



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:45 PM UTC

PDB ID : 3PTQ / pdb_00003ptq
Title : The crystal structure of rice (*Oryza sativa* L.) Os4BGlu12 with dinitrophenyl 2-deoxy-2-fluoro-beta-D-glucopyranoside
Authors : Sansenya, S.; Opassiri, R.; Kuaprasert, B.; Chen, C.J.; Ketudat Cairns, J.R.
Deposited on : 2010-12-03
Resolution : 2.45 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

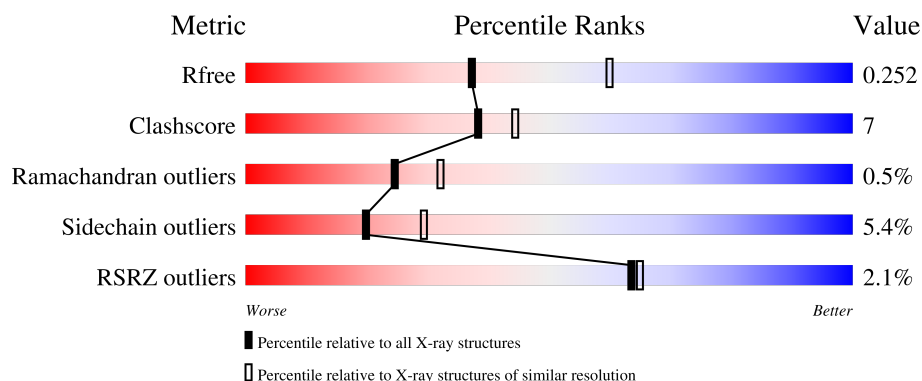
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	505	% 81% 11% .. 5%
1	B	505	3% 78% 15% .. 5%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8081 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 Beta-glucosidase Os4BGlu12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	478	Total	C	N	O	S	0	0	0
			3861	2481	665	704	11			
1	B	478	Total	C	N	O	S	0	0	0
			3861	2481	665	704	11			

There are 38 discrepancies between the modelled and reference sequences:

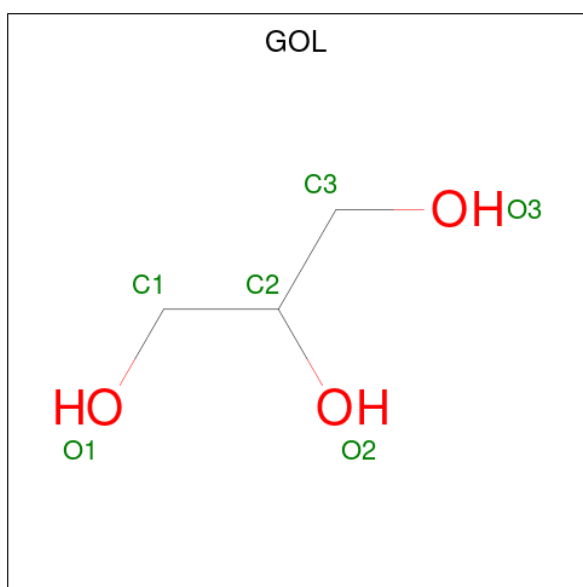
Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	ALA	-	expression tag	UNP Q01KB2
A	-17	MET	-	expression tag	UNP Q01KB2
A	-16	ALA	-	expression tag	UNP Q01KB2
A	-15	ASP	-	expression tag	UNP Q01KB2
A	-14	ILE	-	expression tag	UNP Q01KB2
A	-13	THR	-	expression tag	UNP Q01KB2
A	-12	SER	-	expression tag	UNP Q01KB2
A	-11	LEU	-	expression tag	UNP Q01KB2
A	-10	TYR	-	expression tag	UNP Q01KB2
A	-9	LYS	-	expression tag	UNP Q01KB2
A	-8	LYS	-	expression tag	UNP Q01KB2
A	-7	ALA	-	expression tag	UNP Q01KB2
A	-6	GLY	-	expression tag	UNP Q01KB2
A	-5	SER	-	expression tag	UNP Q01KB2
A	-4	ALA	-	expression tag	UNP Q01KB2
A	-3	ALA	-	expression tag	UNP Q01KB2
A	-2	ALA	-	expression tag	UNP Q01KB2
A	-1	PRO	-	expression tag	UNP Q01KB2
A	0	PHE	-	expression tag	UNP Q01KB2
B	-18	ALA	-	expression tag	UNP Q01KB2
B	-17	MET	-	expression tag	UNP Q01KB2
B	-16	ALA	-	expression tag	UNP Q01KB2
B	-15	ASP	-	expression tag	UNP Q01KB2
B	-14	ILE	-	expression tag	UNP Q01KB2
B	-13	THR	-	expression tag	UNP Q01KB2

