

- Molecule 3 is 6-[3-([1,3]oxazolo[4,5-b]pyridin-2-yl)-2-(trifluoromethyl)phenoxy]-1-(2,4,6-trifluorobenzyl)quinazolin-4(1H)-one (three-letter code: 1NZ) (formula: $C_{28}H_{14}F_6N_4O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C F N O 41 28 6 4 3	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	F	N	O	0	0
			41	28	6	4	3		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Mg	0	0
			2	2		
4	B	2	Total	Mg	0	0
			2	2		

- Molecule 5 is water.

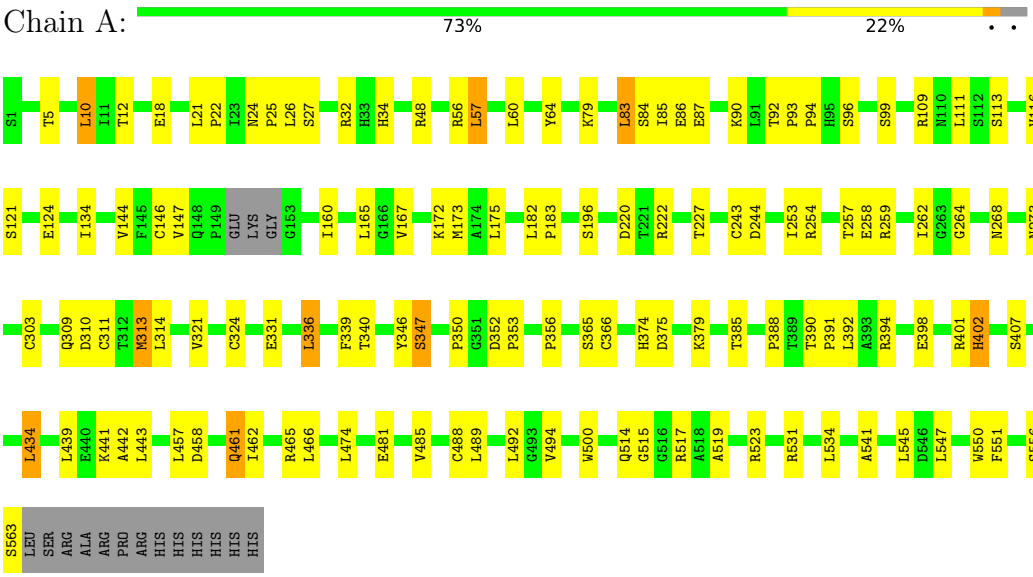
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	178	Total	O	0	0
			178	178		
5	B	146	Total	O	0	0
			146	146		

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.

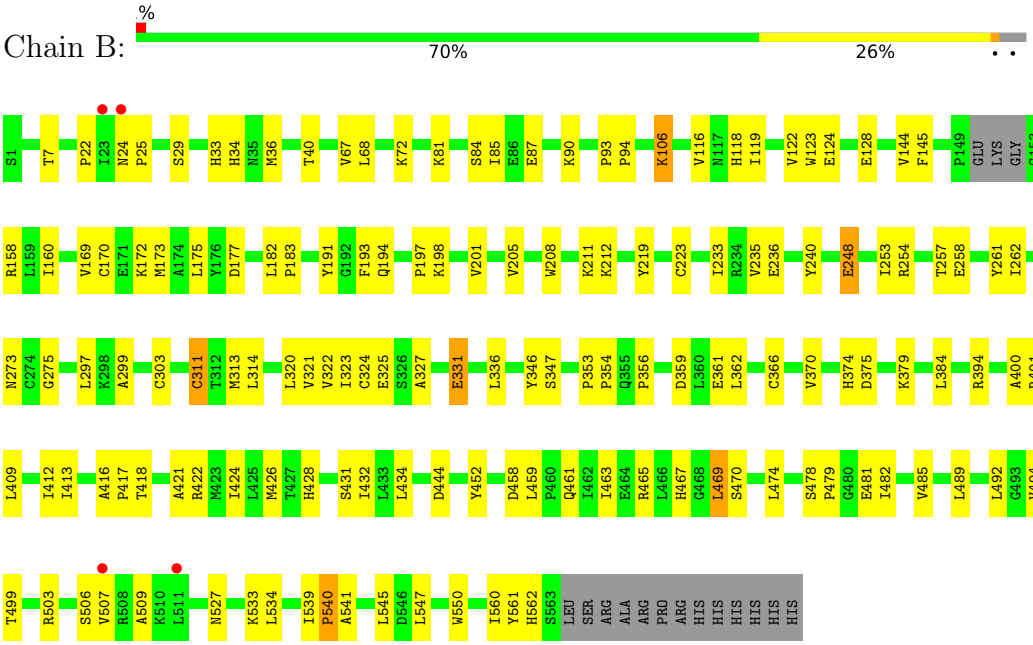
• Molecule 1: Genome polyprotein

Chain A:



• Molecule 1: Genome polyprotein

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	106.82Å 107.76Å 135.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.90 39.26 – 2.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-2.90) 94.1 (39.26-2.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.75 (at 2.90Å)	Xtriage
Refinement program	CNX 2002	Depositor
R, R_{free}	0.195 , 0.252 0.192 , 0.245	Depositor DCC
R_{free} test set	3334 reflections (9.96%)	wwPDB-VP
Wilson B-factor (Å^2)	54.3	Xtriage
Anisotropy	0.457	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 45.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.019 for k,h,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	9146	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MG, 1NZ

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	0.36	0/4457	0.63	1/6049 (0.0%)
1	B	0.34	0/4457	0.59	0/6049
All	All	0.35	0/8914	0.61	1/12098 (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	196	SER	N-CA-C	-5.08	97.29	111.00

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	4362	0	4374	104	0
1	B	4362	0	4374	111	0
2	A	6	0	8	1	0
2	B	6	0	8	0	0
3	A	41	0	14	0	0
3	B	41	0	14	1	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	178	0	0	12	0
5	B	146	0	0	11	0
All	All	9146	0	8792	216	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 12.

