



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:53 AM UTC

PDB ID : 9W5X / pdb_00009w5x
Title : Crystal structure of Namat in complex with nicotinamide
Authors : Bao, H.; Xu, L.
Deposited on : 2025-08-02
Resolution : 2.40 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

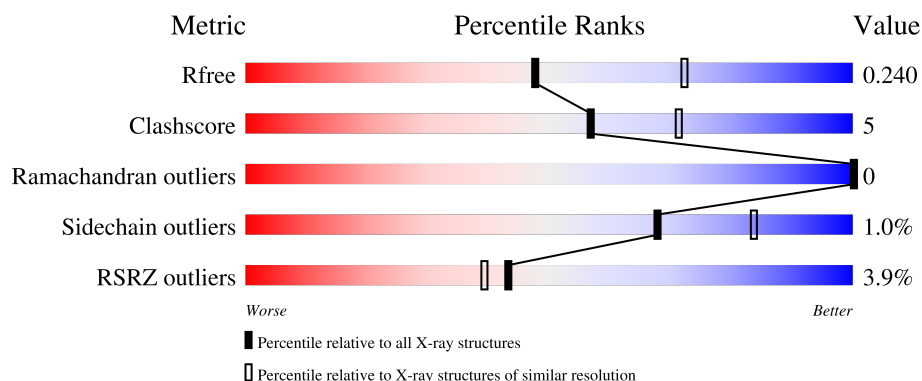
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	491	2% 89% 10% .
1	B	491	5% 85% 14% .
1	C	491	4% 83% 15% .
1	D	491	4% 91% 9% .

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
2	GOL	C	502	-	-	X	-

2 Entry composition [i](#)

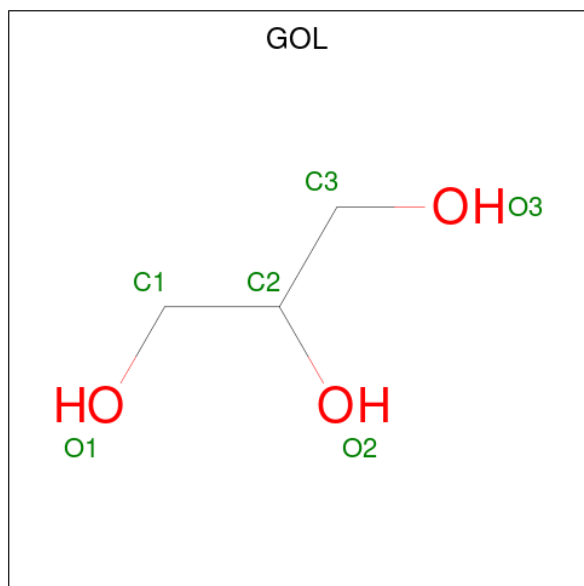
There are 5 unique types of molecules in this entry. The entry contains 16323 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Nicotinamide phosphoribosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	482	Total	C	N	O	S	0	0	0
			3863	2482	629	740	12			
1	B	484	Total	C	N	O	S	0	0	0
			3880	2492	632	744	12			
1	C	486	Total	C	N	O	S	0	0	0
			3893	2499	634	748	12			
1	D	489	Total	C	N	O	S	0	0	0
			3916	2513	638	752	13			

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



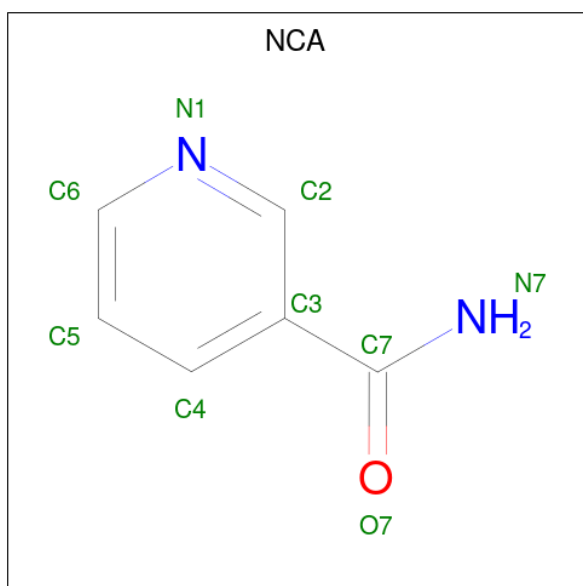
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		

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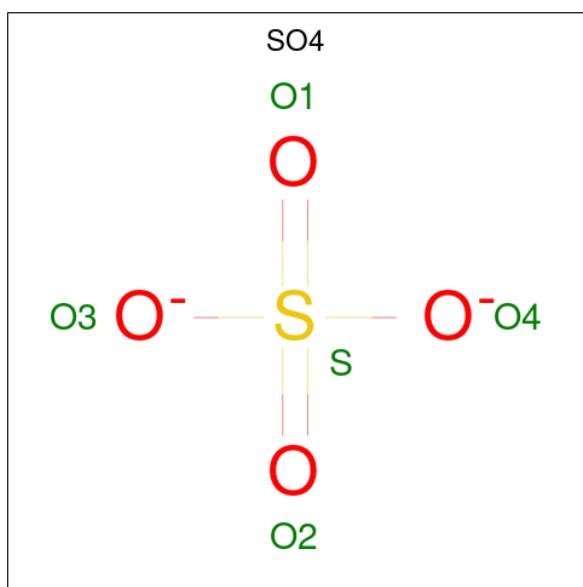
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is NICOTINAMIDE (CCD ID: NCA) (formula: $C_6H_6N_2O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			9	6	2	1		
3	B	1	Total	C	N	O	0	0
			9	6	2	1		
3	C	1	Total	C	N	O	0	0
			9	6	2	1		
3	D	1	Total	C	N	O	0	0
			9	6	2	1		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		

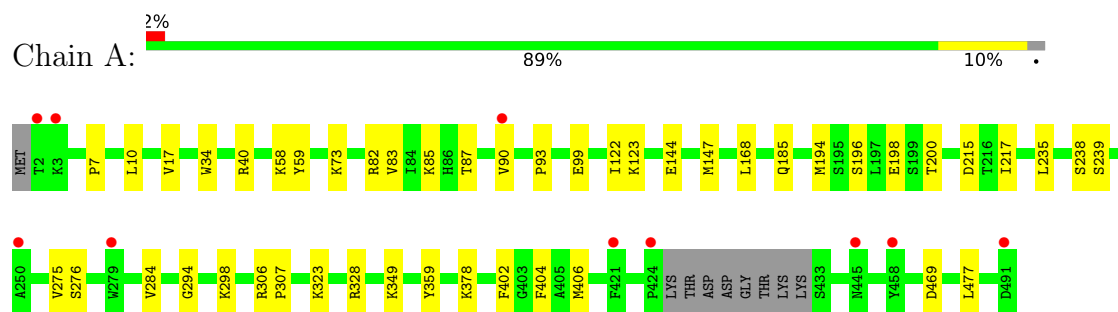
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	173	Total	O	0	0
			173	173		
5	B	134	Total	O	0	0
			134	134		
5	C	128	Total	O	0	0
			128	128		
5	D	175	Total	O	0	0
			175	175		

