



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 05:49 PM UTC

PDB ID : 2WD8 / pdb_00002wd8
Title : PTERIDINE REDUCTASE 1 (PTR1) FROM TRYPANOSOMA BRUCEI IN
COMPLEX WITH NADP AND DDD00071204
Authors : Robinson, D.A.; Wyatt, P.G.; Spinks, D.; Brenk, R.
Deposited on : 2009-03-20
Resolution : 2.10 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

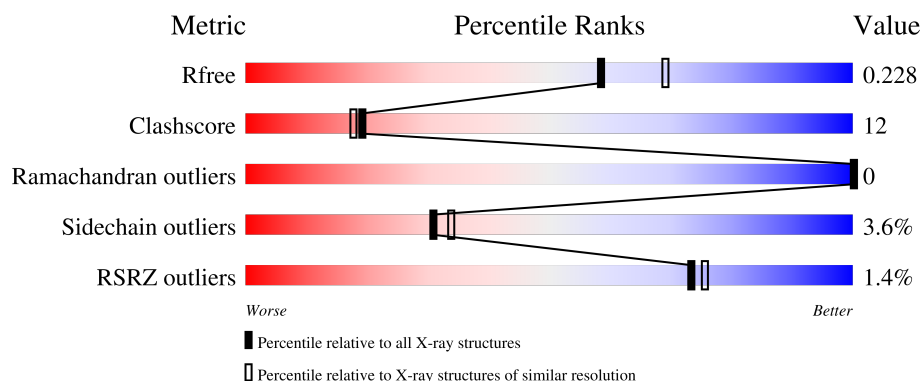
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	268	0% 76% 16% 7%
1	B	268	75% 17% 7%
1	C	268	4% 73% 18% 7%
1	D	268	76% 15% 7%

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:

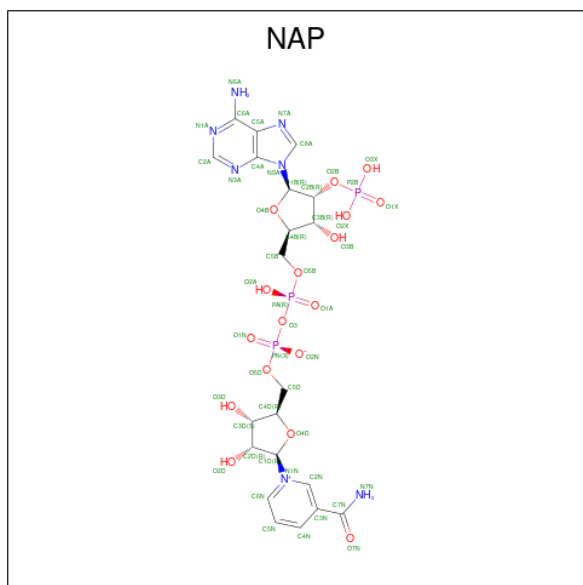
Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CL	A	1269	-	-	X	-

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 PTERIDINE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	249	Total 1870	C 1178	N 327	O 353	S 12	0	4	0
1	B	248	Total 1866	C 1176	N 326	O 352	S 12	0	5	0
1	C	249	Total 1857	C 1167	N 327	O 352	S 11	0	1	0
1	D	249	Total 1860	C 1169	N 327	O 353	S 11	0	2	0

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	B	1	Total 48	C 21	N 7	O 17	P 3	0	0

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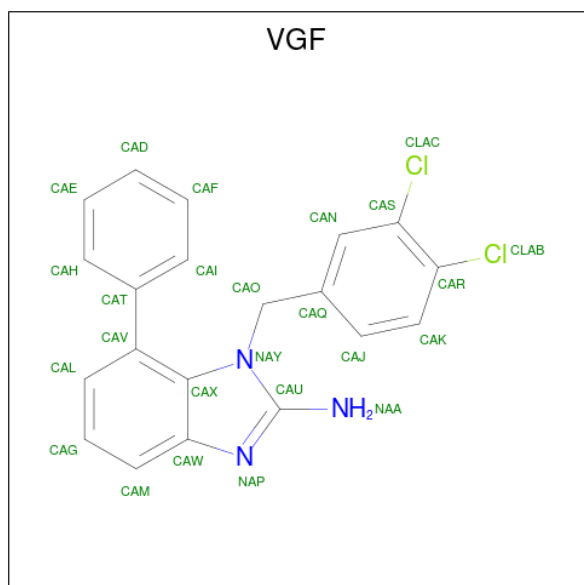
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		
3	C	1	Total	Cl	0	0
			1	1		

- Molecule 4 is 1-(3,4-DICHLOROBENZYL)-7-PHENYL-1H-BENZIMIDAZOL-2-AMINE (CCD ID: VGF) (formula: C₂₀H₁₅Cl₂N₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	Cl	N	0	0
			25	20	2	3		
4	B	1	Total	C	Cl	N	0	0
			25	20	2	3		
4	C	1	Total	C	Cl	N	0	0
			25	20	2	3		
4	D	1	Total	C	Cl	N	0	0
			25	20	2	3		

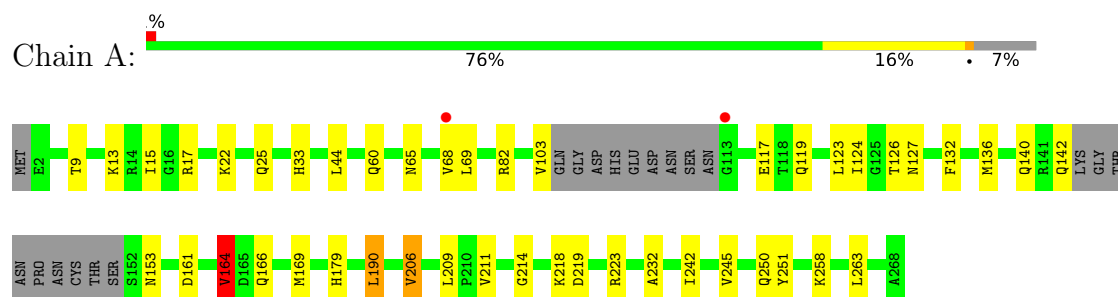
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	181	Total 181	O 181	0	0
5	B	205	Total 205	O 205	0	0
5	C	177	Total 177	O 177	0	0
5	D	170	Total 170	O 170	0	0

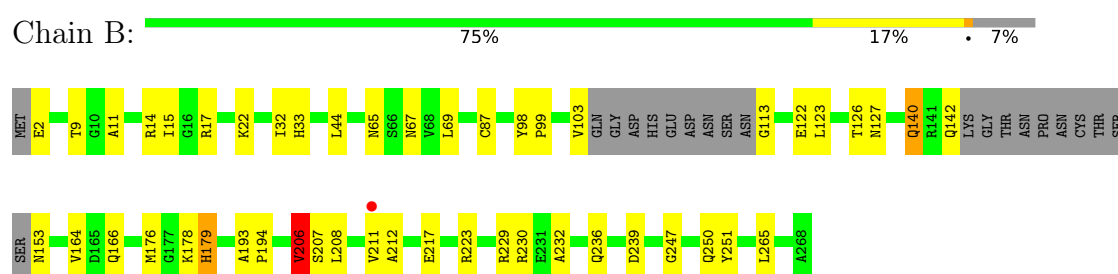
3 Residue-property plots [i](#)

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.