All (216) 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:B:469:LEU:HD23	1:B:469:LEU:H	1.40	0.87
1:A:18:GLU:HG2	1:A:401:ARG:HH22	1.40	0.86
1:A:144:VAL:HB	1:A:394:ARG:HG2	1.58	0.86
1:A:86:GLU:HG3	1:A:111:LEU:HD11	1.61	0.82
1:A:113:SER:HA	1:A:116:VAL:HG12	1.62	0.81
1:B:119:ILE:HD13	1:B:169:VAL:HG11	1.63	0.80
1:A:336:LEU:HD12	1:A:356:PRO:HD3	1.66	0.77
1:B:313:MET:HG2	1:B:322:VAL:HG22	1.68	0.74
1:A:394:ARG:O	1:A:398:GLU:HG3	1.87	0.73
1:A:24:ASN:HD21	1:A:26:LEU:HB2	1.53	0.73
1:A:24:ASN:HD22	1:A:27:SER:H	1.36	0.73
1:B:479:PRO:HG2	5:B:1025:HOH:O	1.89	0.70
1:A:352:ASP:HA	5:A:3152:HOH:O	1.91	0.70
1:A:523:ARG:HG3	1:A:534:LEU:HD12	1.75	0.68
1:B:172:LYS:HE3	1:B:560:ILE:HD13	1.76	0.67
1:B:106:LYS:HA	1:B:106:LYS:HE3	1.75	0.67
1:A:311:CYS:HB3	1:A:324:CYS:HB3	1.75	0.67
1:B:461:GLN:HB3	1:B:545:LEU:HD11	1.76	0.67
1:A:60:LEU:HD13	1:A:64:TYR:CE2	2.30	0.66
1:B:481:GLU:O	1:B:485:VAL:HG23	1.95	0.66
1:B:361:GLU:HG3	1:B:370:VAL:O	1.95	0.66
1:B:418:THR:O	1:B:422:ARG:HG3	1.96	0.66
1:A:515:GLY:HA2	1:A:519:ALA:HB2	1.78	0.65
1:B:434:LEU:HD12	1:B:507:VAL:HG13	1.79	0.65
1:B:123:TRP:HE1	1:B:248:GLU:HG2	1.63	0.64
1:A:488:CYS:HB2	5:A:3141:HOH:O	1.99	0.63
1:B:33:HIS:HB3	1:B:36:MET:HG3	1.81	0.63
1:B:408:TRP:O	1:B:412:ILE:HG13	1.98	0.63
1:B:160:ILE:HB	5:B:1056:HOH:O	1.99	0.62
1:A:21:LEU:HD12	1:A:22:PRO:HD2	1.83	0.61
1:A:388:PRO:HG2	1:A:488:CYS:SG	2.41	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:434:LEU:HG	1:A:439:LEU:HD11	1.83	0.60
1:B:314:LEU:HB3	1:B:321:VAL:CG1	2.32	0.60
1:B:331:GLU:OE1	1:B:331:GLU:N	2.34	0.60
1:B:424:ILE:CD1	1:B:489:LEU:HD21	2.30	0.60
1:A:93:PRO:HG3	1:A:561:TYR:HB2	1.85	0.59
1:A:458:ASP:HA	1:A:461:GLN:NE2	2.17	0.59
1:A:458:ASP:HA	1:A:461:GLN:HE22	1.66	0.59
1:B:424:ILE:HD11	1:B:489:LEU:HD21	1.85	0.59
1:B:469:LEU:H	1:B:469:LEU:CD2	2.15	0.59
1:A:18:GLU:HG2	1:A:401:ARG:NH2	2.16	0.59
1:B:233:ILE:HD13	1:B:261:TYR:O	2.03	0.58
1:A:172:LYS:HE3	1:A:560:ILE:HD13	1.85	0.58
1:B:22:PRO:O	1:B:25:PRO:HG3	2.03	0.58
1:B:175:LEU:HD21	1:B:253:ILE:HG12	1.85	0.58
1:B:219:TYR:HB3	1:B:320:LEU:HD23	1.86	0.58
1:A:346:TYR:O	1:A:347:SER:HB3	2.03	0.58
1:B:191:TYR:CZ	1:B:193:PHE:HB2	2.39	0.57
1:A:24:ASN:ND2	1:A:26:LEU:HB2	2.18	0.57
1:B:303:CYS:HB3	1:B:311:CYS:SG	2.45	0.56
1:B:428:HIS:O	1:B:432:ILE:HG12	2.05	0.56
1:B:469:LEU:HD23	1:B:469:LEU:N	2.17	0.56
1:A:183:PRO:HG2	5:A:3122:HOH:O	2.06	0.56
1:B:144:VAL:HB	1:B:394:ARG:HG2	1.87	0.56
1:B:545:LEU:HD23	5:B:1014:HOH:O	2.06	0.56
1:B:374:HIS:O	1:B:474:LEU:HA	2.07	0.55
1:B:498:ARG:HG3	1:B:499:THR:N	2.21	0.55
1:B:29:SER:HB2	5:B:1113:HOH:O	2.07	0.54
1:B:421:ALA:O	1:B:426:MET:HG3	2.07	0.54
1:B:489:LEU:HD22	1:B:494:VAL:HG11	1.88	0.54
1:B:197:PRO:HB2	1:B:467:HIS:HE1	1.73	0.54
1:A:385:THR:HG21	1:A:481:GLU:OE1	2.08	0.54
1:A:314:LEU:HB3	1:A:321:VAL:CG1	2.39	0.53
1:B:545:LEU:HA	5:B:1014:HOH:O	2.08	0.53
1:A:109:ARG:HG2	1:A:109:ARG:HH11	1.73	0.53
1:B:90:LYS:O	1:B:90:LYS:HG2	2.09	0.53
1:B:303:CYS:CB	1:B:311:CYS:HG	2.20	0.53
1:B:191:TYR:O	1:B:194:GLN:HG2	2.09	0.53
1:A:175:LEU:HD21	1:A:253:ILE:HG12	1.91	0.52
1:A:331:GLU:OE1	1:A:331:GLU:N	2.30	0.52
1:B:22:PRO:HG3	1:B:401:ARG:CZ	2.40	0.52
1:A:481:GLU:O	1:A:485:VAL:HG23	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:561:TYR:HE2	1:A:563:SER:HB2	1.75	0.52
