

Full wwPDB X-ray Structure Validation Report (i)

Nov 16, 2023 – 04:36 AM JST

PDB ID : 6KTK

Title: Crystal structure of scyllo-inositol dehydrogenase R178A mutant, complexed

with NADH and L-glucono-1,5-lactone, from Paracoccus laeviglucosivorans

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mura, A.; Yajima, S.

Deposited on : 2019-08-28

Resolution : 1.65 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 : 2.36

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)

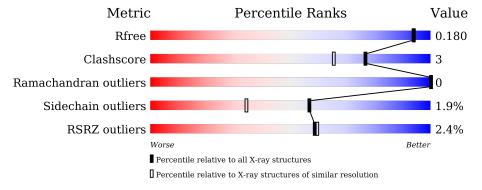
Validation Pipeline (wwPDB-VP) : 2.36

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 1.65 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},\ {\rm resolution\ range}(\mathring{\rm A})) \end{array}$
R_{free}	130704	1827 (1.66-1.66)
Clashscore	141614	1931 (1.66-1.66)
Ramachandran outliers	138981	1891 (1.66-1.66)
Sidechain outliers	138945	1891 (1.66-1.66)
RSRZ outliers	127900	1791 (1.66-1.66)

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	380	91%	6% •
1	В	380	87%	9% • •
1	С	380	90%	7% •
1	D	380	89%	8% •



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 12419 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 Scyllo-inositol dehydrogenase with L-glucose dehydrogenase activity.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Λ	367	Total	С	N	О	S	0	7	0
1	A	307	2827	1772	516	521	18	0	'	
1	В	366	Total C N	О	S	0	0	0		
1	Б	300	2779	1741	507	513	18	0	0	
1	С	368	Total	С	N	О	S	0	5	0
1		300	2823	1770	511	524	18	0	9	
1	D	368	Total	С	N	О	S	0	3	0
1	ע	300	2810	1762	511	519	18)	

There are 40 discrepancies between the modelled and reference sequences:

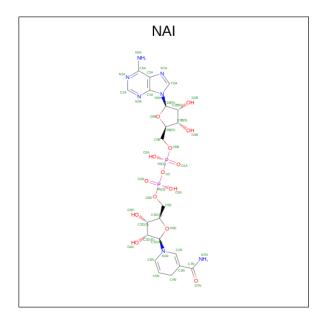
Chain	Residue	Modelled	Actual	Comment	Reference
A	72	SER	ASN	See sequence details	UNP K7ZP76
A	178	ALA	ARG	engineered mutation	UNP K7ZP76
A	373	LEU	-	expression tag	UNP K7ZP76
A	374	GLU	-	expression tag	UNP K7ZP76
A	375	HIS	-	expression tag	UNP K7ZP76
A	376	HIS	-	expression tag	UNP K7ZP76
A	377	HIS	-	expression tag	UNP K7ZP76
A	378	HIS	-	expression tag	UNP K7ZP76
A	379	HIS	-	expression tag	UNP K7ZP76
A	380	HIS	-	expression tag	UNP K7ZP76
В	72	SER	ASN	See sequence details	UNP K7ZP76
В	178	ALA	ARG	engineered mutation	UNP K7ZP76
В	373	LEU	-	expression tag	UNP K7ZP76
В	374	GLU	-	expression tag	UNP K7ZP76
В	375	HIS	-	expression tag	UNP K7ZP76
В	376	HIS	-	expression tag	UNP K7ZP76
В	377	HIS	-	expression tag	UNP K7ZP76
В	378	HIS	-	expression tag	UNP K7ZP76
В	379	HIS	-	expression tag	UNP K7ZP76
В	380	HIS	-	expression tag	UNP K7ZP76



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Chain	Residue	Modelled	Actual	Comment	Reference
С	72	SER	ASN	See sequence details	UNP K7ZP76
С	178	ALA	ARG	engineered mutation	UNP K7ZP76
С	373	LEU	-	expression tag	UNP K7ZP76
С	374	GLU	-	expression tag	UNP K7ZP76
С	375	HIS	-	expression tag	UNP K7ZP76
С	376	HIS	-	expression tag	UNP K7ZP76
С	377	HIS	-	expression tag	UNP K7ZP76
С	378	HIS	-	expression tag	UNP K7ZP76
С	379	HIS	-	expression tag	UNP K7ZP76
С	380	HIS	-	expression tag	UNP K7ZP76
D	72	SER	ASN	See sequence details	UNP K7ZP76
D	178	ALA	ARG	engineered mutation	UNP K7ZP76
D	373	LEU	-	expression tag	UNP K7ZP76
D	374	GLU	-	expression tag	UNP K7ZP76
D	375	HIS	-	expression tag	UNP K7ZP76
D	376	HIS	-	expression tag	UNP K7ZP76
D	377	HIS	-	expression tag	UNP K7ZP76
D	378	HIS	-	expression tag	UNP K7ZP76
D	379	HIS	-	expression tag	UNP K7ZP76
D	380	HIS	-	expression tag	UNP K7ZP76

• Molecule 2 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (three-letter code: NAI) (formula: $C_{21}H_{29}N_7O_{14}P_2$).