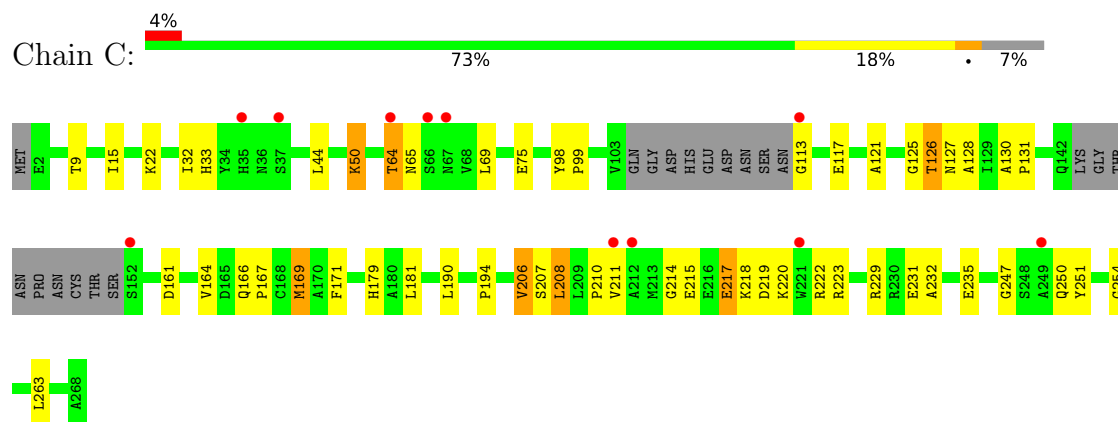
• Molecule 1: PTERIDINE REDUCTASE



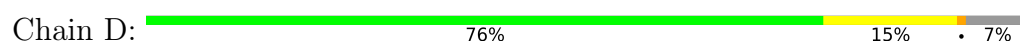
• Molecule 1: PTERIDINE REDUCTASE

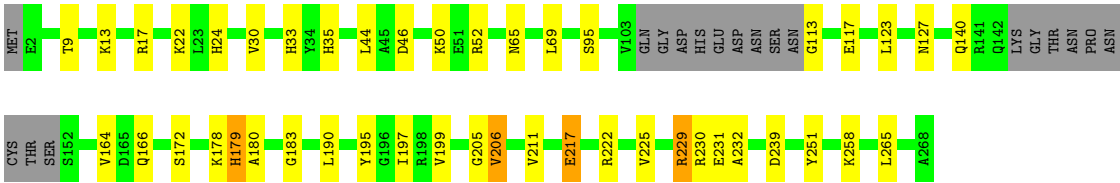


• Molecule 1: PTERIDINE REDUCTASE



• Molecule 1: PTERIDINE REDUCTASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.64Å 89.80Å 83.06Å 90.00° 115.55° 90.00°	Depositor
Resolution (Å)	30.00 – 2.10 30.00 – 2.10	Depositor EDS
% Data completeness (in resolution range)	84.4 (30.00-2.10) 84.6 (30.00-2.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.158 , 0.226 0.160 , 0.228	Depositor DCC
R_{free} test set	2496 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	25.1	Xtriage
Anisotropy	0.940	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.022 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8432	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 30.86 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2180e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: CL, NAP, VGF

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	0.79	0/1909	0.94	1/2589 (0.0%)
1	B	0.74	0/1908	0.92	1/2588 (0.0%)
1	C	0.78	0/1887	0.97	1/2560 (0.0%)
1	D	0.73	0/1893	0.94	1/2568 (0.0%)
All	All	0.76	0/7597	0.94	4/10305 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	164	VAL	CB-CA-C	-6.64	102.36	112.05
1	B	206	VAL	CB-CA-C	-5.83	102.14	110.83
1	D	30	VAL	N-CA-C	5.49	116.03	108.12
1	C	64	THR	N-CA-C	5.11	116.50	109.15