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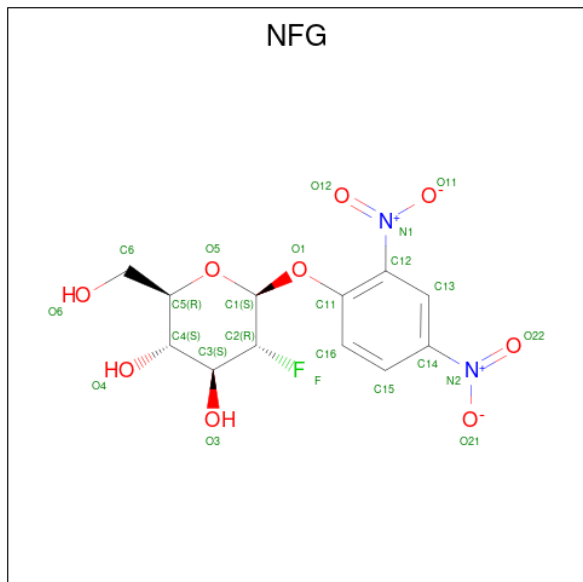
Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	SER	-	expression tag	UNP Q01KB2
B	-11	LEU	-	expression tag	UNP Q01KB2
B	-10	TYR	-	expression tag	UNP Q01KB2
B	-9	LYS	-	expression tag	UNP Q01KB2
B	-8	LYS	-	expression tag	UNP Q01KB2
B	-7	ALA	-	expression tag	UNP Q01KB2
B	-6	GLY	-	expression tag	UNP Q01KB2
B	-5	SER	-	expression tag	UNP Q01KB2
B	-4	ALA	-	expression tag	UNP Q01KB2
B	-3	ALA	-	expression tag	UNP Q01KB2
B	-2	ALA	-	expression tag	UNP Q01KB2
B	-1	PRO	-	expression tag	UNP Q01KB2
B	0	PHE	-	expression tag	UNP Q01KB2

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 3 is 2,4-dinitrophenyl 2-deoxy-2-fluoro-beta-D-glucopyranoside (CCD ID: NFG) (formula: $C_{12}H_{13}FN_2O_9$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	0	0
			24	12	1	2	9		
3	B	1	Total	C	F	N	O	0	0
			24	12	1	2	9		

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

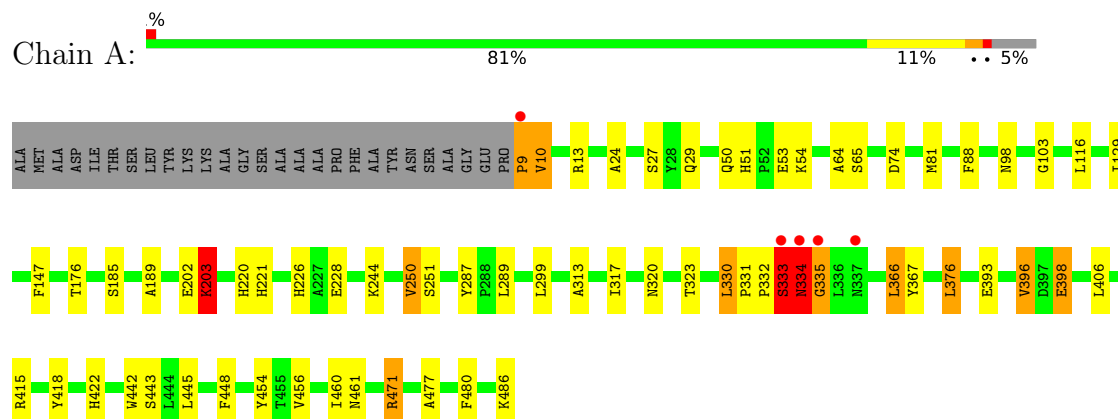
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	165	Total	O	0	0
			165	165		
5	B	115	Total	O	0	0
			115	115		

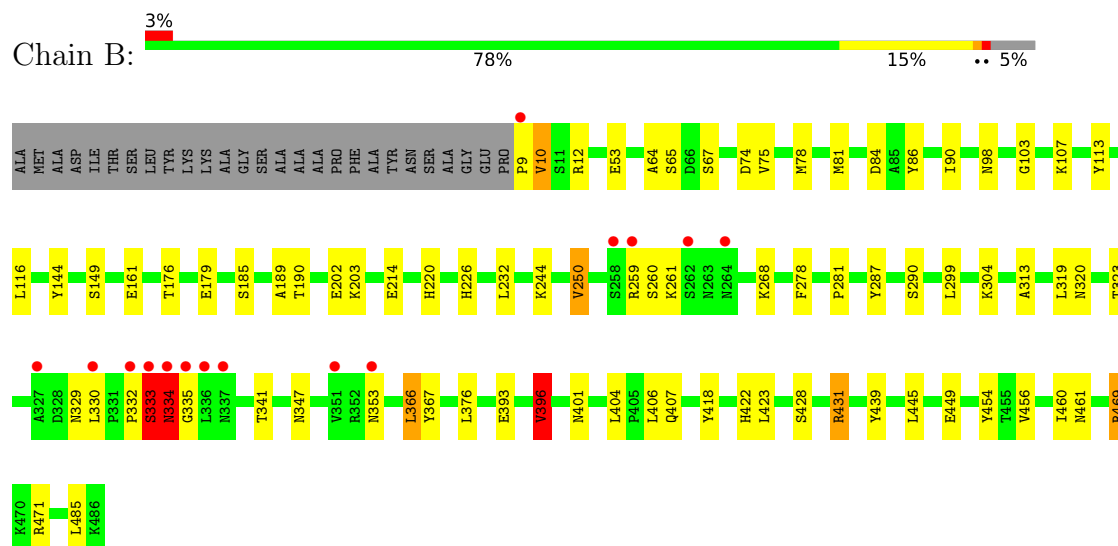
3 Residue-property plots [i](#)