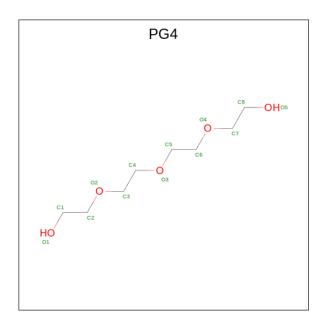
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
9	Λ	1	Total	С	N	О	Р	0	0
2	A	1	44	21	7	14	2	U	U



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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	D	1	Total	С	N	О	Р	0	0
2	Ъ	1	44	21	7	14	2	U	0
9	C	1	Total	С	N	О	Р	0	0
2	C	1	44	21	7	14	2	U	0
9	D	1	Total	С	N	О	Р	0	0
2	ט	1	44	21	7	14	2	U	

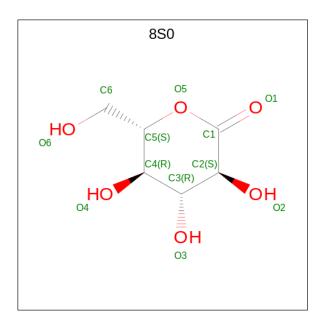
• Molecule 3 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 13 8 5	0	0
3	D	1	Total C O 13 8 5	0	0

• Molecule 4 is L-glucono-1,5-lactone (three-letter code: 8S0) (formula: $C_6H_{10}O_6$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
1	Λ	1	Total C O	0	0
4	A	1	12 6 6	U	U
1	В	1	Total C O	0	0
4	Б	1	12 6 6	U	0
1	С	1	Total C O	0	0
4		1	12 6 6	U	U
1	D	1	Total C O	0	0
4	ש	1	12 6 6	U	U

• Molecule 5 is water.

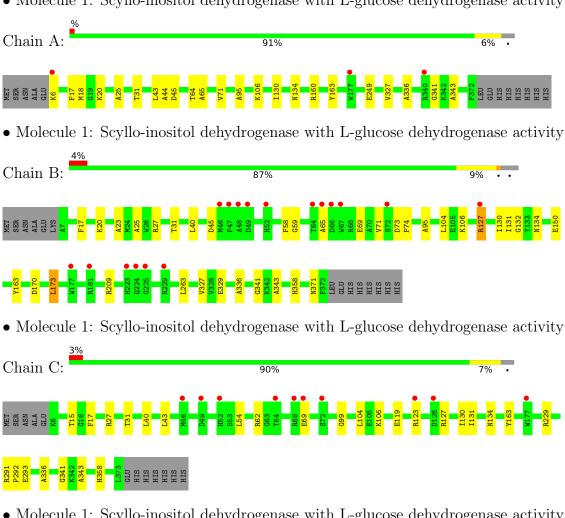
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	253	Total O 253 253	0	0
5	В	204	Total O 204 204	0	0
5	С	233	Total O 233 233	0	0
5	D	240	Total O 240 240	0	0



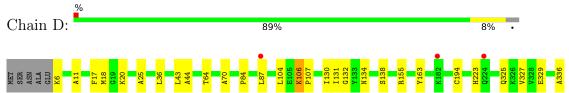
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Scyllo-inositol dehydrogenase with L-glucose dehydrogenase activity



• Molecule 1: Scyllo-inositol dehydrogenase with L-glucose dehydrogenase activity









4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	90.61Å 127.56Å 137.57Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.40 - 1.65	Depositor
Resolution (A)	48.77 - 1.65	EDS
% Data completeness	99.6 (48.40-1.65)	Depositor
(in resolution range)	99.6 (48.77-1.65)	EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.98 (at 1.65Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
D D.	0.160 , 0.171	Depositor
R, R_{free}	0.170 , 0.180	DCC
R_{free} test set	9602 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	16.8	Xtriage
Anisotropy	0.342	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38, 40.1	EDS
L-test for twinning ²	$ < L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	12419	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.98% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 8S0, PG4, NAI

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		
IVIOI	Wioi Chain		# Z > 5	RMSZ	# Z > 5	
1	A	0.59	0/2914	0.75	0/3950	
1	В	0.60	0/2845	0.74	0/3858	
1	С	0.60	0/2904	0.76	0/3937	
1	D	0.60	0/2885	0.74	0/3911	
All	All	0.60	0/11548	0.75	0/15656	

There are no bond length outliers.

There are no bond angle outliers.

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	2827	0	2761	12	0
1	В	2779	0	2694	23	0
1	С	2823	0	2744	13	0
1	D	2810	0	2735	22	0
2	A	44	0	27	1	0
2	В	44	0	27	0	0
2	С	44	0	27	0	0
2	D	44	0	27	1	0
3	A	13	0	18	1	0



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Mol	Chain	Non-H	H(model)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
3	D	13	0	18	6	0
4	A	12	0	0	0	0
4	В	12	0	0	0	0
4	С	12	0	0	0	0
4	D	12	0	0	0	0
5	A	253	0	0	0	0
5	В	204	0	0	1	0
5	С	233	0	0	1	0
5	D	240	0	0	0	0
All	All	12419	0	11078	67	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 3.

All (67) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}({ m \AA})$	overlap(Å)
1:D:223:HIS:NE2	3:D:402:PG4:H42	1.79	0.96
1:B:127:ARG:HA	1:B:127:ARG:HE	1.41	0.83
1:D:106:LYS:HD2	1:D:194:CYS:SG	2.20	0.81
1:B:71:VAL:CG1	1:B:95:ALA:HA	2.15	0.77
1:D:223:HIS:HD2	3:D:402:PG4:H82	1.55	0.72
1:B:71:VAL:HG11	1:B:95:ALA:HA	1.73	0.69
1:D:223:HIS:CD2	3:D:402:PG4:H82	2.27	0.68
1:B:27:ARG:HG2	1:B:40:LEU:HD11	1.76	0.67
1:C:62:ARG:NH2	1:C:69:GLU:OE2	2.27	0.66
1:D:106:LYS:HE3	1:D:107:PRO:HD3	1.84	0.60
1:B:170:ASP:HB3	1:B:173:LEU:HD22	1.81	0.60
1:B:336:ALA:HA	1:B:341:GLY:O	2.07	0.54
1:D:336:ALA:HA	1:D:341:GLY:O	2.08	0.54
1:D:6:LYS:HG3	1:D:36:LEU:HD12	1.92	0.52
1:D:223:HIS:HD2	3:D:402:PG4:C8	2.22	0.51
1:C:130:ILE:HD12	1:C:343:ALA:HB1	1.93	0.50
1:A:6:LYS:HG2	1:A:6:LYS:O	2.12	0.50
1:D:130:ILE:HD12	1:D:343:ALA:HB1	1.94	0.49
1:B:23:ALA:O	1:B:27:ARG:HG3	2.12	0.49
1:D:106:LYS:O	1:D:106:LYS:HE2	2.14	0.48
1:A:71:VAL:HG13	1:A:95:ALA:HA	1.94	0.48
1:D:138:SER:HB3	1:D:325:GLN:HE21	1.80	0.47
1:B:71:VAL:HG11	1:B:95:ALA:CA	2.43	0.47
1:B:127:ARG:HA	1:B:127:ARG:NE	2.20	0.47