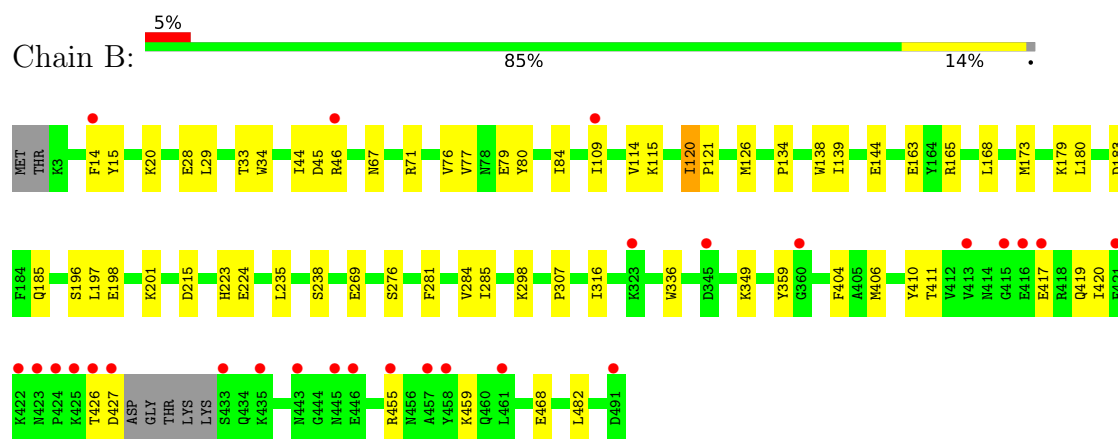
3 Residue-property plots [i](#)

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.

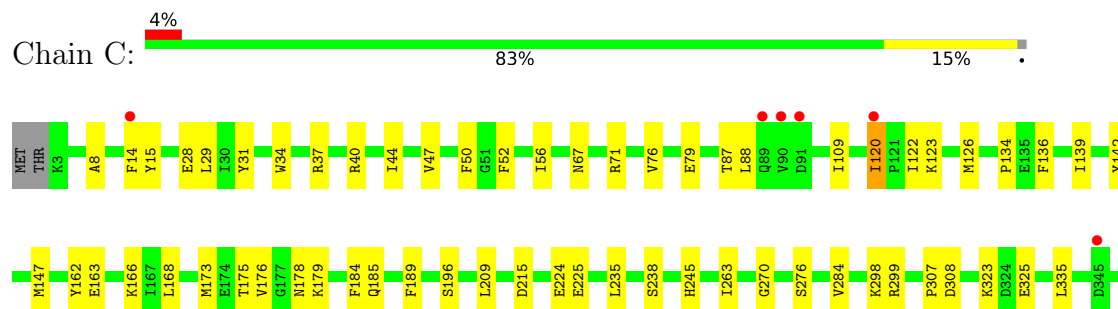
- Molecule 1: Nicotinamide phosphoribosyltransferase

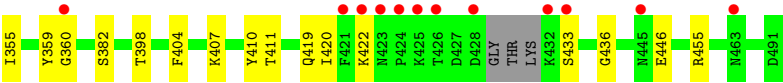


- Molecule 1: Nicotinamide phosphoribosyltransferase

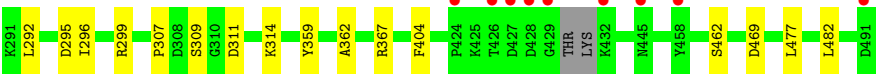
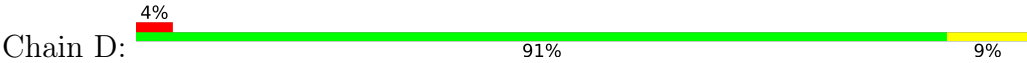


- Molecule 1: Nicotinamide phosphoribosyltransferase





● Molecule 1: Nicotinamide phosphoribosyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	64.06Å 104.74Å 119.67Å 109.31° 101.55° 89.97°	Depositor
Resolution (Å)	38.79 – 2.40 38.79 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.6 (38.79-2.40) 97.6 (38.79-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 2.39Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.223 , 0.240 0.224 , 0.240	Depositor DCC
R_{free} test set	5320 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å ²)	28.0	Xtriage
Anisotropy	0.251	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	16323	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.83% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, SO4, NCA

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	0.15	0/3948	0.39	0/5352
1	B	0.14	0/3965	0.37	0/5374
1	C	0.15	0/3978	0.37	0/5392
1	D	0.15	0/4001	0.40	0/5421
All	All	0.15	0/15892	0.39	0/21539