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: Beta-glucosidase Os4BGlu12



• Molecule 1: Beta-glucosidase Os4BGlu12



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	114.11Å 114.11Å 184.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.45 30.00 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.8 (30.00-2.45) 99.8 (30.00-2.45)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.03 (at 2.44Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.209 , 0.251 0.207 , 0.252	Depositor DCC
R_{free} test set	2292 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	33.8	Xtriage
Anisotropy	0.002	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 25.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8081	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.54% 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, 0.333 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, ZN, NFG

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	0/3979	0.85	8/5392 (0.1%)
1	B	0.57	0/3979	0.85	3/5392 (0.1%)
All	All	0.57	0/7958	0.85	11/10784 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	5
All	All	0	8

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	250	VAL	CB-CA-C	-7.05	101.17	111.68
1	B	250	VAL	CB-CA-C	-6.88	101.42	111.68
1	A	396	VAL	CB-CA-C	-6.05	101.02	110.52
1	A	335	GLY	CA-C-N	-5.57	113.91	122.60
1	A	335	GLY	C-N-CA	-5.57	113.91	122.60
1	B	10	VAL	N-CA-C	5.41	120.58	109.34
1	B	396	VAL	CB-CA-C	-5.34	102.14	110.52
1	A	203	LYS	N-CA-C	5.05	116.47	111.07
1	A	9	PRO	CA-C-N	5.03	131.02	121.97
1	A	9	PRO	C-N-CA	5.03	131.02	121.97
1	A	129	ILE	N-CA-C	5.00	115.06	107.80

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	333	SER	Peptide
1	A	334	ASN	Peptide
1	A	9	PRO	Peptide
1	B	332	PRO	Peptide
1	B	333	SER	Peptide
1	B	334	ASN	Peptide
1	B	485	LEU	Peptide
1	B	9	PRO	Peptide

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	3861	0	3703	42	0
1	B	3861	0	3703	62	0
2	A	24	0	32	2	0
2	B	6	0	8	1	0
3	A	24	0	13	0	0
3	B	24	0	13	3	0
4	A	1	0	0	0	0
5	A	165	0	0	1	0
5	B	115	0	0	6	0
All	All	8081	0	7472	105	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 7.