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Continuea from pre		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:18:MET:HG3	2:A:401:NAI:C2N	2.45	0.47
1:B:25:ALA:HA	1:B:327:VAL:HG22	1.96	0.47
1:C:358:HIS:HE1	5:C:514:HOH:O	1.99	0.46
1:C:15:THR:HB	1:C:54:LEU:HD13	1.96	0.46
1:D:11:ALA:HB1	1:D:70:ALA:HB1	1.97	0.46
1:A:20:LYS:HE3	1:B:31:THR:O	2.15	0.46
1:B:27:ARG:HD2	1:B:58:PHE:O	2.15	0.45
1:D:223:HIS:NE2	3:D:402:PG4:C4	2.66	0.45
1:D:25:ALA:HA	1:D:327:VAL:HG22	1.98	0.44
1:B:27:ARG:NH2	1:B:59:GLY:HA3	2.32	0.44
1:D:84:PRO:HD2	1:D:87:LEU:HD12	1.98	0.44
1:A:31:THR:O	1:B:20:LYS:HE3	2.18	0.44
1:A:130:ILE:HD12	1:A:343:ALA:HB1	2.00	0.44
1:C:336:ALA:HA	1:C:341:GLY:O	2.17	0.43
1:A:45:ASP:O	1:A:65:ALA:HA	2.18	0.43
1:B:358:HIS:HE1	5:B:520:HOH:O	2.01	0.43
1:B:209:ARG:HD3	1:B:371:ASN:HD21	1.84	0.43
1:D:44:ALA:HA	1:D:64:THR:O	2.19	0.43
1:A:336:ALA:HA	1:A:341:GLY:O	2.19	0.42
1:C:31:THR:O	1:D:20:LYS:HE3	2.18	0.42
1:C:43:LEU:C	1:C:43:LEU:HD23	2.39	0.42
1:C:291:ARG:HA	1:C:292:PRO:HD3	1.93	0.42
1:A:25:ALA:HA	1:A:327:VAL:HG22	2.01	0.42
1:B:132:GLY:HA2	1:B:329:GLU:OE1	2.20	0.42
1:C:27:ARG:HG2	1:C:40:LEU:HD11	2.02	0.42
1:D:104:LEU:O	1:D:131:ILE:HA	2.19	0.42
1:C:119:GLU:OE2	1:C:123:ARG:NH1	2.39	0.41
1:B:130:ILE:HD12	1:B:343:ALA:HB1	2.02	0.41
1:D:43:LEU:C	1:D:43:LEU:HD23	2.41	0.41
3:A:402:PG4:H62	3:A:402:PG4:H41	1.86	0.41
1:C:99:GLY:O	1:C:127:ARG:HD2	2.20	0.41
1:B:104:LEU:O	1:B:131:ILE:HA	2.20	0.41
1:B:45:ASP:O	1:B:65:ALA:HA	2.21	0.41
1:B:150:GLU:OE2	1:C:293:GLU:OE2	2.38	0.41
1:D:223:HIS:CE1	3:D:402:PG4:H42	2.52	0.41
1:A:44:ALA:HA	1:A:64:THR:O	2.20	0.41
1:B:263:LEU:C	1:B:263:LEU:HD23	2.42	0.41
1:D:18:MET:HG3	2:D:401:NAI:C2N	2.51	0.41
1:D:132:GLY:HA2	1:D:329:GLU:OE1	2.21	0.41
1:A:43:LEU:HD23	1:A:43:LEU:C	2.41	0.40
1:A:160:ARG:HD3	1:A:249:GLU:OE1	2.20	0.40



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Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:B:73:ASP:HA	1:B:74:PRO:HD3	1.97	0.40
1:C:104:LEU:O	1:C:131:ILE:HA	2.22	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	Percer	$_{ m tiles}$
1	A	372/380~(98%)	366 (98%)	6 (2%)	0	100	100
1	В	364/380~(96%)	359 (99%)	5 (1%)	0	100	100
1	\mathbf{C}	371/380~(98%)	364 (98%)	7 (2%)	0	100	100
1	D	369/380~(97%)	362 (98%)	7 (2%)	0	100	100
All	All	$1476/1520 \ (97\%)$	1451 (98%)	25 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	282/287~(98%)	278 (99%)	4 (1%)	67 46
1	В	$274/287 \ (96\%)$	267 (97%)	7 (3%)	46 21
1	С	281/287~(98%)	276 (98%)	5 (2%)	59 36



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Mol	Chain	Analysed	Rotameric	Outliers	Percentile	es
1	D	279/287 (97%)	274 (98%)	5 (2%)	59 36	
All	All	1116/1148 (97%)	1095 (98%)	21 (2%)	57 34	

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	PHE
1	A	106	LYS
1	A	134	ASN
1	A	163	TYR
1	В	17	PHE
1	В	69	GLU
1	В	106	LYS
1	В	127	ARG
1	В	134	ASN
1	В	163	TYR
1	В	173	LEU
1	С	17	PHE
1	C C C	106	LYS
1	С	134	ASN
1	С	163	TYR
1	С	229	ARG
1	D	17	PHE
1	D	106	LYS
1	D	134	ASN
1	D	155	ARG
1	D	163	TYR