1:A:485:VAL:O	1:A:489:LEU:HG	2.10	0.52
1:A:303:CYS:HB3	1:A:311:CYS:SG	2.49	0.52
1:B:254:ARG:NH2	1:B:258:GLU:HG2	2.25	0.51
1:A:57:LEU:HD23	1:A:57:LEU:O	2.10	0.51
1:B:182:LEU:HB3	1:B:183:PRO:HD3	1.93	0.51
1:B:470:SER:O	1:B:474:LEU:HG	2.10	0.51
1:A:461:GLN:HG2	1:A:541:ALA:HB3	1.92	0.51
1:B:128:GLU:HA	5:B:1001:HOH:O	2.09	0.51
1:B:257:THR:O	1:B:262:ILE:HG23	2.10	0.51
1:A:561:TYR:CE2	1:A:563:SER:HB2	2.46	0.51
1:B:375:ASP:OD1	1:B:379:LYS:HB3	2.11	0.51
1:B:24:ASN:N	1:B:25:PRO:HD3	2.26	0.51
1:B:359:ASP:HB3	1:B:362:LEU:HD12	1.93	0.51
1:A:402:HIS:HD2	5:A:3271:HOH:O	1.94	0.51
1:A:24:ASN:ND2	1:A:26:LEU:H	2.08	0.50
1:B:311:CYS:HA	1:B:324:CYS:HB3	1.93	0.50
1:B:534:LEU:N	1:B:534:LEU:HD12	2.26	0.50
1:A:336:LEU:O	1:A:339:PHE:HB3	2.11	0.50
1:B:145:PHE:CZ	1:B:155:LYS:HD2	2.47	0.50
1:A:21:LEU:HD23	1:A:34:HIS:HB2	1.92	0.50
1:A:85:ILE:HG12	1:A:173:MET:SD	2.52	0.50
1:B:211:LYS:HE3	1:B:323:ILE:HG22	1.93	0.50
1:A:466:LEU:HD22	1:A:551:PHE:HE2	1.76	0.50
1:B:191:TYR:CE2	1:B:193:PHE:HB2	2.47	0.50
1:B:346:TYR:O	1:B:347:SER:HB3	2.12	0.50
1:A:556:SER:HB2	5:A:3147:HOH:O	2.11	0.49
1:A:254:ARG:NH2	1:A:258:GLU:HG2	2.26	0.49
1:B:444:ASP:HA	1:B:452:TYR:O	2.12	0.49
1:A:79:LYS:HE3	1:A:244:ASP:OD1	2.12	0.49
1:A:32:ARG:N	1:A:32:ARG:HD2	2.26	0.49
1:B:233:ILE:CD1	1:B:262:ILE:HA	2.42	0.49
1:B:353:PRO:HG3	5:B:1130:HOH:O	2.13	0.48
1:A:146:CYS:SG	1:A:492:LEU:HD21	2.53	0.48
1:B:233:ILE:HD13	1:B:262:ILE:HA	1.96	0.48
1:A:390:THR:HB	1:A:391:PRO:HD3	1.96	0.48
1:A:458:ASP:O	1:A:462:ILE:HG13	2.13	0.48
1:A:465:ARG:NH1	1:A:545:LEU:O	2.46	0.48
1:B:93:PRO:HG3	1:B:561:TYR:HB2	1.96	0.48
1:A:222:ARG:HD2	5:A:3112:HOH:O	2.13	0.48
1:A:5:THR:O	1:A:275:GLY:HA3	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:CYS:CB	1:A:311:CYS:SG	3.03	0.47
1:A:423:MET:CE	1:A:424:ILE:HD11	2.45	0.47
1:B:303:CYS:CB	1:B:311:CYS:SG	3.02	0.47
1:B:336:LEU:CD2	1:B:356:PRO:HD3	2.44	0.47
1:B:205:VAL:O	1:B:208:TRP:HB3	2.14	0.47
1:B:327:ALA:O	1:B:331:GLU:HB2	2.15	0.47
1:A:120:ARG:O	1:A:124:GLU:HG2	2.14	0.47
1:A:160:ILE:HA	1:A:282:SER:OG	2.15	0.47
1:B:494:VAL:O	3:B:602:1NZ:H13	2.14	0.47
1:A:374:HIS:O	1:A:474:LEU:HA	2.15	0.47
1:B:321:VAL:HG13	1:B:321:VAL:O	2.15	0.47
1:B:314:LEU:O	1:B:321:VAL:HG12	2.15	0.47
1:A:257:THR:O	1:A:262:ILE:HG23	2.15	0.46
1:B:527:ASN:O	1:B:533:LYS:HG3	2.15	0.46
1:A:84:SER:OG	1:A:87:GLU:HG3	2.14	0.46
1:B:299:ALA:HB3	1:B:313:MET:HE1	1.96	0.46
1:B:7:THR:HG23	1:B:275:GLY:HA2	1.98	0.46
1:A:182:LEU:HD12	1:A:243:CYS:SG	2.56	0.46
1:A:336:LEU:HD23	1:A:336:LEU:HA	1.72	0.46
1:A:531:ARG:HG3	5:A:3128:HOH:O	2.15	0.46
1:A:10:LEU:O	1:A:12:THR:HG23	2.15	0.46
1:A:134:ILE:HG13	1:A:259:ARG:HB3	1.98	0.46
1:A:353:PRO:HD2	5:A:3152:HOH:O	2.15	0.46
1:B:81:LYS:HG2	1:B:177:ASP:OD2	2.16	0.46
1:B:85:ILE:HD11	1:B:119:ILE:HB	1.98	0.46
1:B:201:VAL:CG2	1:B:384:LEU:HB2	2.46	0.46
1:B:539:ILE:HG23	1:B:540:PRO:HD2	1.97	0.46
1:A:113:SER:HA	1:A:116:VAL:CG1	2.38	0.45
1:B:93:PRO:HA	1:B:94:PRO:HD3	1.84	0.45
1:B:458:ASP:HA	1:B:461:GLN:OE1	2.17	0.45
1:B:158:ARG:HG3	5:B:1144:HOH:O	2.17	0.45
1:A:375:ASP:OD1	1:A:379:LYS:HB3	2.17	0.45
1:B:313:MET:CG	1:B:322:VAL:HG22	2.44	0.45
1:B:170:CYS:HA	1:B:173:MET:HE3	1.99	0.45