All (105) 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:333:SER:H	1:B:334:ASN:HA	1.15	1.10
1:B:74:ASP:OD1	1:B:471:ARG:NH1	1.97	0.97
1:A:323:THR:HG22	1:A:367:TYR:O	1.66	0.96
1:B:334:ASN:H	1:B:335:GLY:CA	1.79	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:333:SER:N	1:B:334:ASN:HA	1.83	0.91
1:B:161:GLU:HG3	1:B:232:LEU:HD21	1.54	0.89
1:A:65:SER:O	1:A:471:ARG:NH2	2.05	0.89
1:A:323:THR:HG21	1:A:367:TYR:H	1.38	0.87
1:B:176:THR:OG1	1:B:226:HIS:HD2	1.60	0.84
1:B:323:THR:HG22	1:B:367:TYR:O	1.79	0.81
1:B:323:THR:HG21	1:B:367:TYR:H	1.44	0.80
1:A:176:THR:OG1	1:A:226:HIS:HD2	1.65	0.80
1:B:78:MET:HE3	5:B:591:HOH:O	1.83	0.77
1:B:78:MET:CE	5:B:591:HOH:O	2.33	0.74
1:A:323:THR:CG2	1:A:367:TYR:H	2.01	0.73
1:B:334:ASN:H	1:B:335:GLY:HA2	1.54	0.72
1:A:332:PRO:HB2	1:A:334:ASN:OD1	1.90	0.72
1:B:334:ASN:N	1:B:335:GLY:CA	2.49	0.71
1:B:431:ARG:HH11	1:B:431:ARG:HG2	1.55	0.69
1:B:333:SER:N	1:B:334:ASN:CA	2.56	0.68
1:B:64:ALA:O	1:B:469:ARG:HD3	1.95	0.66
1:B:202:GLU:HG3	1:B:203:LYS:H	1.61	0.66
1:A:330:LEU:HD23	1:A:331:PRO:HD2	1.77	0.65
1:A:202:GLU:HG3	1:A:203:LYS:H	1.63	0.64
1:B:65:SER:O	1:B:471:ARG:NH2	2.31	0.64
1:B:78:MET:HE1	1:B:86:TYR:HB2	1.80	0.63
1:B:323:THR:CG2	1:B:367:TYR:H	2.12	0.63
1:B:268:LYS:NZ	5:B:577:HOH:O	2.32	0.62
1:A:442:TRP:CD2	1:A:443:SER:HB3	2.36	0.61
1:A:398:GLU:OE2	1:A:415:ARG:NH1	2.31	0.61
1:B:334:ASN:H	1:B:335:GLY:HA3	1.66	0.61
1:B:323:THR:HG21	1:B:367:TYR:N	2.14	0.61
1:B:202:GLU:HG3	1:B:203:LYS:N	2.16	0.60
1:B:334:ASN:N	1:B:335:GLY:HA3	2.15	0.60
1:A:189:ALA:O	1:A:202:GLU:HG2	2.01	0.59
1:B:189:ALA:O	1:B:202:GLU:HG2	2.03	0.59
1:A:323:THR:HG21	1:A:367:TYR:N	2.15	0.59
1:B:323:THR:HG21	1:B:366:LEU:HA	1.84	0.59
1:A:323:THR:HG23	1:A:366:LEU:HD13	1.84	0.58
1:A:29:GLN:HG2	1:A:448:PHE:O	2.04	0.58
1:B:81:MET:HE1	1:B:460:ILE:HG21	1.86	0.58
1:A:81:MET:HE1	1:A:460:ILE:HG21	1.86	0.58
1:B:81:MET:CE	1:B:460:ILE:HG21	2.36	0.56
1:A:323:THR:CG2	1:A:367:TYR:N	2.70	0.55
1:B:445:LEU:HD11	1:B:471:ARG:NH1	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:78:MET:HE1	1:B:86:TYR:CB	2.37	0.54
1:B:320:ASN:CG	1:B:393:GLU:HB2	2.33	0.54
1:A:74:ASP:OD1	1:A:471:ARG:NH1	2.41	0.53
1:B:431:ARG:HH11	1:B:431:ARG:CG	2.21	0.52
1:B:185:SER:O	1:B:189:ALA:HB3	2.09	0.52
1:B:330:LEU:HG	1:B:347:ASN:HB2	1.91	0.52
1:A:176:THR:OG1	1:A:226:HIS:CD2	2.56	0.51
1:A:202:GLU:HG3	1:A:203:LYS:N	2.26	0.50
1:A:81:MET:HE3	1:A:477:ALA:HA	1.93	0.50
1:B:334:ASN:O	1:B:334:ASN:OD1	2.29	0.50
1:A:13:ARG:HD3	1:A:486:LYS:HD2	1.91	0.50
1:A:333:SER:N	1:A:334:ASN:HA	2.26	0.49
1:A:323:THR:HG21	1:A:366:LEU:HA	1.94	0.49
1:B:176:THR:OG1	1:B:226:HIS:CD2	2.52	0.49
3:B:1002:NFG:O11	3:B:1002:NFG:H4	2.12	0.49
1:A:88:PHE:HB2	2:A:3966:GOL:H2	1.94	0.48
1:B:98:ASN:OD1	1:B:103:GLY:HA3	2.14	0.48
1:A:98:ASN:OD1	1:A:103:GLY:HA3	2.13	0.47
1:A:445:LEU:HD23	1:A:461:ASN:HB2	1.96	0.47
1:A:320:ASN:CG	1:A:393:GLU:HB2	2.40	0.46
1:B:78:MET:HE1	1:B:86:TYR:CG	2.50	0.46
1:A:226:HIS:HE1	1:A:313:ALA:O	1.98	0.46
1:B:396:VAL:HG13	1:B:418:TYR:CE2	2.50	0.46
1:A:27:SER:HA	2:A:3966:GOL:H12	1.96	0.46
1:A:64:ALA:HA	1:A:454:TYR:OH	2.16	0.46
1:A:418:TYR:O	1:A:422:HIS:HD2	1.98	0.46
1:A:81:MET:CE	1:A:480:PHE:HB2	2.47	0.45
1:A:332:PRO:HB2	1:A:334:ASN:CG	2.42	0.45
1:A:244:LYS:HG3	5:A:652:HOH:O	2.17	0.44
1:B:226:HIS:HE1	1:B:313:ALA:O	2.00	0.44
1:B:422:HIS:HE1	5:B:518:HOH:O	2.00	0.44
1:A:147:PHE:O	1:A:221:HIS:HD2	2.01	0.44
1:B:422:HIS:CE1	5:B:518:HOH:O	2.70	0.44
1:B:67:SER:HB3	2:B:3967:GOL:H31	2.00	0.44
1:A:220:HIS:HD2	1:A:287:TYR:OH	2.00	0.44
1:A:251:SER:HB3	1:A:376:LEU:HD11	1.99	0.44
1:B:81:MET:HE1	1:B:460:ILE:HD13	1.98	0.44
1:B:78:MET:HE1	1:B:86:TYR:CD1	2.53	0.43
1:B:323:THR:CG2	1:B:367:TYR:N	2.78	0.43
1:A:24:ALA:O	1:A:443:SER:HB2	2.19	0.43
1:B:75:VAL:O	1:B:78:MET:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:396:VAL:HG13	1:B:418:TYR:CD2	2.54	0.43
1:B:190:THR:HA	1:B:202:GLU:HG2	2.01	0.43
1:B:214:GLU:OE1	5:B:598:HOH:O	2.21	0.43
1:A:185:SER:O	1:A:189:ALA:HB3	2.19	0.43
1:B:90:ILE:HG23	1:B:113:TYR:CE2	2.54	0.43
1:B:401:ASN:HB3	1:B:404:LEU:HD12	1.99	0.43
1:B:179:GLU:OE1	3:B:1002:NFG:H16	2.19	0.43
1:B:445:LEU:HD23	1:B:461:ASN:HB2	2.01	0.42
1:B:64:ALA:HA	1:B:454:TYR:OH	2.20	0.42
1:B:220:HIS:HD2	1:B:287:TYR:OH	2.03	0.42
1:A:398:GLU:OE2	1:A:415:ARG:NH2	2.51	0.42
1:B:423:LEU:HD21	1:B:439:TYR:CE1	2.55	0.42
1:B:179:GLU:OE2	3:B:1002:NFG:H1	2.19	0.41
1:B:449:GLU:O	1:B:449:GLU:HG3	2.20	0.41
1:B:144:TYR:CD2	1:B:149:SER:HB3	2.55	0.41
1:A:81:MET:HE2	1:A:480:PHE:CB	2.50	0.41
1:B:278:PHE:C	1:B:281:PRO:HD2	2.46	0.41
1:A:51:HIS:HB3	1:A:54:LYS:HG3	2.01	0.40
1:B:12:ARG:HH22	1:B:84:ASP:CG	2.29	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	476/505 (94%)	458 (96%)	15 (3%)	3 (1%)	21	27
1	B	476/505 (94%)	459 (96%)	15 (3%)	2 (0%)	30	37
All	All	952/1010 (94%)	917 (96%)	30 (3%)	5 (0%)	24	32