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	3863	0	3818	31	0
1	B	3880	0	3835	45	0
1	C	3893	0	3841	54	0
1	D	3916	0	3874	23	0
2	A	6	0	8	0	0
2	C	18	0	24	6	0
2	D	6	0	8	0	0
3	A	9	0	6	1	0
3	B	9	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	9	0	6	0	0
3	D	9	0	6	0	0
4	A	30	0	0	0	0
4	B	20	0	0	0	0
4	C	15	0	0	0	0
4	D	30	0	0	0	0
5	A	173	0	0	1	0
5	B	134	0	0	0	0
5	C	128	0	0	1	0
5	D	175	0	0	0	0
All	All	16323	0	15432	142	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (142) 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:173:MET:HE2	1:B:179:LYS:HD3	1.62	0.82
1:B:34:TRP:HE3	1:B:406:MET:HG3	1.47	0.78
1:C:175:THR:HG21	1:C:382:SER:H	1.54	0.72
1:C:120:ILE:HD13	1:C:126:MET:HB3	1.73	0.69
1:B:411:THR:HG22	1:B:420:ILE:HD11	1.76	0.68
1:A:144:GLU:HG2	1:A:406:MET:HG2	1.76	0.67
1:B:114:VAL:HG11	1:B:120:ILE:HD11	1.77	0.67
1:B:144:GLU:HG2	1:B:406:MET:HE2	1.77	0.66
1:C:270:GLY:O	1:C:299:ARG:NH2	2.25	0.65
1:C:122:ILE:HG22	1:C:123:LYS:HG3	1.80	0.63
1:C:109:ILE:HD11	1:C:139:ILE:HG23	1.81	0.62
1:A:235:LEU:HD11	1:A:238:SER:HB2	1.80	0.62
1:B:34:TRP:CE3	1:B:406:MET:HG3	2.34	0.62
1:A:73:LYS:HD2	1:A:99:GLU:HG2	1.80	0.62
1:B:120:ILE:HG21	1:B:126:MET:HG2	1.83	0.61
1:C:433:SER:HB2	2:C:502:GOL:H12	1.83	0.60
1:A:82:ARG:NH2	1:B:224:GLU:OE2	2.32	0.60
1:B:46:ARG:HG2	1:B:121:PRO:HA	1.84	0.59
1:C:40:ARG:HH11	1:C:40:ARG:HG2	1.68	0.58
1:D:469:ASP:HB3	1:D:477:LEU:HD13	1.85	0.57
1:C:14:PHE:CD2	1:D:217:ILE:HG12	2.40	0.56
1:C:335:LEU:HD22	1:C:355:ILE:HG12	1.87	0.55
1:B:235:LEU:HD11	1:B:238:SER:HB3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:235:LEU:HD11	1:C:238:SER:HB3	1.89	0.55
1:C:14:PHE:HZ	1:C:87:THR:OG1	1.90	0.55
1:C:175:THR:HG23	1:C:176:VAL:HG23	1.89	0.55
1:B:109:ILE:HD11	1:B:139:ILE:HG23	1.89	0.54
1:C:14:PHE:CE1	1:C:88:LEU:HG	2.41	0.54
1:B:168:LEU:HD13	1:B:185:GLN:HB3	1.89	0.54
1:D:76:VAL:O	1:D:79:GLU:HG2	2.07	0.54
1:D:311:ASP:HB3	1:D:314:LYS:HB2	1.90	0.54
1:C:196:SER:HB2	1:D:198:GLU:HG2	1.89	0.54
1:C:37:ARG:HH12	2:C:503:GOL:H2	1.72	0.54
1:A:215:ASP:OD2	3:A:502:NCA:H4	2.08	0.53
1:A:349:LYS:NZ	5:A:606:HOH:O	2.42	0.53
1:C:184:PHE:HE1	1:C:238:SER:OG	1.92	0.52
1:C:31:TYR:HB3	1:C:410:TYR:HB3	1.91	0.52
1:B:276:SER:HB3	1:B:284:VAL:HG11	1.92	0.52
1:D:223:HIS:CE1	1:D:482:LEU:HD13	2.44	0.52
1:A:294:GLY:O	1:A:298:LYS:HG3	2.09	0.52
1:C:168:LEU:HD13	1:C:185:GLN:HB3	1.90	0.52
1:D:34:TRP:CH2	1:D:404:PHE:HB3	2.44	0.52
1:D:235:LEU:HD11	1:D:238:SER:HB3	1.92	0.52
1:A:217:ILE:HG12	1:B:14:PHE:CE2	2.44	0.52
1:B:165:ARG:NH1	1:B:183:ASP:OD1	2.39	0.51
1:B:316:ILE:HD11	1:B:359:TYR:HB2	1.92	0.51
1:A:122:ILE:HG22	1:A:123:LYS:HD2	1.93	0.50
1:C:433:SER:CB	2:C:502:GOL:H12	2.41	0.50
1:C:419:GLN:HG2	1:C:436:GLY:N	2.27	0.50
1:D:307:PRO:HG2	1:D:359:TYR:CD2	2.46	0.50
1:D:109:ILE:HD11	1:D:139:ILE:HG23	1.93	0.50
1:C:14:PHE:HE1	1:C:88:LEU:HG	1.77	0.49
1:C:323:LYS:NZ	5:C:605:HOH:O	2.44	0.49
1:B:411:THR:CG2	1:B:420:ILE:HD11	2.43	0.49
1:C:76:VAL:O	1:C:79:GLU:HG2	2.13	0.49
1:A:276:SER:HB3	1:A:284:VAL:HG11	1.95	0.49
1:C:422:LYS:H	2:C:502:GOL:H11	1.77	0.49
1:B:307:PRO:HG2	1:B:359:TYR:CD2	2.49	0.48
1:D:73:LYS:HD2	1:D:99:GLU:HG3	1.96	0.48
1:D:277:ASP:OD2	1:D:309:SER:OG	2.32	0.48
1:B:223:HIS:CE1	1:B:482:LEU:HD13	2.49	0.47
1:B:298:LYS:HB3	1:B:298:LYS:HE3	1.66	0.47
1:C:8:ALA:O	1:C:142:TYR:OH	2.30	0.47
1:A:198:GLU:HG2	1:B:196:SER:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:LYS:HD2	1:B:138:TRP:CD1	2.50	0.47
1:A:215:ASP:OD1	1:A:239:SER:OG	2.34	0.46
1:C:225:GLU:OE1	1:D:6:TYR:OH	2.27	0.46
1:C:136:PHE:O	1:C:139:ILE:HG22	2.15	0.46
1:C:307:PRO:HG2	1:C:359:TYR:CD2	2.49	0.46
1:A:34:TRP:CH2	1:A:404:PHE:HB3	2.51	0.46
1:A:90:VAL:HG23	1:A:93:PRO:HG3	1.98	0.46
1:C:420:ILE:HG23	1:D:249:CYS:HB3	1.98	0.46
1:D:85:LYS:HG3	1:D:90:VAL:O	2.16	0.46
1:C:455:ARG:HD3	1:C:455:ARG:HA	1.67	0.46
1:C:276:SER:HB3	1:C:284:VAL:HG11	1.97	0.46
1:C:407:LYS:HE2	2:C:502:GOL:O2	2.16	0.46
1:B:455:ARG:HA	1:B:455:ARG:HD3	1.69	0.46
1:C:173:MET:HE3	1:C:179:LYS:HD3	1.98	0.46
1:C:224:GLU:OE2	1:D:82:ARG:NH2	2.41	0.46
1:A:58:LYS:HD3	1:A:59:TYR:CE2	2.51	0.45
1:D:295:ASP:O	1:D:299:ARG:HG3	2.16	0.45
1:A:307:PRO:HG2	1:A:359:TYR:CD2	2.52	0.44
1:B:179:LYS:HE2	1:B:179:LYS:HB2	1.88	0.44
1:C:29:LEU:O	1:C:411:THR:HA	2.17	0.44
1:B:426:THR:O	1:B:427:ASP:HB2	2.16	0.44
1:A:323:LYS:O	1:A:328:ARG:NH2	2.51	0.44
1:A:147:MET:HG2	1:A:406:MET:HE1	1.98	0.44
1:A:168:LEU:HD13	1:A:185:GLN:HB3	2.00	0.44
1:B:33:THR:O	1:B:406:MET:HA	2.17	0.44
1:B:281:PHE:O	1:B:285:ILE:HG12	2.17	0.44
1:B:336:TRP:CE2	1:B:349:LYS:HD3	2.52	0.44
1:C:325:GLU:H	1:C:325:GLU:HG3	1.62	0.44
1:A:40:ARG:HG2	1:A:40:ARG:HH11	1.83	0.44
1:B:420:ILE:N	1:B:420:ILE:HD12	2.33	0.44
1:B:34:TRP:CH2	1:B:404:PHE:HB3	2.53	0.44
1:D:263:ILE:HG13	1:D:264:THR:HG23	2.00	0.44
1:A:7:PRO:HG2	1:A:10:LEU:HD12	2.01	0.43
1:D:83:VAL:O	1:D:87:THR:HG23	2.17	0.43
1:A:215:ASP:HA	1:B:14:PHE:HD2	1.84	0.43
1:B:45:ASP:OD1	1:B:45:ASP:N	2.49	0.43
1:C:28:GLU:O	1:C:134:PRO:HA	2.17	0.43
1:C:162:TYR:CE2	1:C:166:LYS:HG3	2.54	0.43
1:B:44:ILE:HD11	1:B:163:GLU:HG2	2.01	0.43
1:C:14:PHE:CZ	1:C:87:THR:OG1	2.71	0.43
1:A:196:SER:HB2	1:B:198:GLU:HG2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:76:VAL:O	1:B:79:GLU:HG2	2.19	0.43
1:C:34:TRP:CH2	1:C:404:PHE:HB3	2.54	0.43
1:B:197:LEU:HG	1:B:201:LYS:HE3	1.99	0.43
1:C:67:ASN:O	1:C:71:ARG:HD3	2.18	0.43
1:C:50:PHE:CD1	1:C:209:LEU:HD11	2.54	0.43
1:A:275:VAL:HA	1:A:306:ARG:O	2.19	0.42
1:A:217:ILE:HG12	1:B:14:PHE:CD2	2.54	0.42
1:B:80:TYR:O	1:B:84:ILE:HG12	2.19	0.42
1:A:83:VAL:O	1:A:87:THR:OG1	2.30	0.42
1:C:298:LYS:HA	1:C:298:LYS:HD2	1.85	0.42
1:B:410:TYR:OH	1:B:417:GLU:HG2	2.20	0.42
1:B:455:ARG:O	1:B:459:LYS:HG3	2.19	0.42
1:A:469:ASP:HB3	1:A:477:LEU:HD13	2.03	0.41
1:C:263:ILE:O	1:C:299:ARG:HD2	2.20	0.41
1:A:402:PHE:HB2	1:A:404:PHE:CE2	2.56	0.41
1:B:419:GLN:C	1:B:420:ILE:HD12	2.45	0.41
1:B:29:LEU:O	1:B:411:THR:HA	2.21	0.41
1:C:245:HIS:HE1	1:C:308:ASP:OD2	2.02	0.41
1:B:67:ASN:O	1:B:71:ARG:HD3	2.20	0.41
1:B:115:LYS:NZ	1:B:468:GLU:OE2	2.43	0.41
1:C:147:MET:HE2	1:C:147:MET:HB2	1.83	0.41
1:C:179:LYS:HE2	1:C:179:LYS:HB2	1.86	0.41
1:D:290:ARG:HH11	1:D:290:ARG:HG3	1.85	0.41
1:A:378:LYS:HE3	1:A:378:LYS:HB3	1.80	0.41
1:A:194:MET:HG3	1:A:200:THR:HA	2.03	0.41
1:C:29:LEU:O	1:C:411:THR:HG23	2.21	0.41
1:C:173:MET:HE1	1:C:178:ASN:HA	2.03	0.41
1:A:85:LYS:HG3	1:A:90:VAL:O	2.21	0.41
1:D:292:LEU:O	1:D:296:ILE:HG13	2.21	0.41
1:C:189:PHE:CE2	1:C:360:GLY:HA3	2.56	0.40
1:C:323:LYS:N	1:C:323:LYS:HD2	2.35	0.40
1:D:73:LYS:O	1:D:77:VAL:HG23	2.21	0.40
1:C:398:THR:OG1	2:C:501:GOL:H11	2.21	0.40
1:B:28:GLU:O	1:B:134:PRO:HA	2.22	0.40
1:C:44:ILE:HD11	1:C:163:GLU:HG2	2.02	0.40
1:C:52:PHE:O	1:C:56:ILE:HG13	2.21	0.40
1:D:362:ALA:HB1	1:D:367:ARG:NH1	2.37	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	478/491 (97%)	471 (98%)	7 (2%)	0	100	100
1	B	480/491 (98%)	470 (98%)	10 (2%)	0	100	100
1	C	482/491 (98%)	474 (98%)	8 (2%)	0	100	100
1	D	485/491 (99%)	473 (98%)	12 (2%)	0	100	100
All	All	1925/1964 (98%)	1888 (98%)	37 (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	427/435 (98%)	426 (100%)	1 (0%)	87	94
1	B	429/435 (99%)	423 (99%)	6 (1%)	59	79
1	C	430/435 (99%)	425 (99%)	5 (1%)	63	81
1	D	433/435 (100%)	427 (99%)	6 (1%)	59	79
All	All	1719/1740 (99%)	1701 (99%)	18 (1%)	68	84