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1870	0	1907	50	0
1	B	1866	0	1905	39	0
1	C	1857	0	1882	53	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1860	0	1887	40	0
2	A	48	0	25	1	0
2	B	48	0	25	4	0
2	D	48	0	25	2	0
3	A	1	0	0	1	1
3	C	1	0	0	0	0
4	A	25	0	15	6	0
4	B	25	0	15	2	0
4	C	25	0	15	3	0
4	D	25	0	15	3	0
5	A	181	0	0	28	0
5	B	205	0	0	19	1
5	C	177	0	0	26	0
5	D	170	0	0	22	0
All	All	8432	0	7716	181	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (181) 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:C:164:VAL:HB	5:C:2116:HOH:O	1.36	1.25
1:A:206:VAL:HB	5:A:2122:HOH:O	1.45	1.16
1:B:126:THR:HB	5:B:2104:HOH:O	1.51	1.10
1:A:126:THR:HB	5:A:2081:HOH:O	1.55	1.04
1:C:164:VAL:CB	5:C:2116:HOH:O	2.00	1.01
1:D:197:ILE:HG22	5:D:2117:HOH:O	1.65	0.96
1:D:206:VAL:HG23	5:D:2119:HOH:O	1.72	0.90
1:A:140:GLN:HB3	5:A:2086:HOH:O	1.73	0.89
1:C:65:ASN:HB2	1:C:125:GLY:HA3	1.57	0.87
2:B:269:NAP:H51A	5:B:2086:HOH:O	1.76	0.86
1:C:64:THR:HG21	5:C:2054:HOH:O	1.75	0.86
1:C:161:ASP:O	1:C:164:VAL:HG13	1.76	0.86
1:C:206:VAL:HG13	4:C:1270:VGF:HAN	1.57	0.85
1:D:199:VAL:CG2	5:D:2117:HOH:O	2.23	0.85
1:C:164:VAL:CG1	5:C:2116:HOH:O	2.22	0.85
1:A:206:VAL:HG22	4:A:1270:VGF:CAN	2.07	0.83
5:B:2067:HOH:O	1:D:117:GLU:HG3	1.80	0.81
1:D:222:ARG:HD3	1:D:231:GLU:OE2	1.80	0.81
1:B:142:GLN:NE2	5:B:2111:HOH:O	2.12	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:269:NAP:H6N	5:B:2120:HOH:O	1.80	0.80
1:C:65:ASN:HB2	1:C:125:GLY:CA	2.12	0.78
1:A:126:THR:OG1	5:A:2080:HOH:O	2.01	0.78
1:C:121:ALA:O	1:C:125:GLY:HA3	1.84	0.77
1:C:127:ASN:CG	5:C:2095:HOH:O	2.28	0.77
1:C:128:ALA:HA	5:C:2096:HOH:O	1.84	0.77
1:A:60:GLN:HG3	5:A:2042:HOH:O	1.86	0.76
1:D:127:ASN:ND2	5:D:2079:HOH:O	2.17	0.76
5:A:2113:HOH:O	1:B:265:LEU:HB3	1.86	0.74
1:A:206:VAL:HG22	4:A:1270:VGF:HAN	1.66	0.74
1:B:206:VAL:HG13	4:B:1269:VGF:HAN	1.70	0.74
1:C:127:ASN:ND2	5:C:2095:HOH:O	2.21	0.73
1:B:217:GLU:HG3	5:B:2158:HOH:O	1.90	0.72
1:C:231:GLU:HB3	5:C:2151:HOH:O	1.90	0.72
1:C:179:HIS:ND1	5:C:2129:HOH:O	2.08	0.71
1:B:153:ASN:N	5:B:2117:HOH:O	2.23	0.71
1:D:199:VAL:HG23	5:D:2117:HOH:O	1.84	0.70
1:C:235:GLU:HG2	5:C:2153:HOH:O	1.92	0.69
1:A:206:VAL:HG23	1:A:263:LEU:HD22	1.75	0.68
1:A:127:ASN:ND2	5:A:2080:HOH:O	2.27	0.68
1:D:206:VAL:CG2	5:D:2119:HOH:O	2.33	0.67
1:C:65:ASN:HA	1:C:69:LEU:HD22	1.77	0.67
1:D:113:GLY:HA2	5:D:2071:HOH:O	1.94	0.67
1:C:15:ILE:HG13	1:C:208:LEU:HD11	1.77	0.66
1:A:206:VAL:CG2	4:A:1270:VGF:HAN	2.25	0.66
1:B:179:HIS:HB2	5:D:2106:HOH:O	1.97	0.64
1:D:199:VAL:HG22	5:D:2117:HOH:O	1.90	0.64
1:B:176:MET:HA	5:D:2106:HOH:O	1.97	0.64
1:D:123:LEU:O	1:D:127:ASN:HB2	1.97	0.63
1:A:179:HIS:ND1	5:C:2129:HOH:O	2.22	0.63
1:C:181:LEU:HD13	5:C:2096:HOH:O	1.98	0.63
1:D:22:LYS:HE3	1:D:239:ASP:OD1	2.00	0.61
4:C:1270:VGF:HAO2	4:C:1270:VGF:CAI	2.29	0.61
4:D:1269:VGF:HAO2	4:D:1269:VGF:CAI	2.29	0.61
1:A:206:VAL:CG2	4:A:1270:VGF:CAN	2.79	0.61
1:B:9:THR:HA	1:B:33:HIS:HB3	1.84	0.60
5:A:2103:HOH:O	1:D:166:GLN:HG2	2.00	0.60
1:A:206:VAL:CB	5:A:2122:HOH:O	2.23	0.60
1:C:214:GLY:HA3	5:C:2140:HOH:O	2.02	0.60
1:D:206:VAL:HG22	4:D:1269:VGF:HAN	1.83	0.60
1:B:2:GLU:HA	5:B:2004:HOH:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:87:CYS:HB3	5:B:2111:HOH:O	2.01	0.59
1:C:232:ALA:HB2	1:D:251:TYR:CE2	2.37	0.59
1:A:206:VAL:HG21	4:A:1270:VGF:CLAC	2.39	0.58
1:C:210:PRO:HA	5:C:2139:HOH:O	2.03	0.58
1:D:127:ASN:CG	5:D:2079:HOH:O	2.44	0.58
1:C:164:VAL:HG12	5:C:2116:HOH:O	1.92	0.58
1:D:225:VAL:HG21	5:D:2119:HOH:O	2.03	0.58
1:B:178:LYS:HE3	5:B:2120:HOH:O	2.03	0.58
1:B:179:HIS:CB	5:D:2106:HOH:O	2.51	0.57
1:C:223:ARG:HA	1:C:229:ARG:HB3	1.87	0.57
1:A:127:ASN:CG	5:A:2080:HOH:O	2.48	0.57
1:A:68:VAL:HB	5:A:2049:HOH:O	2.03	0.57
5:A:2108:HOH:O	1:C:190:LEU:CD2	2.52	0.56
1:C:50:LYS:HE2	5:C:2045:HOH:O	2.04	0.56
1:A:206:VAL:CG2	5:A:2122:HOH:O	2.50	0.56
1:A:103:VAL:HB	5:C:2136:HOH:O	2.05	0.56
1:A:132:PHE:O	1:A:136[A]:MET:HG3	2.06	0.56
1:D:172[B]:SER:HB2	5:D:2102:HOH:O	2.05	0.55
1:D:206:VAL:HG22	4:D:1269:VGF:CAN	2.35	0.55
1:A:9:THR:HA	1:A:33:HIS:HB3	1.89	0.55
4:B:1269:VGF:CAI	4:B:1269:VGF:HAO2	2.36	0.55
1:A:65:ASN:HA	1:A:69:LEU:HD22	1.88	0.55
1:C:64:THR:CG2	5:C:2054:HOH:O	2.44	0.54
1:C:65:ASN:HB2	1:C:125:GLY:HA2	1.90	0.54
1:D:183:GLY:HA3	5:D:2106:HOH:O	2.07	0.53
5:A:2113:HOH:O	1:C:167:PRO:HD2	2.09	0.53
1:A:142:GLN:C	5:A:2088:HOH:O	2.51	0.52
1:A:13:LYS:NZ	5:A:2007:HOH:O	2.41	0.52
1:A:124:ILE:HD12	5:A:2110:HOH:O	2.08	0.52
1:D:180:ALA:HA	5:D:2106:HOH:O	2.08	0.52
1:A:250:GLN:HG2	5:B:2178:HOH:O	2.09	0.52
1:D:65:ASN:HA	1:D:69:LEU:HD22	1.92	0.52
1:A:82:ARG:HD2	5:A:2061:HOH:O	2.09	0.52
1:D:46:ASP:O	1:D:50:LYS:HG3	2.09	0.52
1:A:119:GLN:NE2	5:A:2079:HOH:O	2.42	0.52
1:B:17:ARG:HG3	1:B:44:LEU:HD22	1.91	0.52
1:B:113:GLY:HA3	5:B:2096:HOH:O	2.10	0.52
1:A:258:LYS:HE3	5:A:2172:HOH:O	2.10	0.51
5:A:2108:HOH:O	1:C:190:LEU:HD23	2.10	0.51
4:A:1270:VGF:CAI	4:A:1270:VGF:HAO2	2.41	0.51
1:C:217:GLU:HA	1:C:220:LYS:HE2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:223:ARG:HA	1:B:229:ARG:HG3	1.93	0.50
1:C:98:TYR:HB2	1:C:99:PRO:HD2	1.92	0.50
1:C:65:ASN:HB3	1:C:121:ALA:HA	1.92	0.50
1:B:15:ILE:HB	2:B:269:NAP:H51N	1.94	0.50
1:D:164:VAL:HG22	1:D:179:HIS:CD2	2.46	0.50
1:A:211:VAL:HB	5:A:2126:HOH:O	2.11	0.50
1:D:9:THR:HA	1:D:33:HIS:HB3	1.94	0.50
1:B:123:LEU:O	1:B:127:ASN:HB2	2.10	0.50
1:B:208:LEU:HB2	5:B:2203:HOH:O	2.11	0.50
1:A:22:LYS:HG2	1:A:242:ILE:HG13	1.93	0.50
1:B:230:ARG:HB2	5:B:2170:HOH:O	2.10	0.50
5:C:2173:HOH:O	1:D:190:LEU:HB2	2.10	0.50
1:C:179:HIS:CE1	5:C:2129:HOH:O	2.59	0.50
1:A:232:ALA:HB2	1:B:251:TYR:CE2	2.48	0.49
1:C:131:PRO:HB2	5:C:2096:HOH:O	2.13	0.49
1:C:75:GLU:HG3	5:C:2063:HOH:O	2.13	0.49
1:B:212:ALA:HB3	5:B:2149:HOH:O	2.13	0.48
1:D:17:ARG:HG3	1:D:44:LEU:HD22	1.95	0.48
1:B:122:GLU:O	1:B:126:THR:HG23	2.13	0.48
1:C:222:ARG:NH2	5:C:2144:HOH:O	2.45	0.47
1:C:247:GLY:HA2	1:C:250:GLN:HG3	1.96	0.47
1:B:14:ARG:NH2	5:B:2009:HOH:O	2.48	0.47
1:C:251:TYR:CE2	1:D:232:ALA:HB2	2.50	0.47
1:A:219:ASP:O	1:A:223:ARG:HG3	2.15	0.47
1:B:22:LYS:HE3	1:B:239:ASP:OD1	2.15	0.47
2:B:269:NAP:H52N	5:B:2086:HOH:O	2.15	0.46
1:C:9:THR:HA	1:C:33:HIS:HB3	1.96	0.46
1:A:13:LYS:HB2	3:A:1269:CL:CL	2.52	0.46
1:B:98:TYR:HB2	1:B:99:PRO:HD2	1.97	0.46
1:B:11:ALA:HB3	1:B:32:ILE:HG23	1.97	0.46
1:C:130:ALA:HB3	1:C:131:PRO:HD3	1.97	0.45
1:D:95:SER:HA	5:D:2079:HOH:O	2.17	0.45
1:B:103:VAL:HG21	1:D:195:TYR:OH	2.16	0.45
1:C:215:GLU:HA	1:C:218:LYS:HB2	1.97	0.45
1:A:17:ARG:HG3	1:A:44:LEU:HD22	1.99	0.45
1:C:64:THR:HA	1:C:126:THR:HG22	1.98	0.45
1:A:258:LYS:CB	5:A:2172:HOH:O	2.65	0.44
1:D:35:HIS:HB2	2:D:269:NAP:C2A	2.47	0.44
1:D:13:LYS:HB2	5:D:2169:HOH:O	2.17	0.44
1:D:127:ASN:OD1	1:D:178:LYS:HE2	2.17	0.44
1:B:14:ARG:CZ	5:B:2009:HOH:O	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:194:PRO:HG3	5:D:2132:HOH:O	2.17	0.44
1:C:206:VAL:HG22	1:C:263:LEU:HD22	1.99	0.44
1:A:214:GLY:O	1:A:218:LYS:HG3	2.18	0.44
1:C:32:ILE:HG12	1:C:44:LEU:HD23	2.00	0.43
1:A:153:ASN:ND2	1:A:245:VAL:O	2.51	0.43
1:D:205:GLY:O	2:D:269:NAP:H4N	2.18	0.43
1:C:128:ALA:C	1:C:131:PRO:HD2	2.43	0.43
1:A:250:GLN:CD	1:B:236:GLN:HE21	2.26	0.43
1:C:171:PHE:CG	4:C:1270:VGF:HAG	2.53	0.43
1:A:258:LYS:HB2	5:A:2172:HOH:O	2.19	0.42
1:C:113:GLY:HA2	5:C:2086:HOH:O	2.18	0.42
1:A:169:MET:HA	5:A:2108:HOH:O	2.18	0.42
1:C:219:ASP:HA	1:C:222:ARG:HB2	2.00	0.42
1:A:251:TYR:CE2	1:B:232:ALA:HB2	2.54	0.42
1:D:24:HIS:O	1:D:52:ARG:NH1	2.52	0.42
1:D:217:GLU:HB2	5:D:2124:HOH:O	2.19	0.42
1:B:193:ALA:N	1:B:194:PRO:CD	2.82	0.42
1:C:220:LYS:HE3	5:C:2142:HOH:O	2.19	0.42
1:D:229:ARG:NH1	5:D:2132:HOH:O	2.52	0.42
1:B:164:VAL:HG22	1:B:179:HIS:CD2	2.55	0.42
1:A:166:GLN:NE2	5:A:2102:HOH:O	2.52	0.42
1:A:15:ILE:HB	2:A:269:NAP:H51N	2.02	0.41
1:B:247:GLY:HA2	1:B:250:GLN:HG3	2.01	0.41
1:A:123:LEU:O	1:A:127:ASN:HB2	2.20	0.41
1:B:207:SER:O	1:B:208:LEU:C	2.62	0.41
1:C:214:GLY:CA	5:C:2140:HOH:O	2.65	0.41
1:C:254:GLY:HA3	1:D:265:LEU:HD11	2.01	0.41
1:A:190:LEU:CD1	1:C:169:MET:SD	3.08	0.41
1:A:136[B]:MET:HG3	1:A:140:GLN:HE21	1.86	0.41
1:B:65:ASN:HA	1:B:69:LEU:HD22	2.01	0.41
1:A:161:ASP:O	1:A:164:VAL:HG22	2.21	0.41
1:D:258:LYS:HE3	1:D:258:LYS:HB2	1.89	0.41
1:A:169:MET:SD	5:A:2108:HOH:O	2.62	0.40
1:D:206:VAL:HB	5:D:2119:HOH:O	2.22	0.40
1:A:25:GLN:NE2	5:A:2012:HOH:O	2.53	0.40
1:B:67:ASN:HB3	5:B:2018:HOH:O	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1269:CL:CL	5:B:2152:HOH:O[2_545]	2.00	0.20