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	10	VAL
1	A	334	ASN
1	A	10	VAL
1	B	334	ASN
1	A	335	GLY

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	406/423 (96%)	387 (95%)	19 (5%)	23	35
1	B	406/423 (96%)	381 (94%)	25 (6%)	16	23
All	All	812/846 (96%)	768 (95%)	44 (5%)	20	29

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	VAL
1	A	50	GLN
1	A	53	GLU
1	A	116	LEU
1	A	203	LYS
1	A	228	GLU
1	A	250	VAL
1	A	289	LEU
1	A	299	LEU
1	A	317	ILE
1	A	330	LEU
1	A	333	SER
1	A	366	LEU
1	A	376	LEU
1	A	396	VAL
1	A	398	GLU
1	A	406	LEU
1	A	456	VAL
1	A	471	ARG

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Mol	Chain	Res	Type
1	B	53	GLU
1	B	107	LYS
1	B	116	LEU
1	B	244	LYS
1	B	250	VAL
1	B	259	ARG
1	B	260	SER
1	B	261	LYS
1	B	290	SER
1	B	299	LEU
1	B	304	LYS
1	B	319	LEU
1	B	329	ASN
1	B	333	SER
1	B	341	THR
1	B	353	ASN
1	B	366	LEU
1	B	376	LEU
1	B	396	VAL
1	B	406	LEU
1	B	407	GLN
1	B	428	SER
1	B	431	ARG
1	B	456	VAL
1	B	469	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	205	ASN
1	A	220	HIS
1	A	221	HIS
1	A	226	HIS
1	A	360	GLN
1	A	407	GLN
1	A	420	HIS
1	A	422	HIS
1	B	29	GLN
1	B	51	HIS
1	B	220	HIS
1	B	221	HIS
1	B	226	HIS

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Mol	Chain	Res	Type
1	B	238	GLN
1	B	252	HIS
1	B	360	GLN
1	B	371	GLN
1	B	422	HIS
1	B	447	ASN
1	B	466	ASN

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 8 ligands modelled in this entry, 1 is monoatomic - leaving 7 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	A	3968	-	5,5,5	0.36	0	5,5,5	0.44	0
2	GOL	A	3969	-	5,5,5	0.42	0	5,5,5	0.27	0
3	NFG	B	1002	-	25,25,25	1.47	2 (8%)	28,36,36	1.89	5 (17%)
3	NFG	A	1001	-	25,25,25	1.52	3 (12%)	28,36,36	2.39	7 (25%)
2	GOL	A	3970	-	5,5,5	0.34	0	5,5,5	0.45	0
2	GOL	A	3966	-	5,5,5	0.35	0	5,5,5	0.69	0
2	GOL	B	3967	-	5,5,5	0.29	0	5,5,5	0.79	0