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

Mol	Chain	Res	Type
1	В	224	GLN
1	В	358	HIS
1	В	371	ASN
1	С	358	HIS
1	D	278	GLN
1	D	325	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)

10 ligands are 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	Во	ond leng	ths	В	ond ang	les
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	$\mid \# Z > 2$	Counts	RMSZ	# Z > 2
3	PG4	D	402	-	12,12,12	0.28	0	11,11,11	0.22	0
2	NAI	В	401	-	42,48,48	1.03	2 (4%)	47,73,73	1.18	4 (8%)
2	NAI	D	401	-	42,48,48	1.08	3 (7%)	47,73,73	1.15	3 (6%)
2	NAI	С	401	-	42,48,48	1.00	3 (7%)	47,73,73	1.18	4 (8%)
3	PG4	A	402	-	12,12,12	0.16	0	11,11,11	0.19	0
4	8S0	В	402	-	12,12,12	1.46	2 (16%)	15,17,17	0.99	1 (6%)
4	8S0	С	402	-	12,12,12	1.52	2 (16%)	15,17,17	1.24	2 (13%)
2	NAI	A	401	-	42,48,48	0.99	2 (4%)	47,73,73	1.15	3 (6%)
4	8S0	A	403	-	12,12,12	1.44	1 (8%)	15,17,17	1.03	0
4	8S0	D	403	-	12,12,12	1.64	3 (25%)	15,17,17	1.31	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PG4	D	402	-	-	6/10/10/10	-
2	NAI	В	401	-	-	3/25/72/72	0/5/5/5
2	NAI	D	401	-	-	7/25/72/72	0/5/5/5
2	NAI	С	401	-	-	3/25/72/72	0/5/5/5
3	PG4	A	402	-	-	6/10/10/10	-
4	8S0	В	402	-	-	0/2/22/22	0/1/1/1
4	8S0	С	402	-	-	0/2/22/22	0/1/1/1
2	NAI	A	401	-	-	5/25/72/72	0/5/5/5
4	8S0	A	403	-	=	0/2/22/22	0/1/1/1
4	8S0	D	403	-	-	0/2/22/22	0/1/1/1

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$Ideal(\AA)$
4	A	403	8S0	C2-C1	-3.88	1.43	1.52
2	D	401	NAI	C6N-C5N	3.80	1.40	1.33
4	В	402	8S0	C2-C1	-3.57	1.44	1.52
2	В	401	NAI	C6N-C5N	3.44	1.39	1.33
4	С	402	8S0	C2-C1	-3.43	1.44	1.52
2	A	401	NAI	C6N-C5N	3.34	1.39	1.33
2	С	401	NAI	C6N-C5N	3.32	1.39	1.33
4	D	403	8S0	C2-C1	-3.17	1.45	1.52
4	D	403	8S0	O5-C1	3.03	1.39	1.34
4	С	402	8S0	O5-C1	2.89	1.39	1.34
4	D	403	8S0	C3-C2	-2.82	1.48	1.53
2	D	401	NAI	C5A-C4A	2.42	1.47	1.40
2	В	401	NAI	C5A-C4A	2.42	1.47	1.40
2	D	401	NAI	C2A-N3A	2.37	1.35	1.32
2	A	401	NAI	C2A-N3A	2.23	1.35	1.32
4	В	402	8S0	O5-C1	2.19	1.38	1.34
2	С	401	NAI	C5A-C4A	2.16	1.46	1.40
2	С	401	NAI	C2A-N3A	2.02	1.35	1.32

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}(^{o})$
2	С	401	NAI	N3A-C2A-N1A	-4.04	122.36	128.68
4	D	403	8S0	O2-C2-C3	-3.96	102.35	110.53
2	В	401	NAI	N3A-C2A-N1A	-3.94	122.53	128.68
2	D	401	NAI	N3A-C2A-N1A	-3.83	122.70	128.68
2	A	401	NAI	N3A-C2A-N1A	-3.76	122.80	128.68
4	С	402	8S0	O2-C2-C3	-3.26	103.81	110.53



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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
2	В	401	NAI	C1D-N1N-C2N	-2.47	116.99	121.11
2	A	401	NAI	C1B-N9A-C4A	-2.39	122.44	126.64
4	В	402	8S0	O2-C2-C3	-2.35	105.68	110.53
2	D	401	NAI	C2A-N1A-C6A	2.24	122.58	118.75
2	В	401	NAI	PN-O3-PA	-2.19	125.30	132.83
2	С	401	NAI	C1D-N1N-C2N	-2.16	117.52	121.11
2	В	401	NAI	C4A-C5A-N7A	-2.15	107.16	109.40
2	С	401	NAI	C4A-C5A-N7A	-2.14	107.17	109.40
2	A	401	NAI	C1D-N1N-C2N	-2.13	117.56	121.11
2	С	401	NAI	PN-O3-PA	-2.10	125.62	132.83
4	С	402	8S0	C3-C4-C5	-2.08	106.52	110.24
2	D	401	NAI	C1B-N9A-C4A	-2.05	123.04	126.64