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	247/268 (92%)	240 (97%)	7 (3%)	0	100	100
1	B	247/268 (92%)	239 (97%)	8 (3%)	0	100	100
1	C	244/268 (91%)	232 (95%)	12 (5%)	0	100	100
1	D	245/268 (91%)	236 (96%)	9 (4%)	0	100	100
All	All	983/1072 (92%)	947 (96%)	36 (4%)	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	201/214 (94%)	196 (98%)	5 (2%)	42	48
1	B	201/214 (94%)	196 (98%)	5 (2%)	42	48
1	C	198/214 (92%)	187 (94%)	11 (6%)	19	18
1	D	199/214 (93%)	192 (96%)	7 (4%)	32	35
All	All	799/856 (93%)	771 (96%)	28 (4%)	31	35

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	117	GLU
1	A	164	VAL
1	A	190	LEU
1	A	206	VAL
1	A	209	LEU
1	B	140	GLN
1	B	166	GLN
1	B	179	HIS
1	B	206	VAL
1	B	211	VAL
1	C	22	LYS
1	C	50	LYS
1	C	117	GLU
1	C	126	THR
1	C	166	GLN
1	C	169	MET
1	C	206	VAL
1	C	207	SER
1	C	208	LEU
1	C	211	VAL
1	C	217	GLU
1	D	140	GLN
1	D	179	HIS
1	D	206	VAL
1	D	211	VAL
1	D	217	GLU
1	D	229	ARG
1	D	230	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	92	ASN
1	A	140	GLN
1	A	166	GLN
1	A	175	ASN
1	A	179	HIS
1	B	36	ASN
1	B	92	ASN
1	B	166	GLN
1	B	175	ASN
1	B	236	GLN

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Mol	Chain	Res	Type
1	C	92	ASN
1	C	175	ASN
1	C	179	HIS
1	D	54	ASN
1	D	92	ASN
1	D	140	GLN
1	D	179	HIS
1	D	250	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 2 are 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	NAP	A	269	-	50,52,52	1.79	5 (10%)	71,80,80	1.67	14 (19%)
4	VGF	B	1269	-	28,28,28	1.38	4 (14%)	37,40,40	1.28	5 (13%)
2	NAP	B	269	-	50,52,52	1.77	6 (12%)	71,80,80	1.88	13 (18%)
4	VGF	A	1270	-	28,28,28	1.40	5 (17%)	37,40,40	1.25	4 (10%)
4	VGF	D	1269	-	28,28,28	1.39	4 (14%)	37,40,40	1.42	6 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAP	D	269	-	50,52,52	1.69	5 (10%)	71,80,80	1.69	12 (16%)
4	VGF	C	1270	-	28,28,28	1.65	6 (21%)	37,40,40	1.12	4 (10%)

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	NAP	A	269	-	-	0/35/67/67	0/5/5/5
4	VGF	B	1269	-	-	2/8/8/8	0/4/4/4
2	NAP	B	269	-	-	1/35/67/67	0/5/5/5
4	VGF	A	1270	-	-	2/8/8/8	0/4/4/4
4	VGF	D	1269	-	-	2/8/8/8	0/4/4/4
2	NAP	D	269	-	-	1/35/67/67	0/5/5/5
4	VGF	C	1270	-	-	0/8/8/8	0/4/4/4