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	A	3968	-	-	4/4/4/4	-
2	GOL	A	3969	-	-	2/4/4/4	-
3	NFG	B	1002	-	-	0/10/34/34	0/2/2/2
3	NFG	A	1001	-	-	1/10/34/34	0/2/2/2
2	GOL	A	3970	-	-	2/4/4/4	-
2	GOL	A	3966	-	-	4/4/4/4	-
2	GOL	B	3967	-	-	4/4/4/4	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1002	NFG	C12-N1	-4.64	1.37	1.45
3	A	1001	NFG	C12-N1	-4.52	1.37	1.45
3	B	1002	NFG	C14-N2	-3.94	1.35	1.45
3	A	1001	NFG	C14-N2	-3.17	1.37	1.45
3	A	1001	NFG	C2-C1	2.48	1.55	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1001	NFG	C11-O1-C1	7.77	132.33	118.15
3	A	1001	NFG	C15-C14-N2	6.45	124.97	119.34
3	B	1002	NFG	C11-O1-C1	6.27	129.60	118.15
3	B	1002	NFG	C15-C14-N2	3.65	122.53	119.34
3	A	1001	NFG	F-C2-C1	3.35	111.48	107.62
3	B	1002	NFG	F-C2-C1	3.32	111.44	107.62
3	B	1002	NFG	F-C2-C3	3.01	111.42	108.81
3	A	1001	NFG	C3-C4-C5	-2.72	105.30	110.23
3	A	1001	NFG	C13-C14-N2	-2.69	116.42	118.74
3	A	1001	NFG	C1-O5-C5	2.56	118.72	113.72
3	B	1002	NFG	C1-O5-C5	2.43	118.46	113.72
3	A	1001	NFG	O22-N2-C14	2.06	121.65	118.82

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	3966	GOL	O1-C1-C2-C3
2	A	3966	GOL	C1-C2-C3-O3
2	A	3968	GOL	O1-C1-C2-C3
2	A	3969	GOL	C1-C2-C3-O3
2	A	3969	GOL	O2-C2-C3-O3
2	A	3970	GOL	C1-C2-C3-O3
2	B	3967	GOL	C1-C2-C3-O3
2	B	3967	GOL	O2-C2-C3-O3
2	A	3966	GOL	O1-C1-C2-O2
2	A	3968	GOL	O2-C2-C3-O3
2	A	3968	GOL	C1-C2-C3-O3
2	B	3967	GOL	O1-C1-C2-C3
2	A	3966	GOL	O2-C2-C3-O3
2	A	3968	GOL	O1-C1-C2-O2
2	A	3970	GOL	O2-C2-C3-O3
2	B	3967	GOL	O1-C1-C2-O2
3	A	1001	NFG	C2-C1-O1-C11

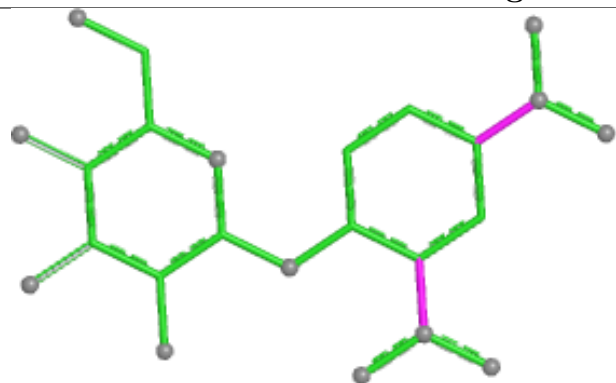
There are no ring outliers.

3 monomers are involved in 6 short contacts:

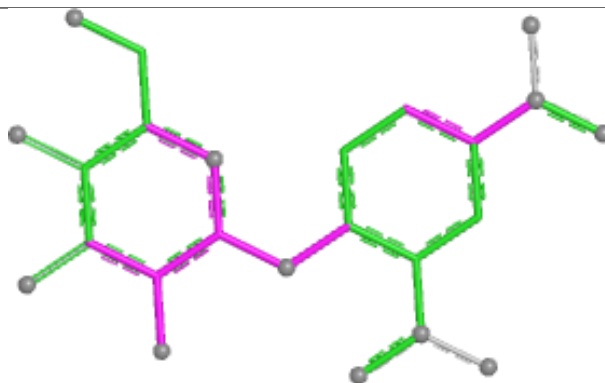
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1002	NFG	3	0
2	A	3966	GOL	2	0
2	B	3967	GOL	1	0

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.