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	VAL
1	B	15	TYR

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Mol	Chain	Res	Type
1	B	77	VAL
1	B	120	ILE
1	B	180	LEU
1	B	215	ASP
1	B	269	GLU
1	C	15	TYR
1	C	47	VAL
1	C	120	ILE
1	C	215	ASP
1	C	446	GLU
1	D	14	PHE
1	D	15	TYR
1	D	91	ASP
1	D	109	ILE
1	D	215	ASP
1	D	462	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	149	ASN
1	A	233	ASN
1	A	460	GLN
1	B	475	GLN
1	C	74	GLN
1	C	89	GLN
1	C	253	GLN
1	C	423	ASN
1	C	442	ASN
1	D	86	HIS
1	D	185	GLN
1	D	233	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

28 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	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	SO4	A	504	-	4,4,4	0.24	0	6,6,6	0.08	0
4	SO4	C	505	-	4,4,4	0.22	0	6,6,6	0.09	0
4	SO4	D	503	-	4,4,4	0.24	0	6,6,6	0.07	0
4	SO4	A	507	-	4,4,4	0.23	0	6,6,6	0.10	0
4	SO4	D	506	-	4,4,4	0.23	0	6,6,6	0.08	0
4	SO4	B	505	-	4,4,4	0.23	0	6,6,6	0.07	0
4	SO4	B	503	-	4,4,4	0.23	0	6,6,6	0.08	0
2	GOL	C	501	-	5,5,5	0.78	0	5,5,5	0.98	0
3	NCA	D	502	-	9,9,9	2.85	4 (44%)	11,11,11	1.35	2 (18%)
4	SO4	B	504	-	4,4,4	0.24	0	6,6,6	0.08	0
2	GOL	C	503	-	5,5,5	0.86	0	5,5,5	1.08	0
2	GOL	A	501	-	5,5,5	0.92	0	5,5,5	1.04	0
3	NCA	A	502	-	9,9,9	2.87	4 (44%)	11,11,11	1.29	1 (9%)
2	GOL	C	502	-	5,5,5	0.82	0	5,5,5	0.99	0
3	NCA	B	501	-	9,9,9	2.86	4 (44%)	11,11,11	1.42	2 (18%)
3	NCA	C	504	-	9,9,9	2.81	3 (33%)	11,11,11	1.92	5 (45%)
4	SO4	A	503	-	4,4,4	0.22	0	6,6,6	0.13	0
4	SO4	D	508	-	4,4,4	0.24	0	6,6,6	0.08	0
4	SO4	D	504	-	4,4,4	0.25	0	6,6,6	0.08	0
4	SO4	A	508	-	4,4,4	0.23	0	6,6,6	0.08	0
4	SO4	D	505	-	4,4,4	0.23	0	6,6,6	0.12	0
4	SO4	D	507	-	4,4,4	0.25	0	6,6,6	0.07	0
4	SO4	C	507	-	4,4,4	0.25	0	6,6,6	0.09	0
4	SO4	A	506	-	4,4,4	0.21	0	6,6,6	0.16	0
4	SO4	A	505	-	4,4,4	0.22	0	6,6,6	0.09	0
4	SO4	B	502	-	4,4,4	0.22	0	6,6,6	0.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	C	506	-	4,4,4	0.22	0	6,6,6	0.08	0
2	GOL	D	501	-	5,5,5	0.86	0	5,5,5	1.08	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
3	NCA	B	501	-	-	0/4/4/4	0/1/1/1
2	GOL	C	501	-	-	0/4/4/4	-
3	NCA	C	504	-	-	0/4/4/4	0/1/1/1
3	NCA	D	502	-	-	0/4/4/4	0/1/1/1
2	GOL	C	503	-	-	0/4/4/4	-
2	GOL	A	501	-	-	4/4/4/4	-
3	NCA	A	502	-	-	0/4/4/4	0/1/1/1
2	GOL	C	502	-	-	0/4/4/4	-
2	GOL	D	501	-	-	4/4/4/4	-