1:A:227:THR:HB	1:A:347:SER:O	2.16	0.45
1:B:459:LEU:O	1:B:463:ILE:HG13	2.16	0.45
1:B:314:LEU:HB3	1:B:321:VAL:HG13	1.98	0.44
1:B:236:GLU:HG2	1:B:240:TYR:CE2	2.53	0.44
1:A:434:LEU:HD21	1:A:514:GLN:HE21	1.83	0.44
1:B:84:SER:OG	1:B:87:GLU:HG3	2.16	0.44
1:A:264:GLY:HA3	5:A:3136:HOH:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:THR:O	1:A:391:PRO:C	2.56	0.44
1:A:268:ASN:HB3	1:A:274:CYS:SG	2.58	0.44
1:A:134:ILE:HG21	1:A:167:VAL:HG21	1.99	0.44
1:B:452:TYR:CE1	1:B:562:HIS:HB2	2.53	0.44
1:A:109:ARG:HG2	1:A:109:ARG:NH1	2.32	0.44
1:B:155:LYS:HA	1:B:156:PRO:HD3	1.81	0.44
1:A:48:ARG:HD3	5:A:3162:HOH:O	2.16	0.43
1:A:56:ARG:HD3	1:A:56:ARG:N	2.33	0.43
1:B:68:LEU:HD21	1:B:235:VAL:HG13	2.00	0.43
1:B:478:SER:O	1:B:482:ILE:HG13	2.18	0.43
1:A:92:THR:HA	1:A:93:PRO:HD3	1.89	0.43
1:A:340:THR:HG21	1:A:350:PRO:HG3	2.01	0.43
1:B:118:HIS:O	1:B:122:VAL:HG23	2.17	0.43
1:B:223:CYS:HB3	5:B:1085:HOH:O	2.17	0.43
1:B:489:LEU:HD23	1:B:494:VAL:HG21	2.00	0.43
1:B:547:LEU:O	1:B:550:TRP:HB2	2.19	0.42
1:A:25:PRO:HG2	1:A:26:LEU:HD22	2.01	0.42
1:B:422:ARG:HA	1:B:426:MET:SD	2.58	0.42
1:A:303:CYS:SG	1:A:313:MET:HE3	2.59	0.42
1:A:365:SER:O	1:A:366:CYS:HB2	2.19	0.42
1:A:423:MET:HE3	1:A:424:ILE:HD11	2.02	0.42
1:A:92:THR:O	1:A:109:ARG:NH1	2.53	0.42
1:B:212:LYS:HB2	1:B:325:GLU:OE2	2.19	0.42
1:B:431:SER:HB3	1:B:507:VAL:HG21	2.02	0.42
1:B:359:ASP:HB3	1:B:362:LEU:CD1	2.50	0.42
1:A:457:LEU:HB2	1:A:517:ARG:HH21	1.85	0.42
1:B:85:ILE:HD13	1:B:116:VAL:HG13	2.01	0.42
1:B:267:THR:CG2	1:B:271:GLY:HA2	2.49	0.42
1:A:430:PHE:O	1:A:434:LEU:HB2	2.20	0.42
1:A:309:GLN:O	1:A:324:CYS:HB2	2.20	0.41
1:B:40:THR:HB	1:B:157:ALA:HB2	2.02	0.41
1:B:67:VAL:CG1	1:B:297:LEU:HD12	2.50	0.41
1:A:90:LYS:HE2	1:A:90:LYS:HB3	1.92	0.41
1:A:303:CYS:CB	1:A:311:CYS:HG	2.34	0.41
1:A:442:ALA:O	1:A:443:LEU:HD23	2.20	0.41
1:B:506:SER:O	1:B:509:ALA:HB3	2.21	0.41
1:A:99:SER:HB2	1:A:165:LEU:HB3	2.02	0.41
1:B:495:PRO:HA	1:B:496:PRO:HD3	1.70	0.41
1:A:24:ASN:ND2	1:A:27:SER:H	2.11	0.41
1:A:182:LEU:N	1:A:183:PRO:HD2	2.35	0.41
1:A:392:LEU:HD21	1:A:424:ILE:HG21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:494:VAL:HG12	1:A:500:TRP:HE1	1.86	0.41
1:B:354:PRO:HA	5:B:1037:HOH:O	2.20	0.41
1:A:93:PRO:HA	1:A:94:PRO:HD3	1.91	0.41
1:B:123:TRP:HZ2	1:B:248:GLU:HB3	1.86	0.41
1:A:24:ASN:OD1	1:A:25:PRO:HD2	2.21	0.40
1:A:79:LYS:HG3	1:A:244:ASP:HB3	2.02	0.40
1:A:254:ARG:HH22	1:A:258:GLU:HG2	1.86	0.40
1:A:398:GLU:OE1	1:A:407:SER:N	2.54	0.40
1:B:539:ILE:HA	1:B:540:PRO:HD3	1.92	0.40
2:A:3001:GOL:H11	5:A:3255:HOH:O	2.20	0.40
1:B:29:SER:O	1:B:503:ARG:NH1	2.54	0.40
1:B:416:ALA:CB	1:B:463:ILE:HG23	2.52	0.40
1:A:441:LYS:HG3	5:A:3157:HOH:O	2.21	0.40
1:A:466:LEU:HD11	1:A:550:TRP:CZ3	2.57	0.40
1:B:72:LYS:NZ	5:B:1137:HOH:O	2.54	0.40
1:B:124:GLU:O	1:B:128:GLU:HG2	2.21	0.40
1:B:201:VAL:O	1:B:205:VAL:HG23	2.22	0.40
1:B:409:LEU:O	1:B:413:ILE:HG13	2.20	0.40
1:A:83:LEU:HG	1:A:87:GLU:HB2	2.03	0.40
1:A:118:HIS:O	1:A:121:SER:HB3	2.22	0.40
1:B:416:ALA:HB3	1:B:417:PRO:HD3	2.04	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	556/576 (96%)	523 (94%)	29 (5%)	4 (1%)	22	54
1	B	556/576 (96%)	520 (94%)	32 (6%)	4 (1%)	22	54
All	All	1112/1152 (96%)	1043 (94%)	61 (6%)	8 (1%)	22	54