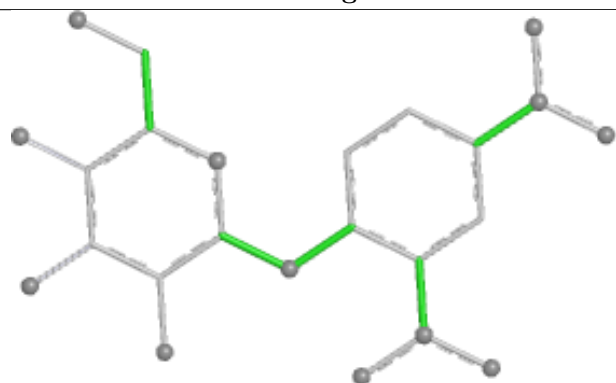
Ligand NFG B 1002



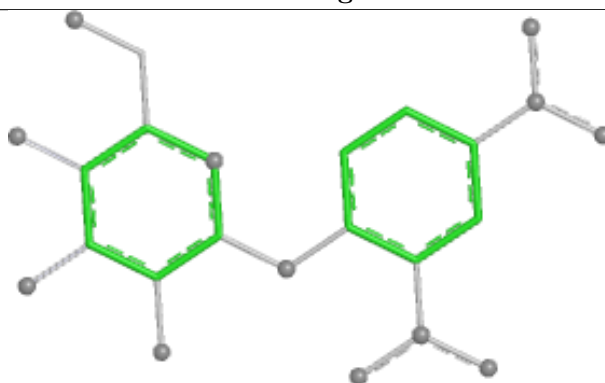
Bond lengths



Bond angles

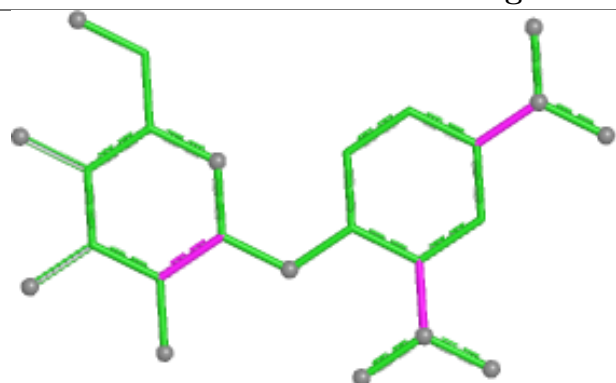


Torsions

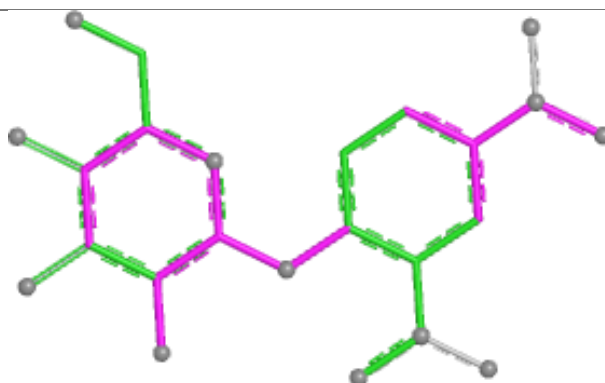


Rings

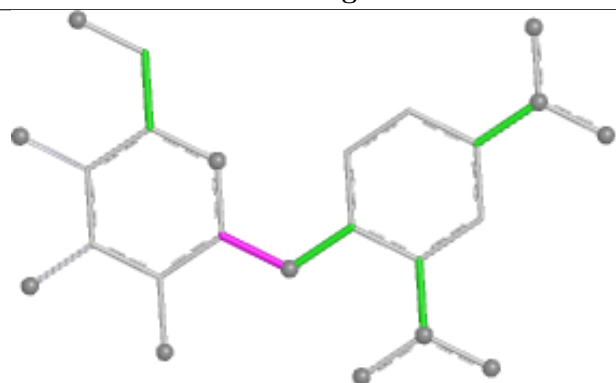
Ligand NFG A 1001



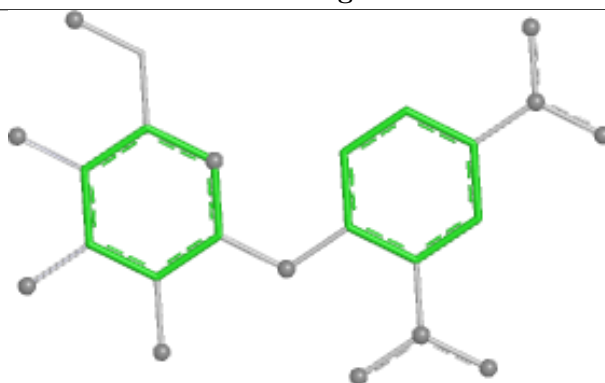
Bond lengths



Bond angles



Torsions



Rings

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, 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	478/505 (94%)	-0.02	5 (1%) 79 80	18, 32, 47, 62	0
1	B	478/505 (94%)	0.12	15 (3%) 51 52	20, 33, 48, 62	0
All	All	956/1010 (94%)	0.05	20 (2%) 63 65	18, 32, 47, 62	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	334	ASN	7.1
1	A	333	SER	6.7
1	B	334	ASN	5.7
1	B	333	SER	4.5
1	B	9	PRO	3.9
1	B	336	LEU	3.6
1	B	258	SER	3.3
1	A	337	ASN	2.5
1	A	335	GLY	2.5
1	B	335	GLY	2.4
1	B	259	ARG	2.3
1	A	9	PRO	2.3
1	B	262	SER	2.3
1	B	327	ALA	2.2
1	B	337	ASN	2.2
1	B	351	VAL	2.1
1	B	264	ASN	2.1
1	B	353	ASN	2.1
1	B	332	PRO	2.0
1	B	330	LEU	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](#)