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	NAI	PA-O3-PN-O5D
3	A	402	PG4	O2-C3-C4-O3
2	A	401	NAI	O4B-C4B-C5B-O5B
3	D	402	PG4	O1-C1-C2-O2
2	D	401	NAI	PN-O3-PA-O1A
3	D	402	PG4	C8-C7-O4-C6
3	A	402	PG4	C6-C5-O3-C4
2	D	401	NAI	PA-O3-PN-O5D
2	A	401	NAI	C3B-C4B-C5B-O5B
3	D	402	PG4	C4-C3-O2-C2
2	В	401	NAI	O4D-C1D-N1N-C2N
2	С	401	NAI	O4D-C1D-N1N-C2N
2	D	401	NAI	PN-O3-PA-O2A
2	D	401	NAI	O4B-C4B-C5B-O5B
2	A	401	NAI	O4D-C1D-N1N-C2N
2	D	401	NAI	O4D-C1D-N1N-C2N
2	С	401	NAI	C2D-C1D-N1N-C2N
3	D	402	PG4	C6-C5-O3-C4
2	В	401	NAI	C2D-C1D-N1N-C2N
2	A	401	NAI	C2D-C1D-N1N-C2N
3	A	402	PG4	O1-C1-C2-O2
3	A	402	PG4	C8-C7-O4-C6
3	A	402	PG4	O3-C5-C6-O4
3	A	402	PG4	O4-C7-C8-O5
2	D	401	NAI	C5B-O5B-PA-O1A



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Mol	Chain	Res	Type	Atoms
2	В	401	NAI	O4B-C4B-C5B-O5B
2	С	401	NAI	O4B-C4B-C5B-O5B
3	D	402	PG4	C3-C4-O3-C5
2	D	401	NAI	C2D-C1D-N1N-C2N
3	D	402	PG4	O3-C5-C6-O4

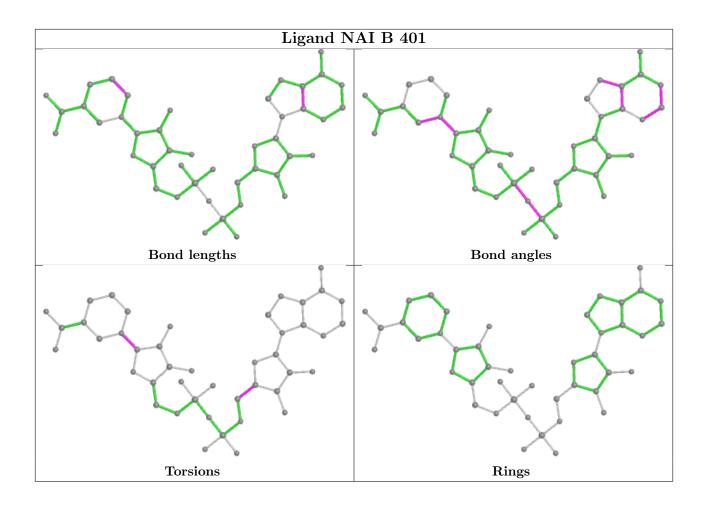
There are no ring outliers.

4 monomers are involved in 9 short contacts:

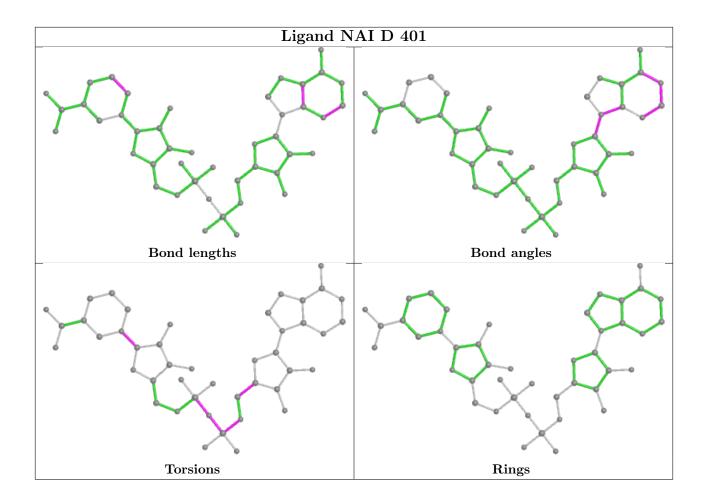
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	402	PG4	6	0
2	D	401	NAI	1	0
3	A	402	PG4	1	0
2	A	401	NAI	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