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	NCA	C7-N7	7.25	1.46	1.33
3	B	501	NCA	C7-N7	7.20	1.46	1.33
3	D	502	NCA	C7-N7	7.14	1.46	1.33
3	C	504	NCA	C7-N7	6.60	1.45	1.33
3	C	504	NCA	C4-C3	-3.62	1.33	1.39
3	C	504	NCA	C3-C7	3.02	1.55	1.50
3	B	501	NCA	C3-C7	2.78	1.54	1.50
3	D	502	NCA	C3-C7	2.66	1.54	1.50
3	D	502	NCA	O7-C7	-2.58	1.19	1.24
3	B	501	NCA	O7-C7	-2.57	1.19	1.24
3	A	502	NCA	O7-C7	-2.57	1.19	1.24
3	A	502	NCA	C3-C7	2.55	1.54	1.50
3	D	502	NCA	C4-C3	-2.31	1.35	1.39
3	A	502	NCA	C4-C3	-2.26	1.36	1.39
3	B	501	NCA	C4-C3	-2.15	1.36	1.39

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	504	NCA	C3-C7-N7	3.23	121.72	117.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	504	NCA	O7-C7-N7	-3.07	118.18	122.62
3	C	504	NCA	C3-C2-N1	-2.76	119.40	123.50
3	B	501	NCA	C3-C2-N1	-2.47	119.83	123.50
3	A	502	NCA	C3-C2-N1	-2.43	119.88	123.50
3	D	502	NCA	C3-C2-N1	-2.38	119.96	123.50
3	C	504	NCA	C6-N1-C2	2.33	120.93	116.85
3	C	504	NCA	C4-C3-C2	2.19	120.05	117.61
3	B	501	NCA	C4-C3-C2	2.19	120.05	117.61
3	D	502	NCA	C4-C3-C2	2.01	119.85	117.61

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	501	GOL	O1-C1-C2-C3
2	A	501	GOL	O1-C1-C2-C3
2	A	501	GOL	C1-C2-C3-O3
2	D	501	GOL	C1-C2-C3-O3
2	A	501	GOL	O1-C1-C2-O2
2	D	501	GOL	O1-C1-C2-O2
2	A	501	GOL	O2-C2-C3-O3
2	D	501	GOL	O2-C2-C3-O3

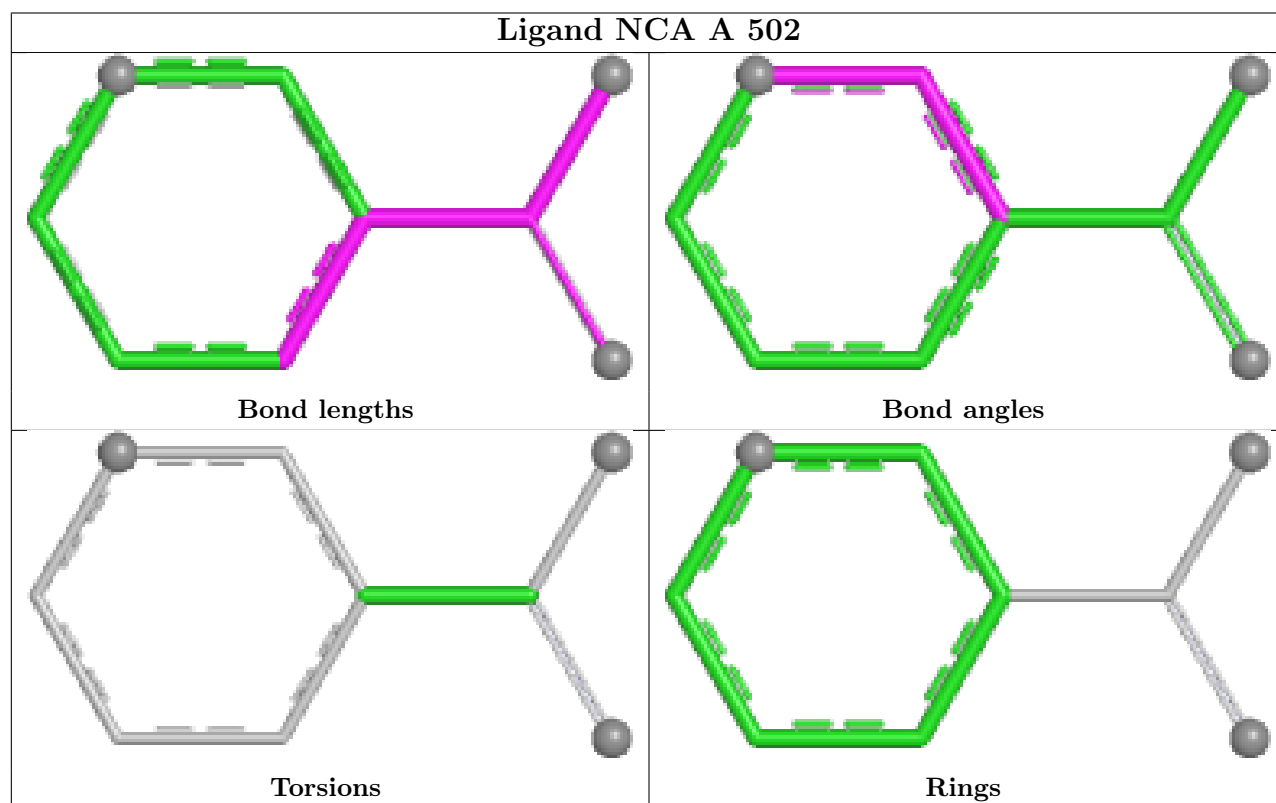
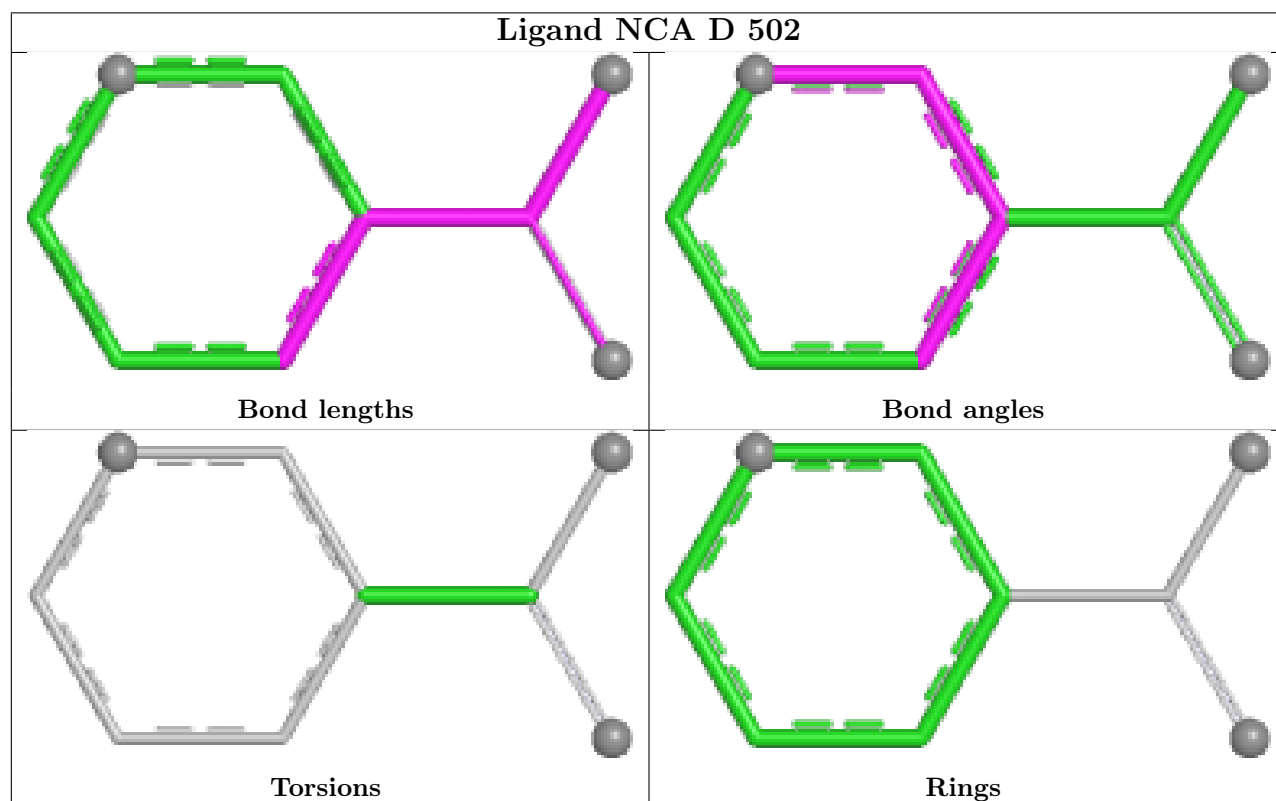
There are no ring outliers.