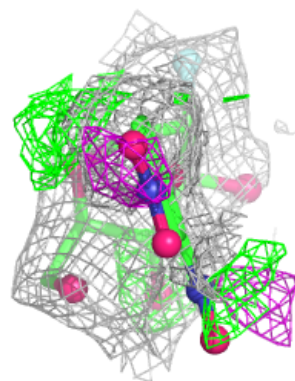
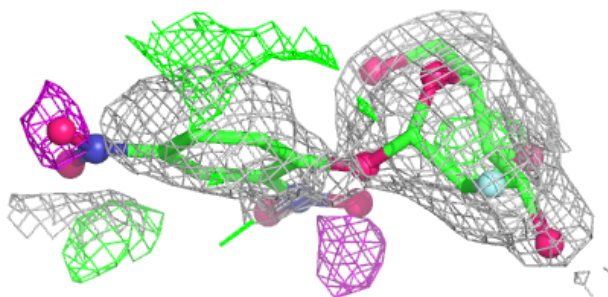
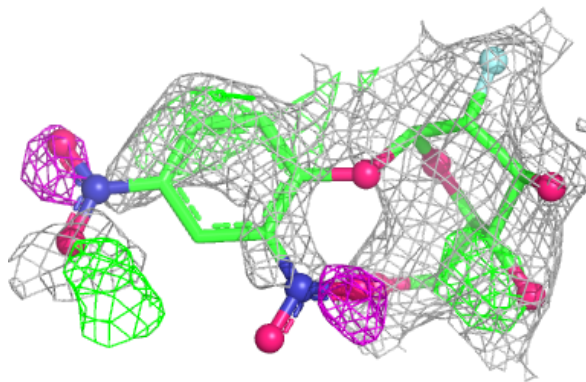
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	NFG	B	1002	24/24	0.67	0.26	54,65,67,67	24
3	NFG	A	1001	24/24	0.70	0.27	57,65,66,66	24
2	GOL	A	3966	6/6	0.82	0.18	37,38,39,39	0
2	GOL	A	3970	6/6	0.86	0.13	42,43,44,45	0
2	GOL	A	3969	6/6	0.91	0.13	50,51,52,53	0
2	GOL	A	3968	6/6	0.92	0.11	49,50,51,52	0
2	GOL	B	3967	6/6	0.93	0.13	38,39,40,41	0
4	ZN	A	487	1/1	1.00	0.02	22,22,22,22	0

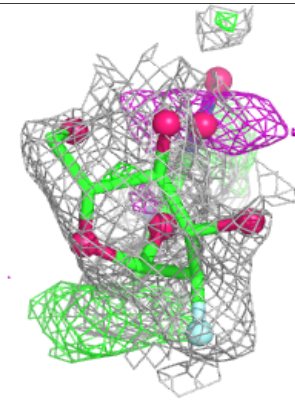
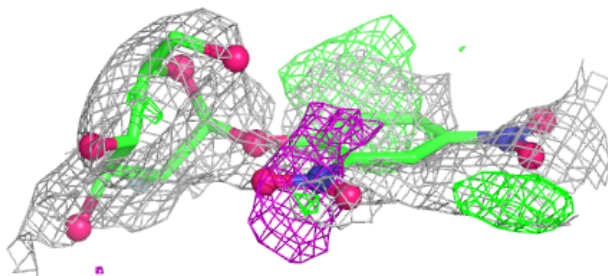
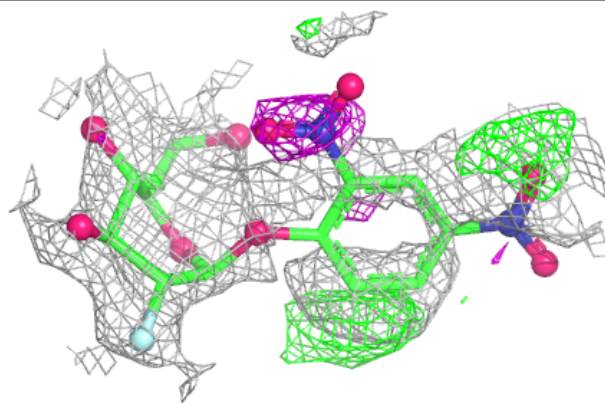
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NFG B 1002:

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

**Electron density around NFG 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.