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	269	NAP	O7N-C7N	9.35	1.41	1.24
2	D	269	NAP	O7N-C7N	9.32	1.41	1.24
2	B	269	NAP	O7N-C7N	9.27	1.41	1.24
4	C	1270	VGF	CAV-CAT	-4.77	1.40	1.49
4	A	1270	VGF	CAV-CAT	-4.47	1.41	1.49
4	D	1269	VGF	CAV-CAT	-3.97	1.42	1.49
2	A	269	NAP	C2N-N1N	3.87	1.39	1.35
4	B	1269	VGF	CAV-CAT	-3.77	1.42	1.49
2	B	269	NAP	C2N-N1N	3.43	1.38	1.35
2	B	269	NAP	C2A-N1A	3.27	1.39	1.33
4	C	1270	VGF	CAX-NAY	-3.26	1.33	1.40
4	C	1270	VGF	CAO-CAQ	3.22	1.57	1.51
2	A	269	NAP	C2A-N1A	3.18	1.39	1.33
2	D	269	NAP	C2N-N1N	3.02	1.38	1.35
4	D	1269	VGF	CAX-NAY	-2.99	1.34	1.40
2	A	269	NAP	C8A-N7A	2.87	1.37	1.31
4	C	1270	VGF	CAW-NAP	-2.70	1.34	1.39
4	A	1270	VGF	CAX-NAY	-2.69	1.35	1.40
2	D	269	NAP	C2A-N1A	2.67	1.38	1.33
4	B	1269	VGF	CAW-NAP	-2.65	1.34	1.39
4	D	1269	VGF	CAW-NAP	-2.63	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1270	VGf	CAW-NAP	-2.60	1.34	1.39
2	B	269	NAP	C2A-N3A	2.57	1.38	1.33
4	B	1269	VGf	CAX-NAY	-2.53	1.35	1.40
2	D	269	NAP	C2A-N3A	2.52	1.38	1.33
4	D	1269	VGf	CAO-CAQ	2.51	1.55	1.51
2	D	269	NAP	C8A-N7A	2.46	1.36	1.31
4	C	1270	VGf	CAU-NAY	-2.40	1.34	1.37
4	B	1269	VGf	CAU-NAY	-2.38	1.34	1.37
2	A	269	NAP	C2A-N3A	2.33	1.38	1.33
2	B	269	NAP	C8A-N7A	2.31	1.36	1.31
4	A	1270	VGf	CAU-NAY	-2.23	1.34	1.37
4	C	1270	VGf	CAU-NAP	2.21	1.35	1.32
4	A	1270	VGf	CAO-CAQ	2.20	1.55	1.51
2	B	269	NAP	PA-O3	2.14	1.61	1.59

All (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	269	NAP	C2B-C1B-N9A	-7.10	102.07	113.75
2	B	269	NAP	N3A-C2A-N1A	-6.11	119.33	128.58
2	A	269	NAP	N3A-C2A-N1A	-5.90	119.65	128.58
2	D	269	NAP	N3A-C2A-N1A	-5.73	119.91	128.58
2	B	269	NAP	O4B-C1B-N9A	5.04	117.77	108.09
2	D	269	NAP	C2B-C1B-N9A	-4.83	105.80	113.75
2	D	269	NAP	O4B-C1B-N9A	4.72	117.16	108.09
2	A	269	NAP	C2B-C1B-N9A	-4.69	106.04	113.75
4	B	1269	VGf	CAW-NAP-CAU	4.57	108.25	105.20
2	D	269	NAP	N9A-C8A-N7A	-4.44	107.64	113.94
2	A	269	NAP	O4B-C1B-N9A	4.30	116.36	108.09
2	A	269	NAP	N9A-C8A-N7A	-4.30	107.83	113.94
2	B	269	NAP	N9A-C8A-N7A	-4.04	108.21	113.94
4	D	1269	VGf	CAW-NAP-CAU	3.84	107.76	105.20
4	D	1269	VGf	CAQ-CAO-NAY	-3.70	107.44	113.46
4	A	1270	VGf	CAQ-CAO-NAY	-3.69	107.45	113.46
2	B	269	NAP	C3N-C7N-N7N	3.65	122.23	117.74
4	D	1269	VGf	CAV-CAX-NAY	3.54	134.41	129.91
2	D	269	NAP	C5A-C4A-N3A	-3.54	121.84	126.72
4	A	1270	VGf	CAV-CAX-NAY	3.46	134.31	129.91
4	B	1269	VGf	CAV-CAX-NAY	3.43	134.27	129.91
2	D	269	NAP	C5A-N7A-C8A	3.42	108.82	103.45
2	A	269	NAP	C5A-N7A-C8A	3.40	108.80	103.45
2	B	269	NAP	C5A-C4A-N3A	-3.26	122.22	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1270	VGf	CAW-NAP-CAU	3.17	107.31	105.20
2	D	269	NAP	C2A-N3A-C4A	3.09	119.37	111.83
2	B	269	NAP	C5A-N7A-C8A	3.09	108.30	103.45
2	B	269	NAP	C2A-N3A-C4A	3.05	119.29	111.83
2	A	269	NAP	C5A-C4A-N3A	-2.97	122.63	126.72
2	A	269	NAP	C2A-N3A-C4A	2.92	118.97	111.83
4	B	1269	VGf	CAQ-CAO-NAY	-2.83	108.86	113.46
4	C	1270	VGf	CAV-CAX-NAY	2.82	133.49	129.91
2	B	269	NAP	C4A-N9A-C8A	2.65	108.52	105.74
4	C	1270	VGf	CAQ-CAO-NAY	-2.63	109.19	113.46
2	A	269	NAP	C4A-C5A-N7A	-2.57	107.64	110.58
2	A	269	NAP	O2A-PA-O3	2.56	114.18	107.27
2	D	269	NAP	C4A-N9A-C8A	2.51	108.37	105.74
2	A	269	NAP	C4A-N9A-C8A	2.45	108.31	105.74
4	B	1269	VGf	CAX-CAW-NAP	-2.42	108.19	110.29
2	B	269	NAP	N3A-C4A-N9A	2.39	131.24	127.17
4	B	1269	VGf	CAO-NAY-CAX	-2.37	124.83	129.06
2	A	269	NAP	C4A-N9A-C1B	-2.35	121.13	126.63
2	D	269	NAP	N3A-C4A-N9A	2.29	131.07	127.17
2	A	269	NAP	C4B-O4B-C1B	-2.27	104.46	109.47
2	B	269	NAP	O7N-C7N-C3N	-2.24	116.85	119.60
2	D	269	NAP	C4A-C5A-N7A	-2.22	108.04	110.58
4	D	1269	VGf	CAX-CAW-NAP	-2.21	108.37	110.29
4	D	1269	VGf	CAK-CAR-CLAB	2.20	122.76	118.42
4	C	1270	VGf	CAW-CAX-NAY	2.20	106.08	104.77
2	D	269	NAP	C6N-N1N-C2N	-2.18	120.02	121.88
2	B	269	NAP	C4A-N9A-C1B	-2.14	121.62	126.63
4	D	1269	VGf	CAO-NAY-CAX	-2.14	125.25	129.06
4	C	1270	VGf	CAX-CAW-NAP	-2.10	108.46	110.29
2	B	269	NAP	O2N-PN-O1N	2.10	122.22	112.44
2	A	269	NAP	C3N-C7N-N7N	2.08	120.30	117.74
4	A	1270	VGf	CAX-CAW-NAP	-2.07	108.49	110.29
2	A	269	NAP	O2N-PN-O1N	2.01	121.82	112.44
2	D	269	NAP	O2N-PN-O1N	2.00	121.76	112.44

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	269	NAP	C5B-O5B-PA-O1A
4	B	1269	VGf	NAY-CAO-CAQ-CAJ
4	D	1269	VGf	NAY-CAO-CAQ-CAJ