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	147	VAL
1	B	541	ALA
1	A	96	SER
1	B	400	ALA
1	B	540	PRO
1	A	310	ASP
1	A	347	SER
1	B	404	PRO

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	477/491 (97%)	466 (98%)	11 (2%)	50 80
1	B	477/491 (97%)	466 (98%)	11 (2%)	50 80
All	All	954/982 (97%)	932 (98%)	22 (2%)	50 80

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	LEU
1	A	57	LEU
1	A	83	LEU
1	A	220	ASP
1	A	273	ASN
1	A	313	MET
1	A	336	LEU
1	A	402	HIS
1	A	434	LEU
1	A	461	GLN
1	A	547	LEU
1	B	34	HIS
1	B	106	LYS
1	B	198	LYS
1	B	248	GLU

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Mol	Chain	Res	Type
1	B	273	ASN
1	B	311	CYS
1	B	331	GLU
1	B	366	CYS
1	B	465	ARG
1	B	469	LEU
1	B	492	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	ASN
1	A	251	GLN
1	A	273	ASN
1	A	438	GLN
1	A	514	GLN
1	A	544	GLN
1	B	24	ASN
1	B	34	HIS
1	B	110	ASN
1	B	148	GLN
1	B	206	ASN
1	B	251	GLN
1	B	273	ASN
1	B	406	ASN
1	B	467	HIS
1	B	514	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 8 ligands modelled in this entry, 4 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	GOL	B	601	-	5,5,5	0.23	0	5,5,5	0.29	0
2	GOL	A	3001	-	5,5,5	0.38	0	5,5,5	0.21	0
3	1NZ	B	602	-	41,46,46	2.39	21 (51%)	54,69,69	2.04	16 (29%)
3	1NZ	A	3002	-	41,46,46	2.31	21 (51%)	54,69,69	1.93	15 (27%)

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	GOL	B	601	-	-	4/4/4/4	-
2	GOL	A	3001	-	-	0/4/4/4	-
3	1NZ	B	602	-	-	2/14/18/18	0/6/6/6
3	1NZ	A	3002	-	-	0/14/18/18	0/6/6/6

All (42) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	3002	1NZ	C25-C26	6.25	1.48	1.40
3	B	602	1NZ	C25-C26	6.23	1.48	1.40
3	B	602	1NZ	C11-N10	5.09	1.46	1.40
3	A	3002	1NZ	C11-N10	4.35	1.45	1.40
3	B	602	1NZ	C6-C1	3.66	1.44	1.38
3	B	602	1NZ	C6-C5	3.64	1.44	1.38
3	B	602	1NZ	C21-C26	3.63	1.46	1.40
3	A	3002	1NZ	C21-C26	3.54	1.45	1.40
3	A	3002	1NZ	C12-C11	3.39	1.46	1.41
3	B	602	1NZ	C12-C11	3.25	1.46	1.41
3	A	3002	1NZ	C6-C1	3.17	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	602	1NZ	C40-N41	3.11	1.38	1.32
3	A	3002	1NZ	C40-N41	3.06	1.38	1.32
3	B	602	1NZ	C2-C3	2.88	1.42	1.37
3	A	3002	1NZ	C24-C25	2.88	1.44	1.40
3	A	3002	1NZ	C13-C12	2.78	1.44	1.39
3	A	3002	1NZ	C39-C38	2.72	1.42	1.36
3	A	3002	1NZ	C6-C5	2.72	1.42	1.38
3	B	602	1NZ	C2-C1	2.71	1.42	1.37
3	A	3002	1NZ	C2-C1	2.70	1.42	1.37
3	A	3002	1NZ	C4-C5	2.67	1.42	1.37
3	B	602	1NZ	C7-N10	2.65	1.50	1.47
3	B	602	1NZ	C39-C38	2.65	1.42	1.36
3	B	602	1NZ	C16-C11	2.63	1.44	1.39
3	A	3002	1NZ	C9-N10	2.61	1.40	1.36
3	A	3002	1NZ	C7-N10	2.59	1.50	1.47
3	B	602	1NZ	C24-C25	2.59	1.44	1.40
3	B	602	1NZ	C4-C5	2.51	1.41	1.37
3	B	602	1NZ	C15-C14	2.51	1.43	1.38
3	B	602	1NZ	C13-C12	2.50	1.43	1.39
3	B	602	1NZ	C27-C26	2.49	1.57	1.51
3	A	3002	1NZ	C12-C17	2.49	1.51	1.48
3	B	602	1NZ	C16-C15	2.42	1.43	1.38
3	B	602	1NZ	C4-C3	2.38	1.41	1.37
3	A	3002	1NZ	C22-C21	2.33	1.44	1.39
3	A	3002	1NZ	C16-C11	2.29	1.43	1.39
3	A	3002	1NZ	C2-C3	2.28	1.41	1.37
3	A	3002	1NZ	C16-C15	2.26	1.42	1.38
3	A	3002	1NZ	C4-C3	2.15	1.41	1.37
3	B	602	1NZ	C22-C21	2.14	1.44	1.39
3	B	602	1NZ	C9-N10	2.12	1.39	1.36
3	A	3002	1NZ	C15-C14	2.09	1.42	1.38