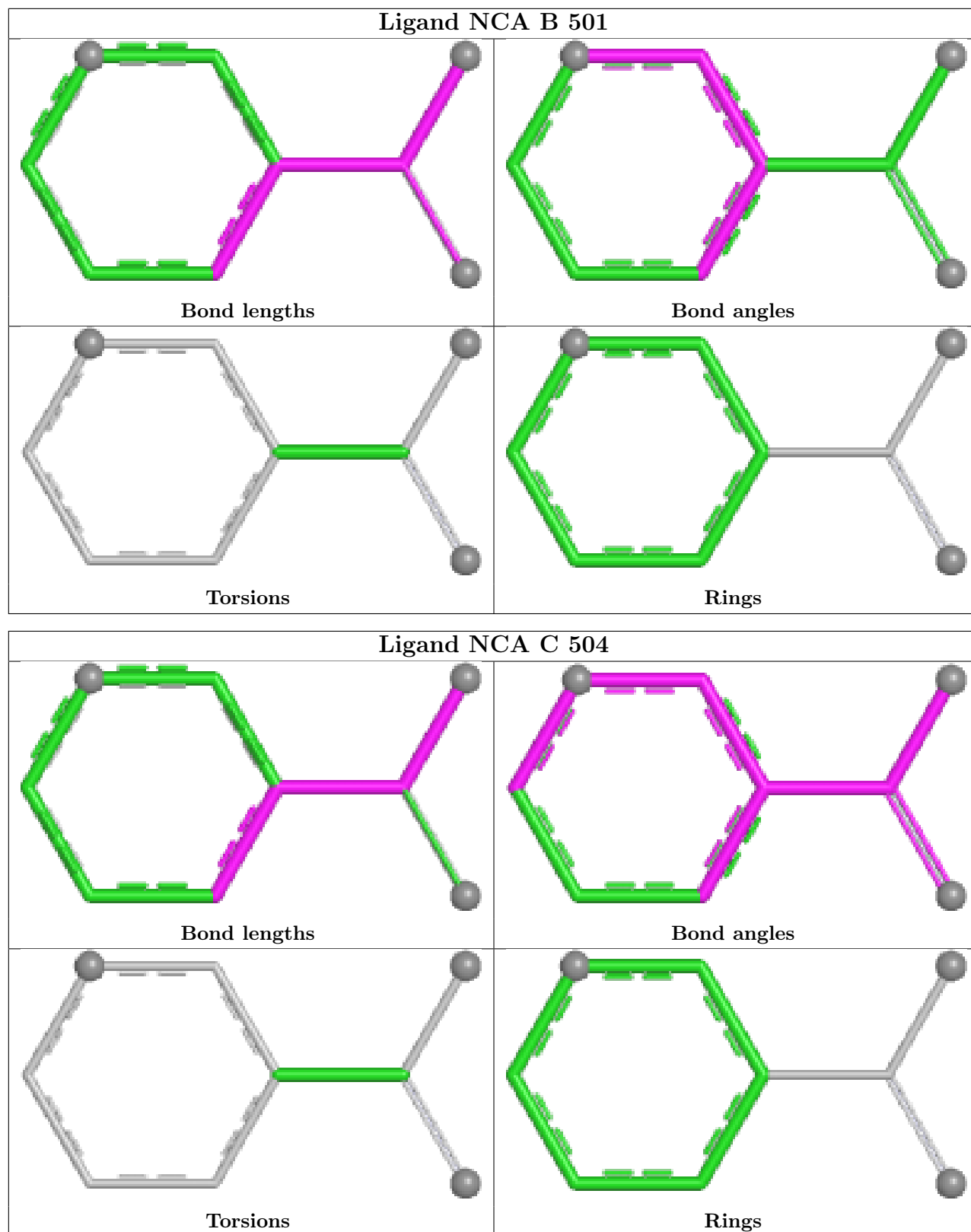
4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501	GOL	1	0
2	C	503	GOL	1	0
3	A	502	NCA	1	0
2	C	502	GOL	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	482/491 (98%)	0.24	10 (2%) 63 59	15, 28, 43, 64	0
1	B	484/491 (98%)	0.43	27 (5%) 30 26	17, 33, 53, 73	0
1	C	486/491 (98%)	0.39	18 (3%) 45 41	18, 34, 56, 89	0
1	D	489/491 (99%)	0.38	20 (4%) 41 37	15, 29, 46, 91	0
All	All	1941/1964 (98%)	0.36	75 (3%) 43 39	15, 31, 51, 91	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	2	THR	7.4
1	A	2	THR	6.6
1	B	423	ASN	5.1
1	D	491	ASP	4.9
1	C	425	LYS	4.6
1	B	421	PHE	4.4
1	D	429	GLY	4.3
1	A	3	LYS	4.0
1	D	3	LYS	4.0
1	C	426	THR	3.9
1	D	426	THR	3.9
1	B	425	LYS	3.7
1	A	424	PRO	3.7
1	D	90	VAL	3.7
1	A	491	ASP	3.6
1	B	360	GLY	3.5
1	C	423	ASN	3.3
1	D	249	CYS	3.3
1	B	445	ASN	3.2
1	D	88	LEU	3.0
1	C	463	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	461	LEU	3.0
1	D	1	MET	3.0
1	C	424	PRO	2.9
1	A	421	PHE	2.9
1	C	433	SER	2.9
1	B	491	ASP	2.9
1	D	424	PRO	2.8
1	C	445	ASN	2.8
1	C	432	LYS	2.8
1	B	323	LYS	2.7
1	B	422	LYS	2.7
1	D	92	ASP	2.7
1	C	14	PHE	2.7
1	B	443	ASN	2.7
1	B	458	TYR	2.7
1	B	417	GLU	2.7
1	C	428	ASP	2.6
1	D	428	ASP	2.6
1	B	426	THR	2.5
1	C	345	ASP	2.5
1	D	14	PHE	2.5
1	B	14	PHE	2.5
1	B	46	ARG	2.5
1	B	415	GLY	2.4
1	B	413	VAL	2.4
1	C	90	VAL	2.4
1	D	432	LYS	2.4
1	B	416	GLU	2.4
1	C	421	PHE	2.3
1	A	90	VAL	2.3
1	D	141	ASN	2.3
1	B	435	LYS	2.3
1	A	458	TYR	2.3
1	A	250	ALA	2.3
1	B	427	ASP	2.3
1	D	445	ASN	2.2
1	C	422	LYS	2.2
1	C	91	ASP	2.2
1	A	445	ASN	2.2
1	C	89	GLN	2.2
1	D	238	SER	2.2
1	D	166	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	120	ILE	2.1
1	B	345	ASP	2.1
1	B	424	PRO	2.1
1	B	457	ALA	2.1
1	D	458	TYR	2.1
1	B	433	SER	2.1
1	A	279	TRP	2.1
1	B	446	GLU	2.1
1	B	455	ARG	2.0
1	B	109	ILE	2.0
1	C	360	GLY	2.0
1	D	427	ASP	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.