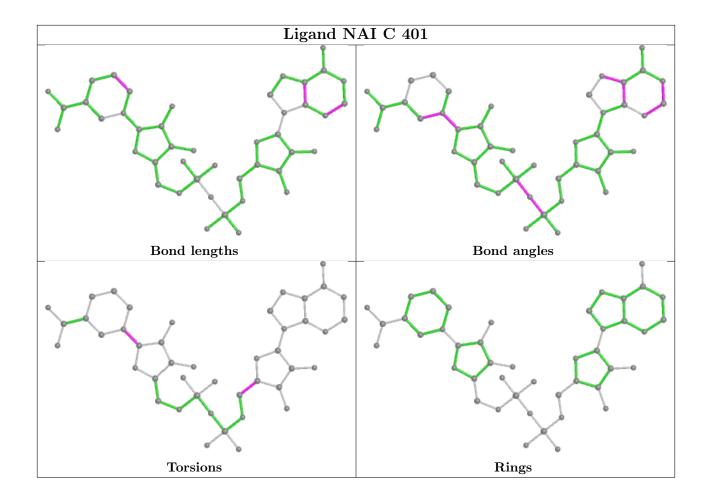




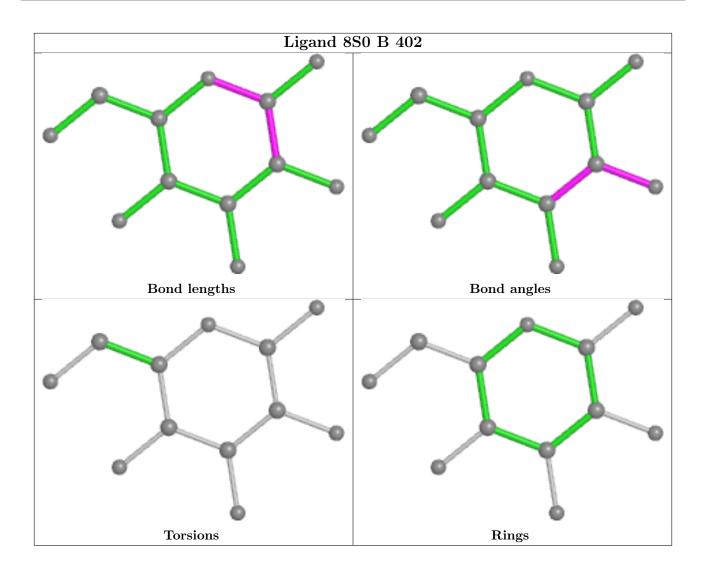




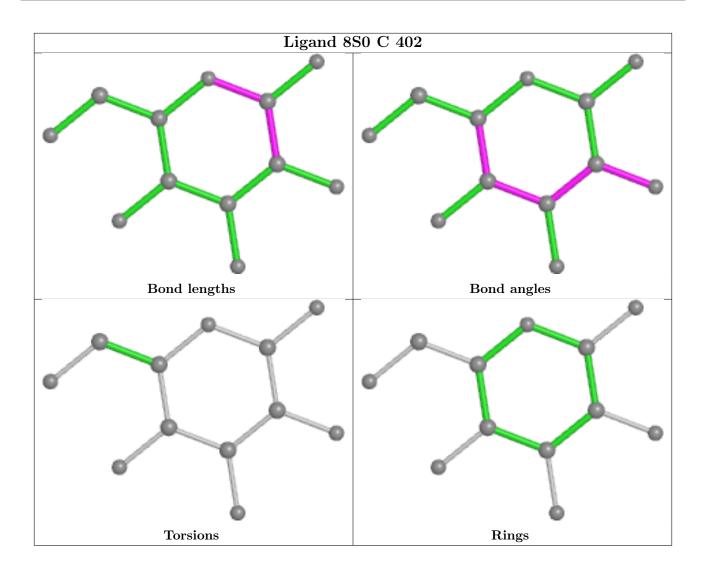




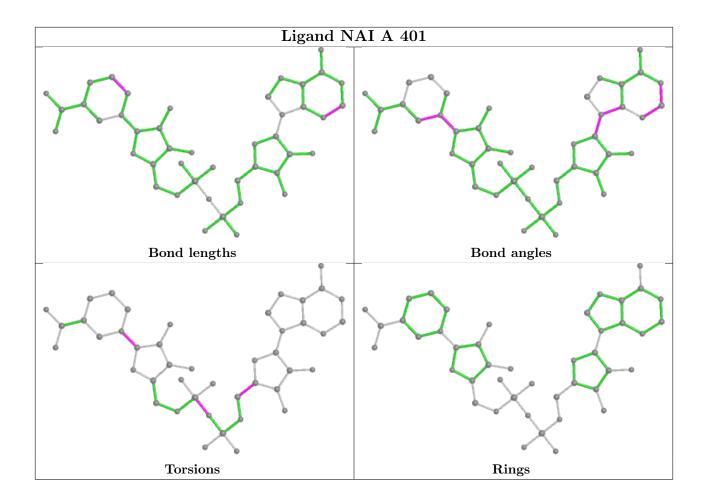




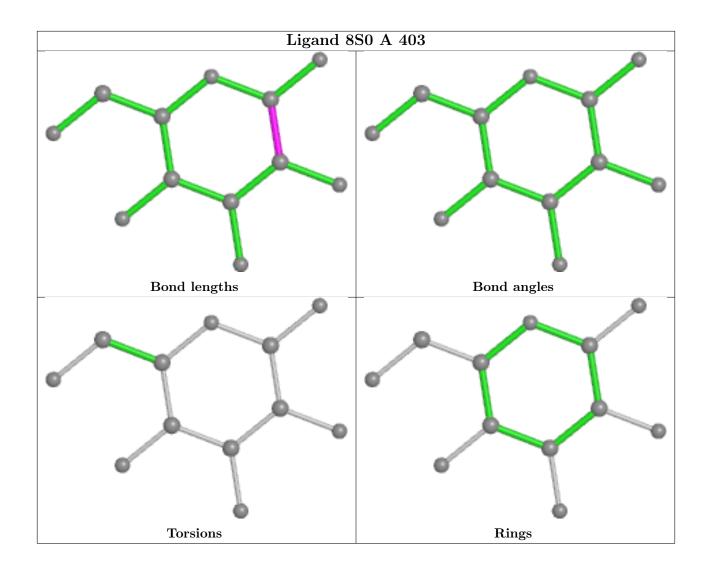




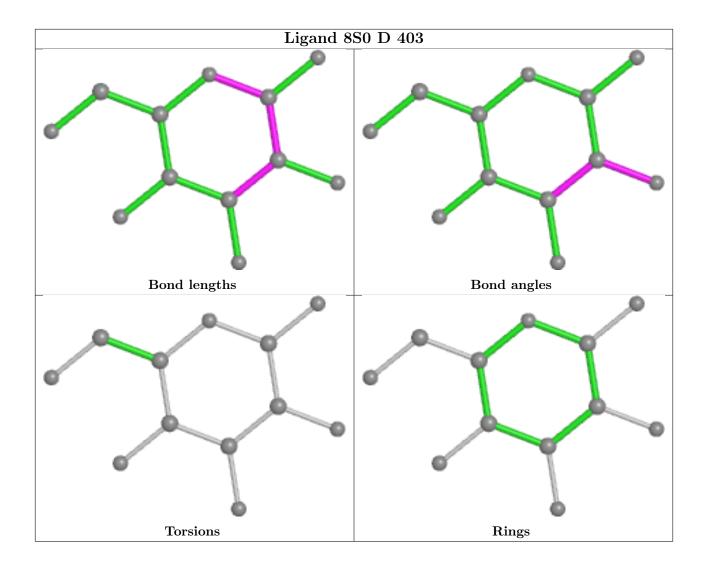












5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ>2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<rsrz></rsrz>	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q < 0.9
1	A	367/380 (96%)	-0.12	3 (0%) 86 88	11, 16, 27, 42	0
1	В	366/380 (96%)	0.21	17 (4%) 32 31	11, 18, 35, 51	0
1	С	368/380 (96%)	0.05	10 (2%) 54 55	11, 17, 33, 48	0
1	D	368/380 (96%)	-0.10	5 (1%) 75 79	11, 16, 28, 42	0
All	All	1469/1520 (96%)	0.01	35 (2%) 59 59	11, 17, 32, 51	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	373	LEU	6.1
1	В	177	TRP	5.5
1	В	224	GLN	3.9
1	С	49[A]	ASP	3.8
1	В	49	ASP	3.8
1	С	177	TRP	3.7
1	В	225	GLY	3.2
1	В	65	ALA	2.9
1	В	52	HIS	2.9
1	В	67	TRP	2.8
1	A	340	ARG	2.7
1	В	48	ALA	2.7
1	С	52	HIS	2.6
1	В	47	PRO	2.6
1	D	87	LEU	2.6
1	С	69	GLU	2.5
1	С	68	ARG	2.5
1	D	224	GLN	2.4
1	С	46	MET	2.4
1	В	46	MET	2.4
1	В	64	THR	2.4



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Mol	Chain	Res	Type	RSRZ
1	С	72	SER	2.3
1	В	229	ARG	2.3
1	С	64	THR	2.3
1	В	72	SER	2.3
1	С	126[A]	ASP	2.3
1	A	177	TRP	2.2
1	В	223	HIS	2.2
1	В	127	ARG	2.1
1	D	182	LYS	2.1