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	602	1NZ	C16-C11-N10	7.64	126.00	121.16
3	A	3002	1NZ	C16-C11-N10	6.76	125.44	121.16
3	B	602	1NZ	C2-C1-C6	-4.24	121.61	124.59
3	A	3002	1NZ	C2-C1-C6	-4.18	121.65	124.59
3	B	602	1NZ	C4-C5-C6	-3.78	121.94	124.59
3	B	602	1NZ	C25-C33-N35	3.78	128.60	123.52
3	A	3002	1NZ	C4-C5-C6	-3.64	122.03	124.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	3002	1NZ	C27-C26-C25	3.38	124.89	120.33
3	A	3002	1NZ	C25-C33-N35	3.36	128.04	123.52
3	B	602	1NZ	C13-C12-C11	3.29	122.57	118.73
3	A	3002	1NZ	C26-C25-C33	3.27	126.80	120.01
3	A	3002	1NZ	C11-C12-C17	-3.20	117.66	120.27
3	A	3002	1NZ	C13-C12-C11	3.02	122.26	118.73
3	B	602	1NZ	C26-C25-C33	2.91	126.05	120.01
3	B	602	1NZ	C27-C26-C25	2.83	124.15	120.33
3	A	3002	1NZ	N10-C9-N8	2.79	128.77	126.36
3	B	602	1NZ	C11-C12-C17	-2.73	118.04	120.27
3	B	602	1NZ	C5-C4-C3	2.68	119.44	116.62
3	B	602	1NZ	C1-C2-C3	2.64	119.39	116.62
3	B	602	1NZ	N10-C9-N8	2.55	128.57	126.36
3	A	3002	1NZ	C1-C2-C3	2.53	119.28	116.62
3	B	602	1NZ	F31-C1-C6	2.47	120.58	117.63
3	B	602	1NZ	C25-C26-C21	-2.42	116.49	118.83
3	B	602	1NZ	F32-C5-C6	2.40	120.49	117.63
3	A	3002	1NZ	C5-C4-C3	2.39	119.13	116.62
3	B	602	1NZ	C16-C11-C12	-2.33	115.44	119.10
3	B	602	1NZ	C4-C3-C2	-2.27	120.65	123.52
3	A	3002	1NZ	C16-C11-C12	-2.21	115.63	119.10
3	A	3002	1NZ	C4-C3-C2	-2.14	120.81	123.52
3	A	3002	1NZ	F31-C1-C6	2.12	120.16	117.63
3	A	3002	1NZ	C25-C26-C21	-2.04	116.86	118.83

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	GOL	O1-C1-C2-O2
2	B	601	GOL	O1-C1-C2-C3
2	B	601	GOL	O2-C2-C3-O3
2	B	601	GOL	C1-C2-C3-O3
3	B	602	1NZ	C21-C26-C27-F29
3	B	602	1NZ	C21-C26-C27-F30

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	3001	GOL	1	0

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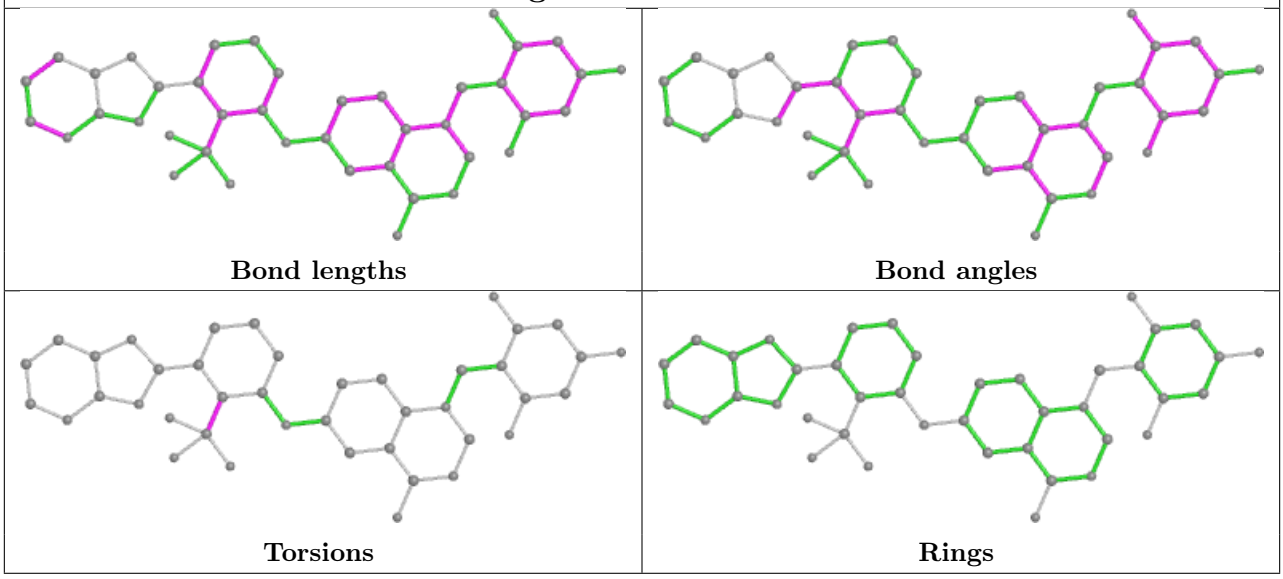
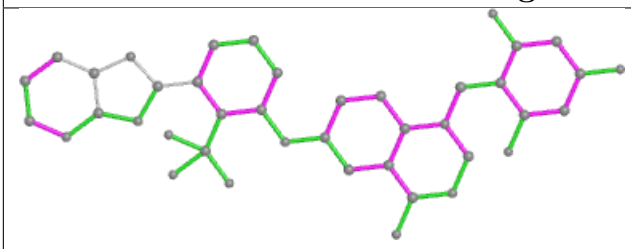
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	602	1NZ	1	0