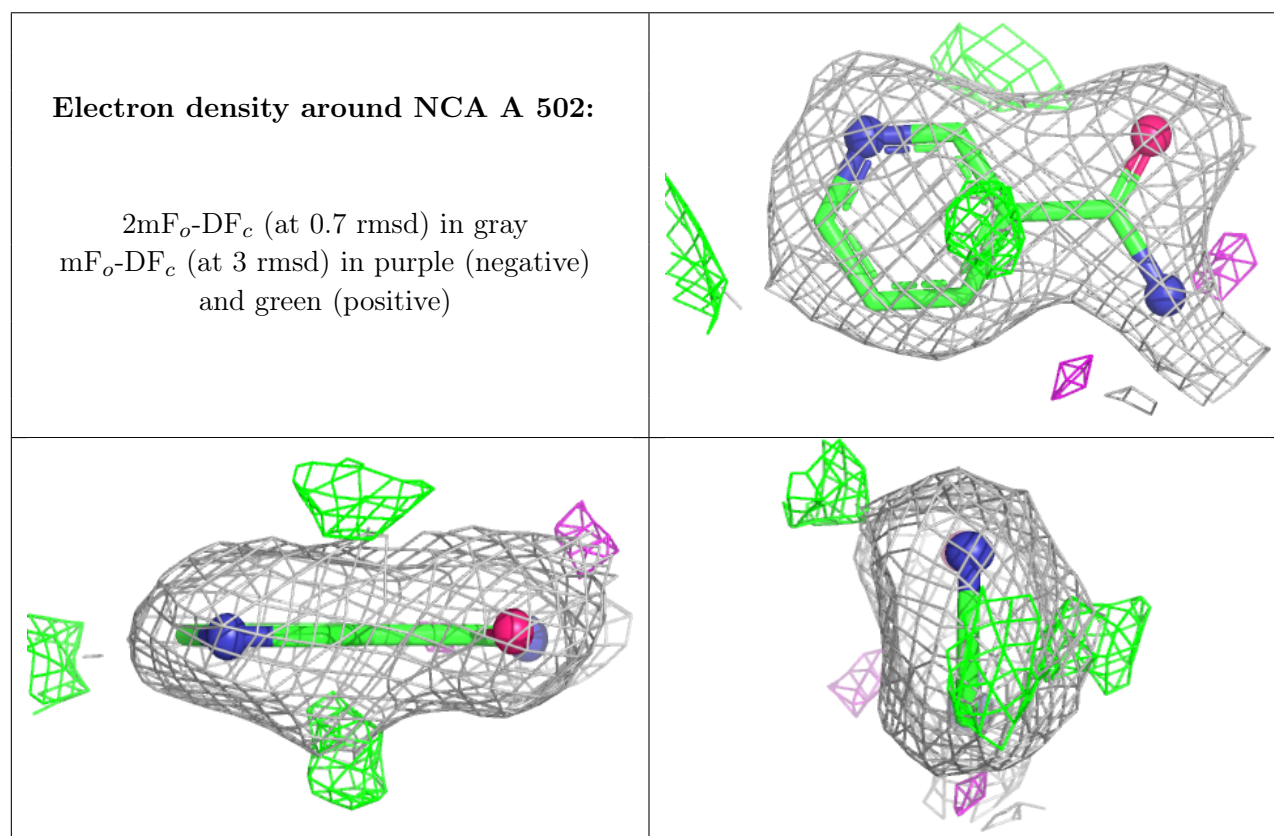
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GOL	C	503	6/6	0.79	0.15	42,46,53,56	0
4	SO4	B	503	5/5	0.80	0.24	52,62,71,80	0
4	SO4	B	505	5/5	0.80	0.18	57,63,71,77	0
4	SO4	A	506	5/5	0.82	0.19	53,55,60,70	0
4	SO4	C	507	5/5	0.82	0.15	56,61,67,71	0
4	SO4	A	504	5/5	0.84	0.15	56,58,71,74	0
2	GOL	A	501	6/6	0.85	0.12	35,37,43,43	0
4	SO4	A	507	5/5	0.86	0.26	35,36,56,57	0
4	SO4	D	505	5/5	0.86	0.17	59,62,69,74	0
4	SO4	D	507	5/5	0.86	0.19	60,61,62,69	0
4	SO4	A	508	5/5	0.87	0.23	40,50,54,71	0

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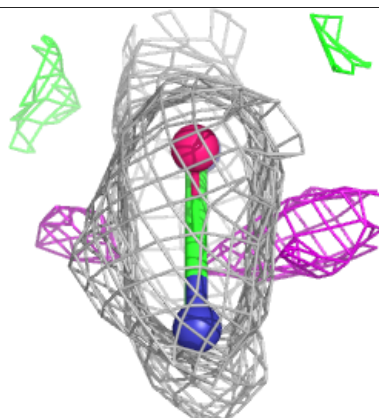
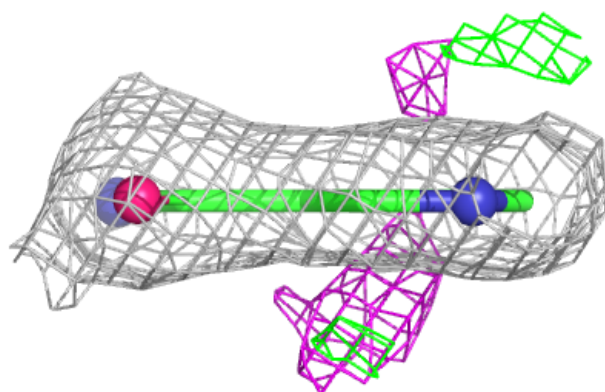
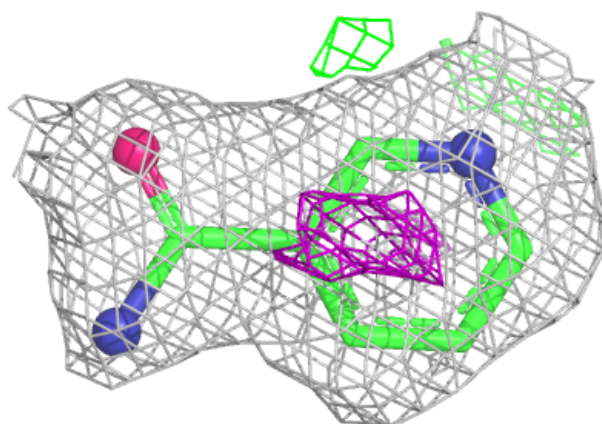
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	SO4	D	504	5/5	0.87	0.27	37,39,48,57	0
2	GOL	D	501	6/6	0.89	0.13	30,34,41,44	0
3	NCA	A	502	9/9	0.90	0.12	24,32,33,38	0
3	NCA	C	504	9/9	0.90	0.14	25,28,30,31	0
2	GOL	C	502	6/6	0.90	0.14	43,54,56,57	0
4	SO4	D	508	5/5	0.90	0.21	42,43,51,61	0
4	SO4	B	504	5/5	0.91	0.23	38,39,46,47	0
3	NCA	D	502	9/9	0.91	0.13	31,31,36,37	0
4	SO4	C	506	5/5	0.91	0.21	37,42,47,54	0
2	GOL	C	501	6/6	0.91	0.10	34,41,45,47	0
4	SO4	D	506	5/5	0.93	0.20	30,33,38,46	0
3	NCA	B	501	9/9	0.93	0.13	27,30,33,36	0
4	SO4	A	505	5/5	0.93	0.19	32,35,41,44	0
4	SO4	C	505	5/5	0.96	0.09	30,30,38,39	0
4	SO4	A	503	5/5	0.96	0.10	34,36,38,49	0
4	SO4	D	503	5/5	0.97	0.07	34,36,38,39	0
4	SO4	B	502	5/5	0.98	0.09	31,34,35,43	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.