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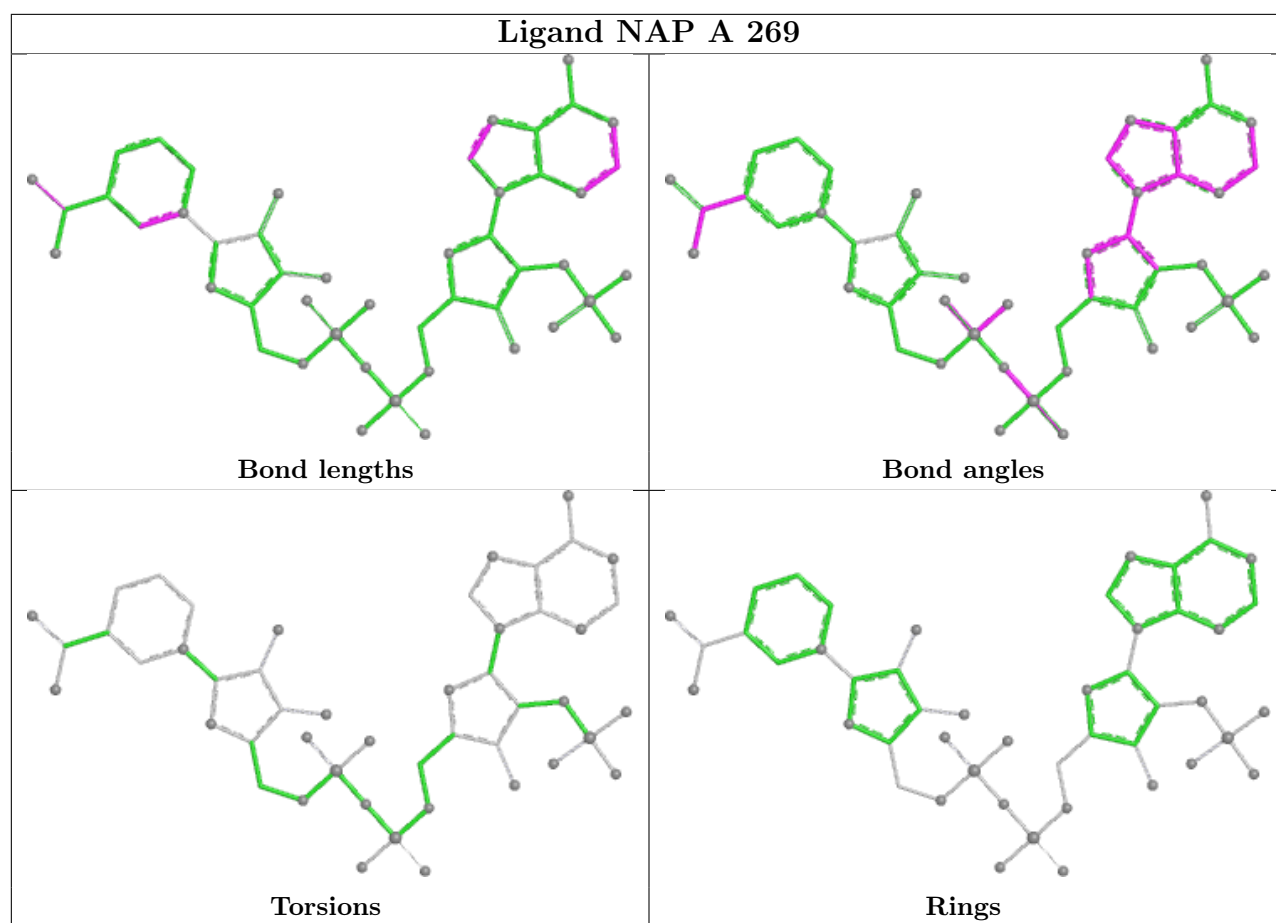
Mol	Chain	Res	Type	Atoms
2	B	269	NAP	C3B-C2B-O2B-P2B
4	D	1269	VGf	NAY-CAO-CAQ-CAN
4	A	1270	VGf	NAY-CAO-CAQ-CAJ
4	A	1270	VGf	CAH-CAT-CAV-CAL
4	B	1269	VGf	NAY-CAO-CAQ-CAN

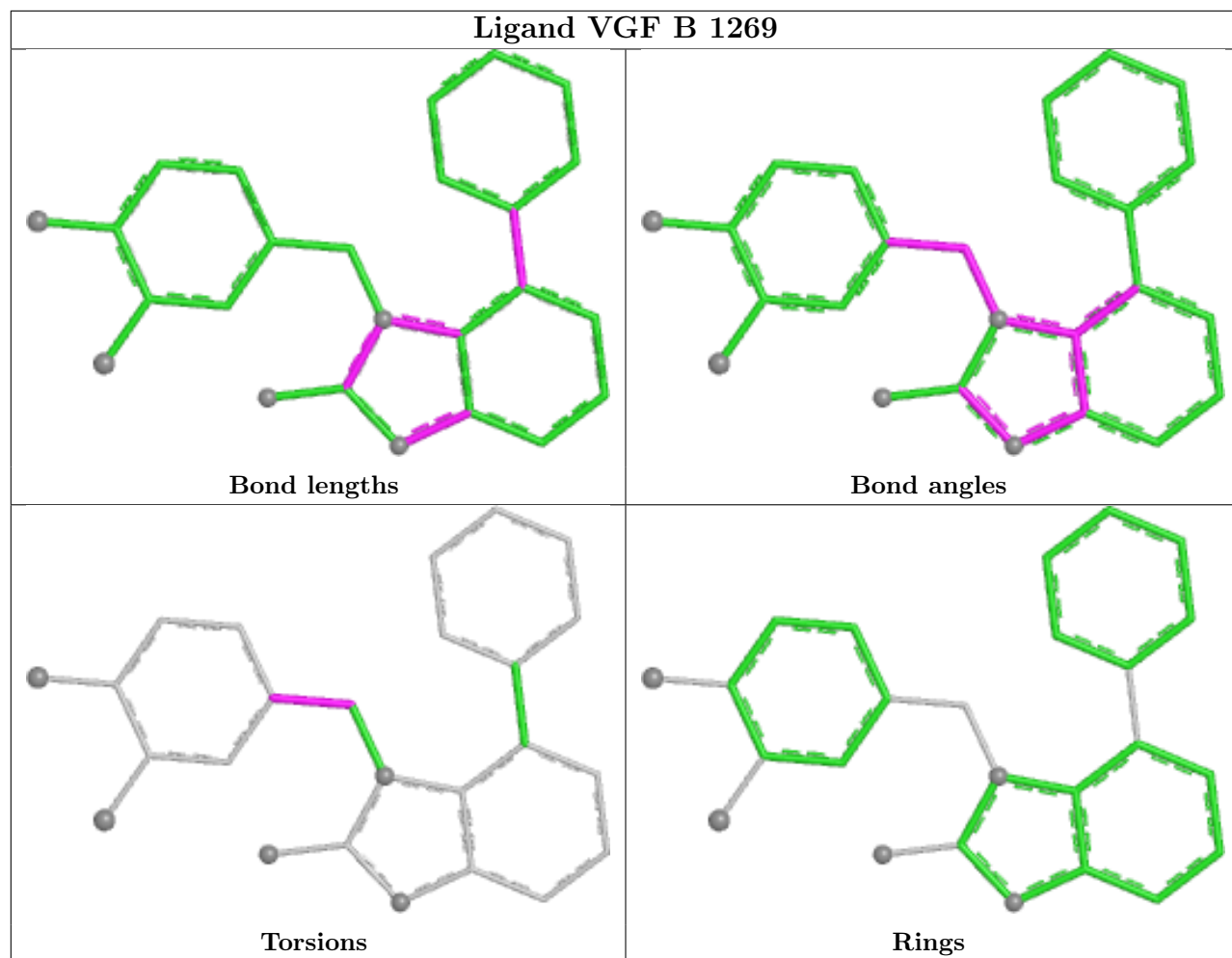
There are no ring outliers.