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.

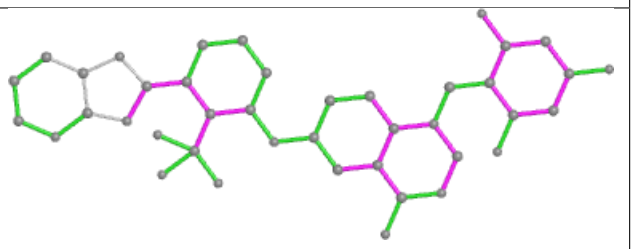
Ligand 1NZ B 602



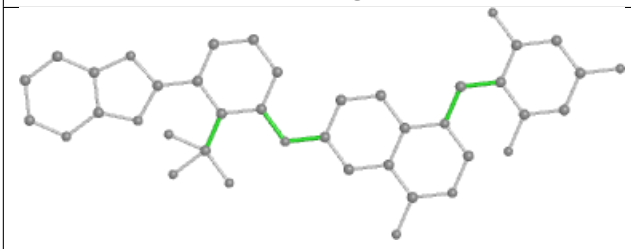
Ligand 1NZ A 3002



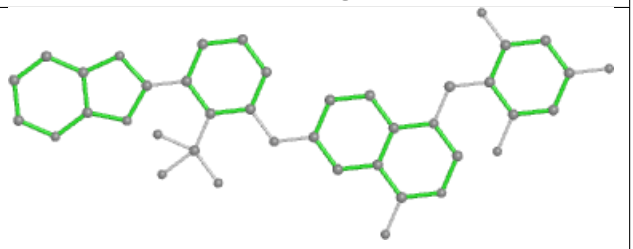
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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^{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	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	560/576 (97%)	-0.46	0 100 100	27, 45, 68, 90	0
1	B	560/576 (97%)	-0.22	4 (0%) 87 87	31, 56, 92, 105	0
All	All	1120/1152 (97%)	-0.34	4 (0%) 92 93	27, 49, 84, 105	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	23	ILE	2.6
1	B	507	VAL	2.5
1	B	511	LEU	2.5
1	B	24	ASN	2.4

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 monosaccharides 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. 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	B-factors(Å^2)	Q<0.9
4	MG	A	3004	1/1	0.70	0.44	64,64,64,64	0