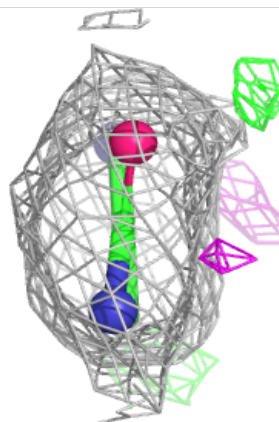
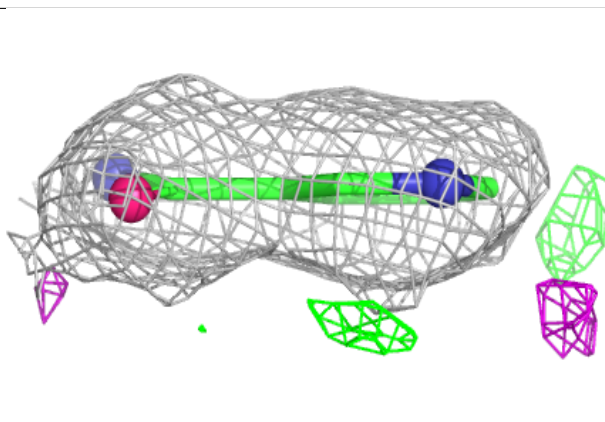
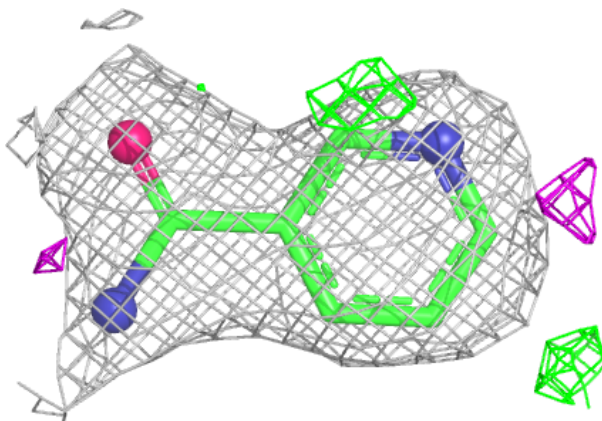


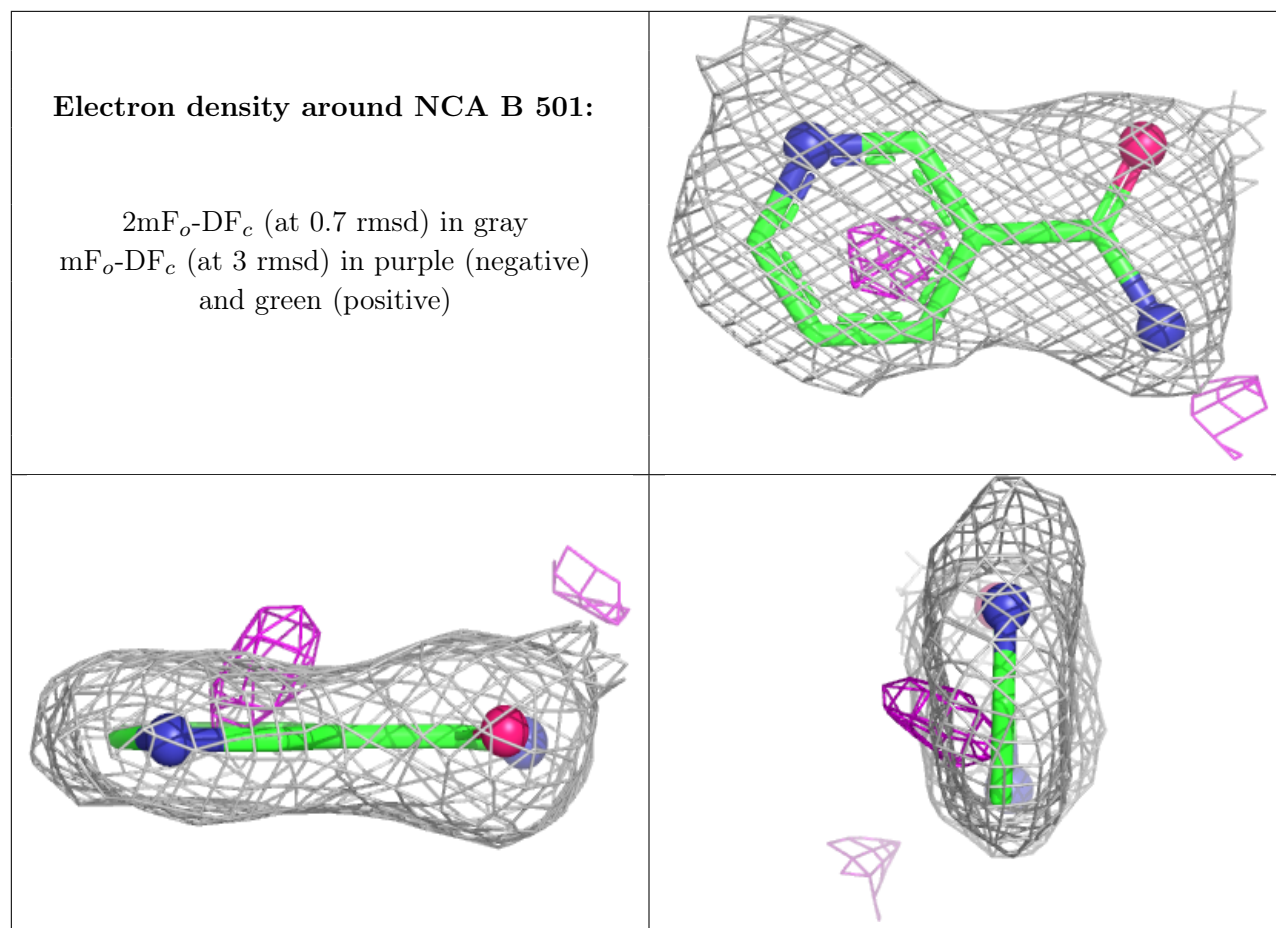
Electron density around NCA C 504:

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

**Electron density around NCA D 502:**

$2mF_o-DF_c$ (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.