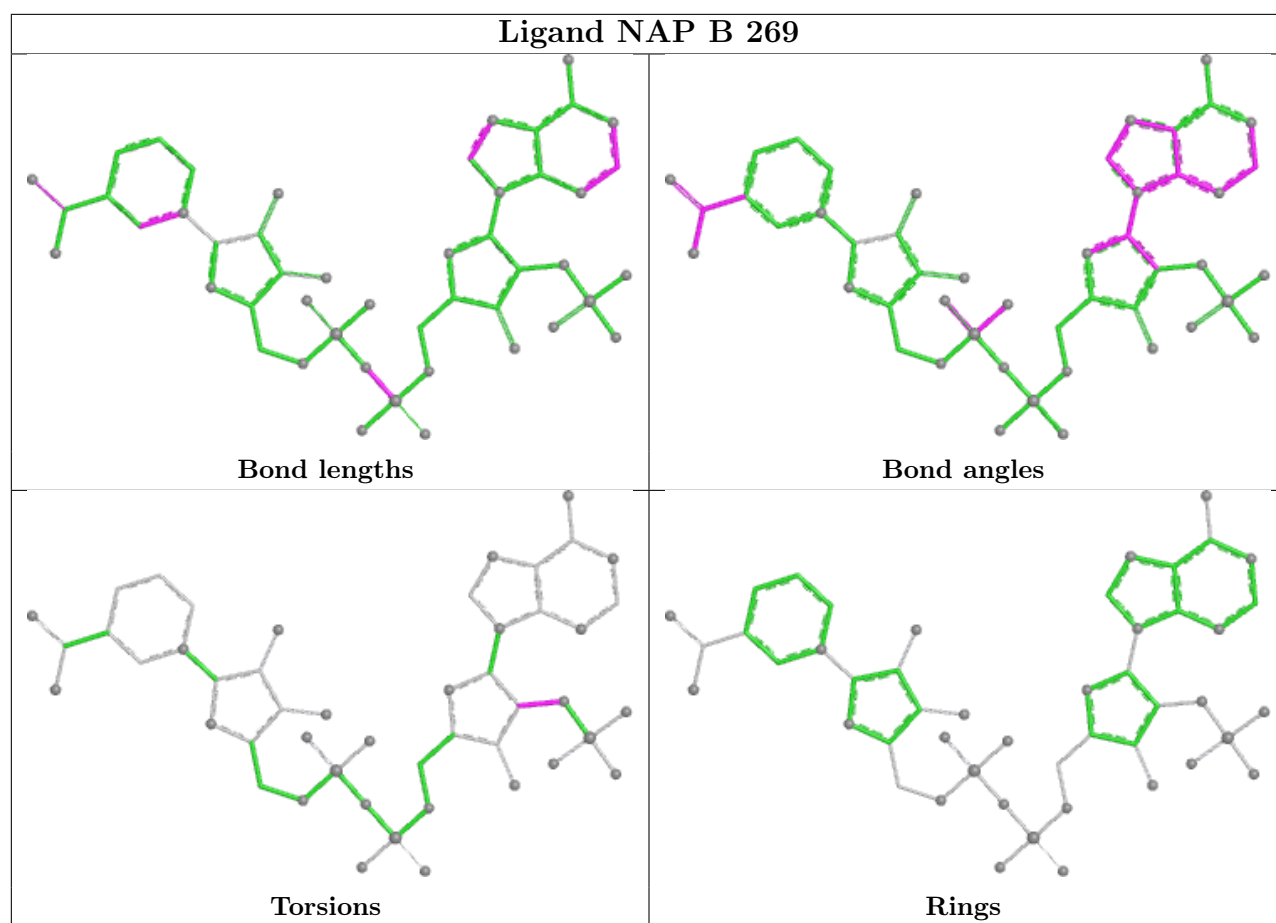
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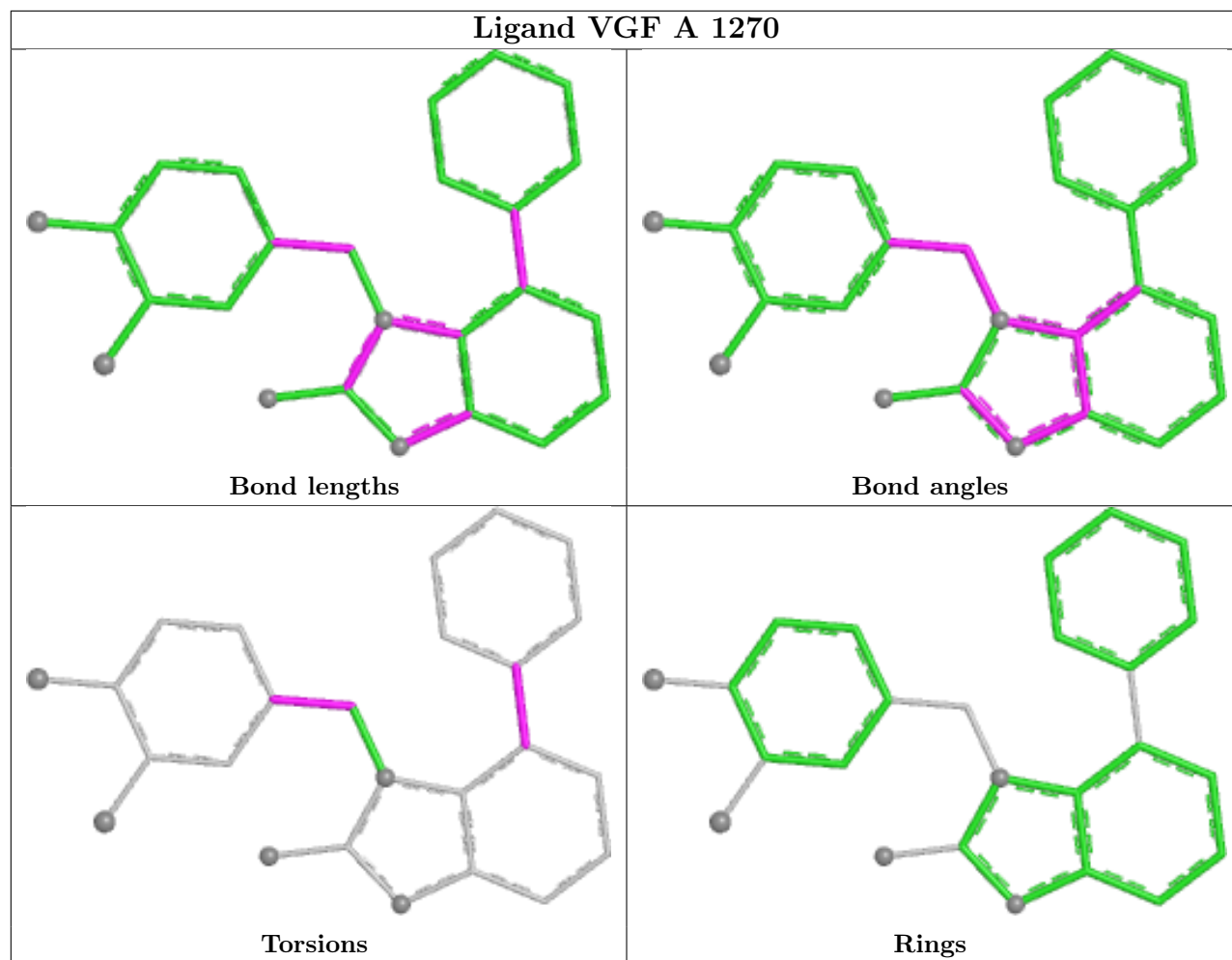
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2	A	269	NAP	1	0
4	B	1269	VGf	2	0
2	B	269	NAP	4	0
4	A	1270	VGf	6	0
4	D	1269	VGf	3	0
2	D	269	NAP	2	0
4	C	1270	VGf	3	0