1	D	340	ARG	2.1
1	A	6	LYS	2.1
1	В	66	ASP	2.1
1	В	181	ARG	2.0
1	С	123	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

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

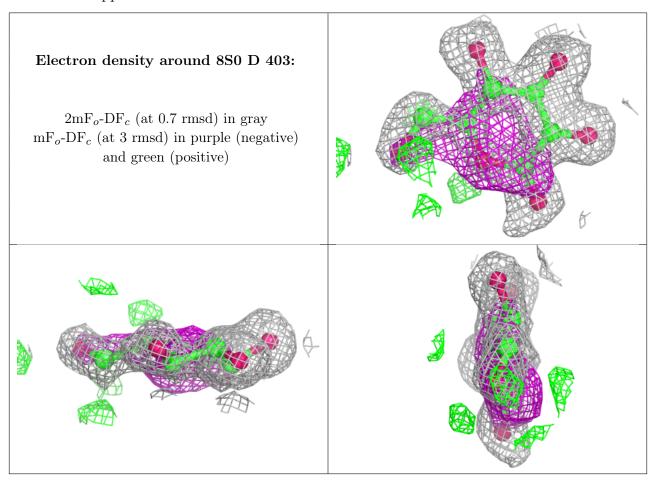
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
4	8S0	D	403	12/12	0.74	0.25	19,25,28,29	0
3	PG4	D	402	13/13	0.81	0.23	35,36,42,43	0
3	PG4	A	402	13/13	0.85	0.13	29,34,38,40	0
2	NAI	В	401	44/44	0.85	0.16	18,26,31,32	0
2	NAI	D	401	44/44	0.85	0.23	24,26,34,36	0
4	8S0	С	402	12/12	0.87	0.21	22,24,27,28	0
2	NAI	С	401	44/44	0.89	0.14	18,23,28,28	0
2	NAI	A	401	44/44	0.89	0.12	16,19,27,33	0
4	8S0	В	402	12/12	0.91	0.18	22,23,25,27	0



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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
4	8S0	A	403	12/12	0.92	0.11	18,20,23,26	0

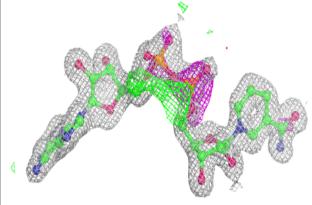
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

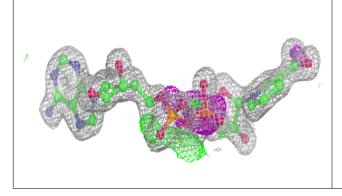


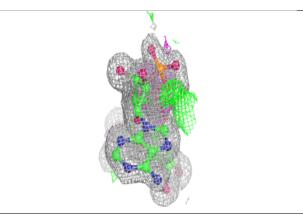


Electron density around NAI B 401:

 $2 {\rm mF}_o\text{-}{\rm DF}_c$ (at 0.7 rmsd) in gray ${\rm mF}_o\text{-}{\rm DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

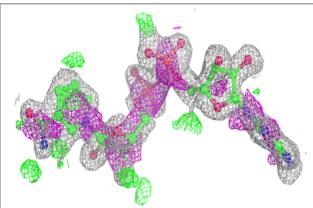


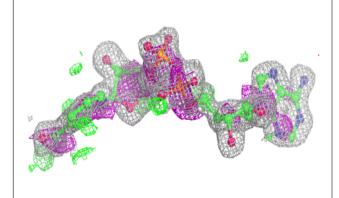


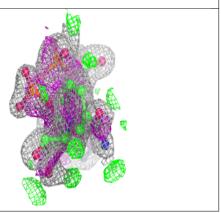


Electron density around NAI D 401:

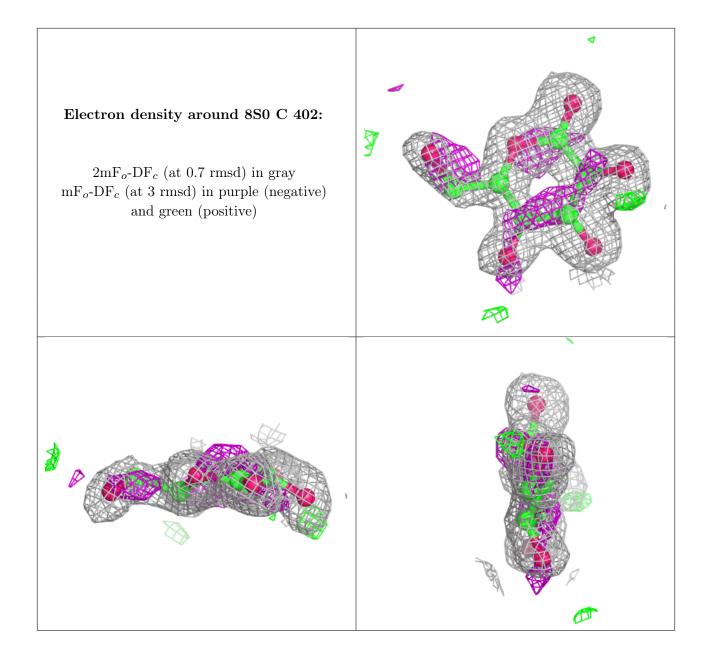
 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)







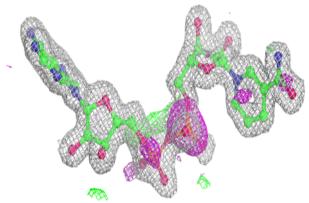


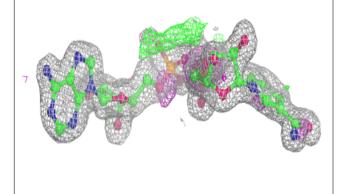


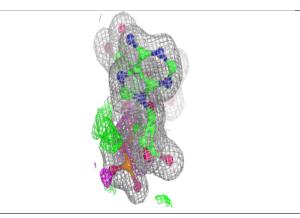


Electron density around NAI C 401:

 $2 {\rm mF}_o\text{-}{\rm DF}_c$ (at 0.7 rmsd) in gray ${\rm mF}_o\text{-}{\rm DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

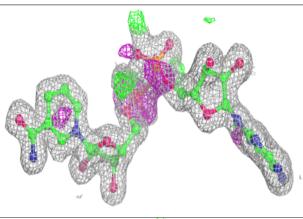


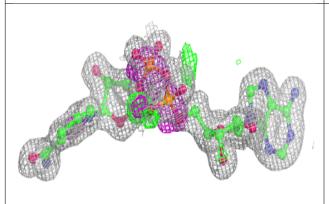


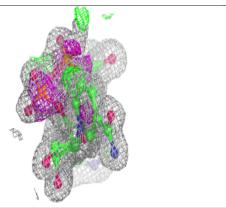


Electron density around NAI A 401:

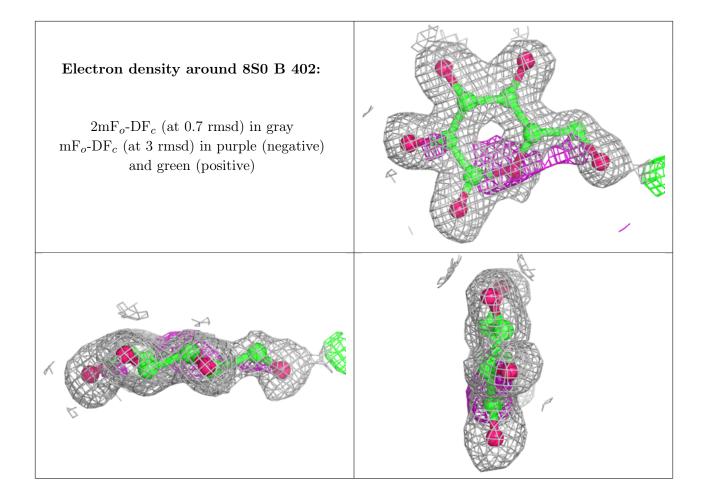
 $2 \mathrm{mF}_o\text{-DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)



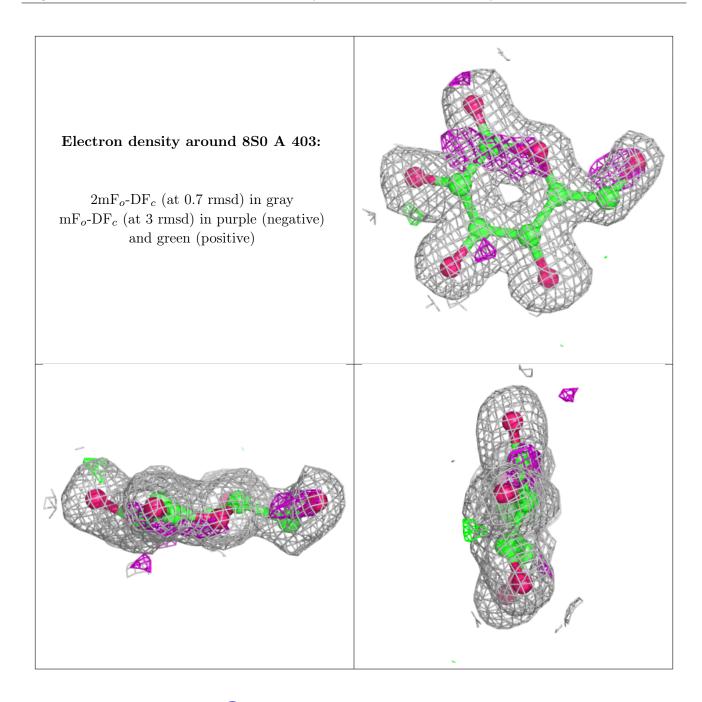












6.5 Other polymers (i)

There are no such residues in this entry.