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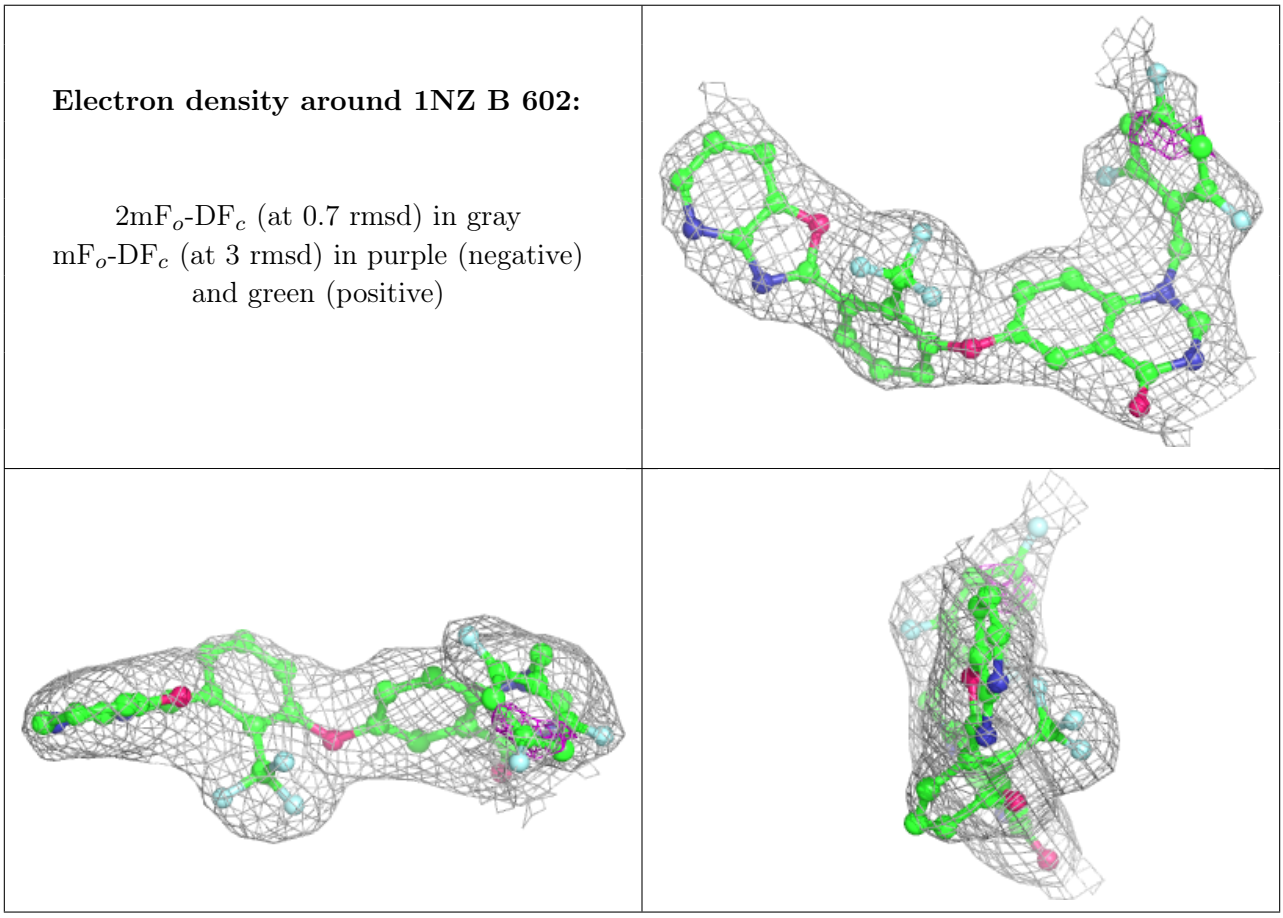
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	MG	B	604	1/1	0.76	0.23	77,77,77,77	0
4	MG	A	3003	1/1	0.89	0.10	36,36,36,36	0
2	GOL	A	3001	6/6	0.92	0.23	61,62,63,63	0
2	GOL	B	601	6/6	0.93	0.26	76,77,77,77	0
3	1NZ	B	602	41/41	0.95	0.17	56,61,71,71	0
3	1NZ	A	3002	41/41	0.95	0.18	45,51,59,60	0
4	MG	B	603	1/1	0.97	0.24	57,57,57,57	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.

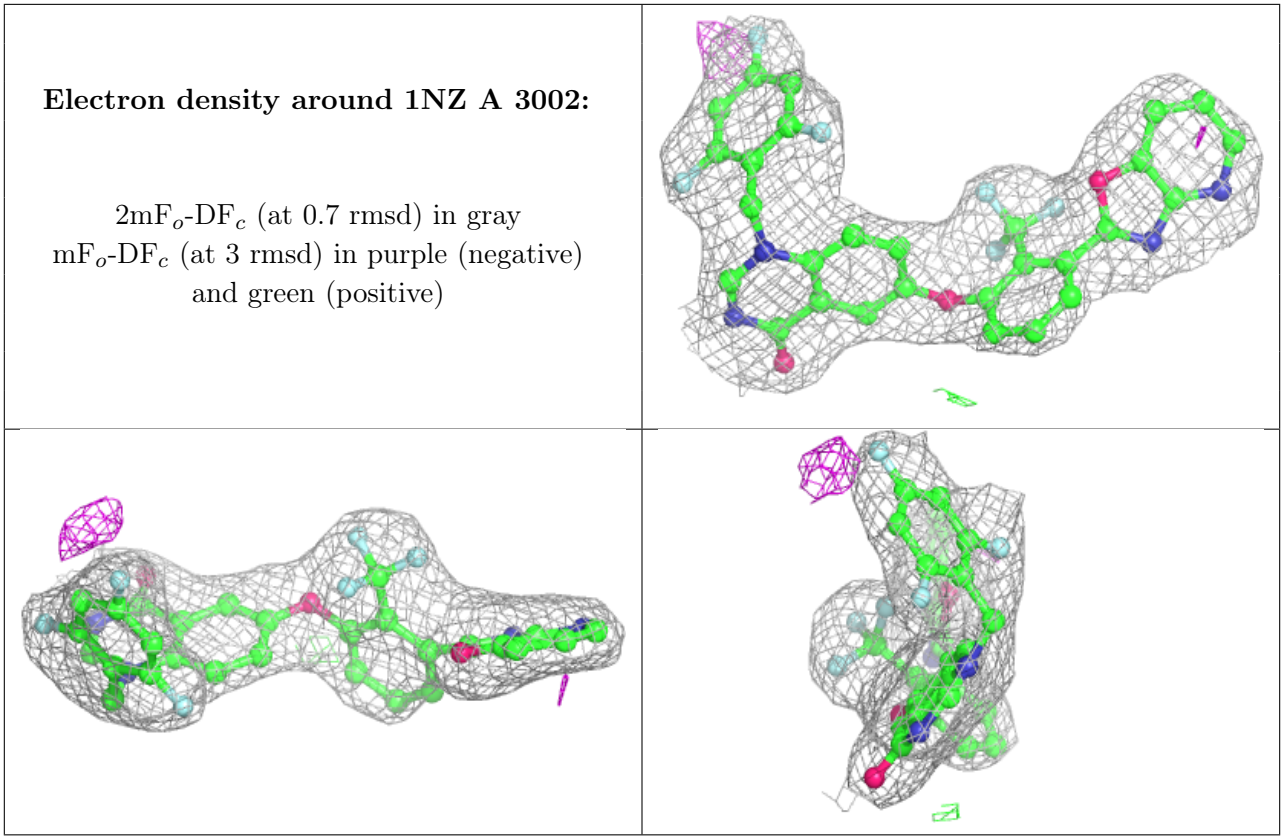
Electron density around 1NZ B 602:

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



Electron density around 1NZ A 3002:

$2mF_o$-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.