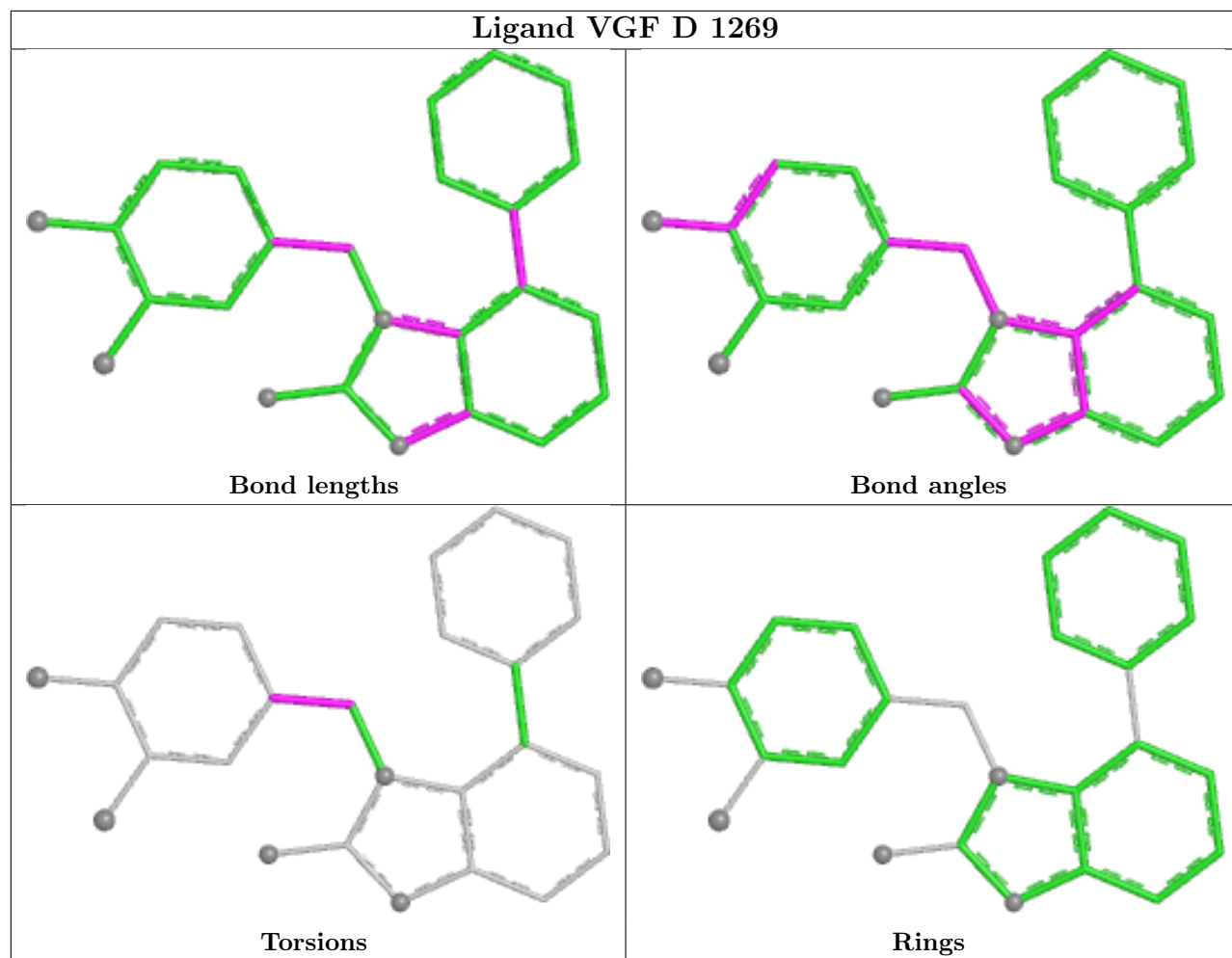
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

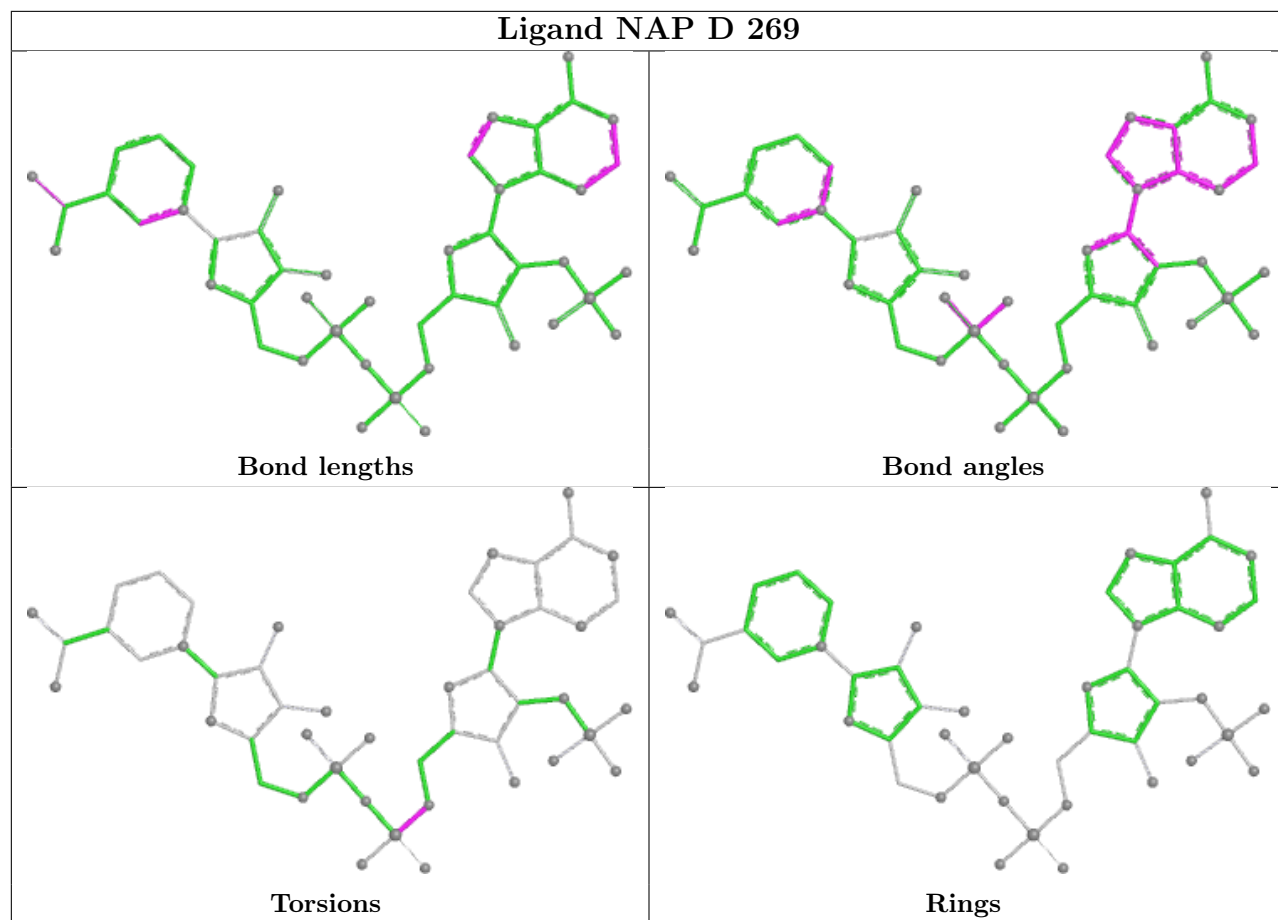


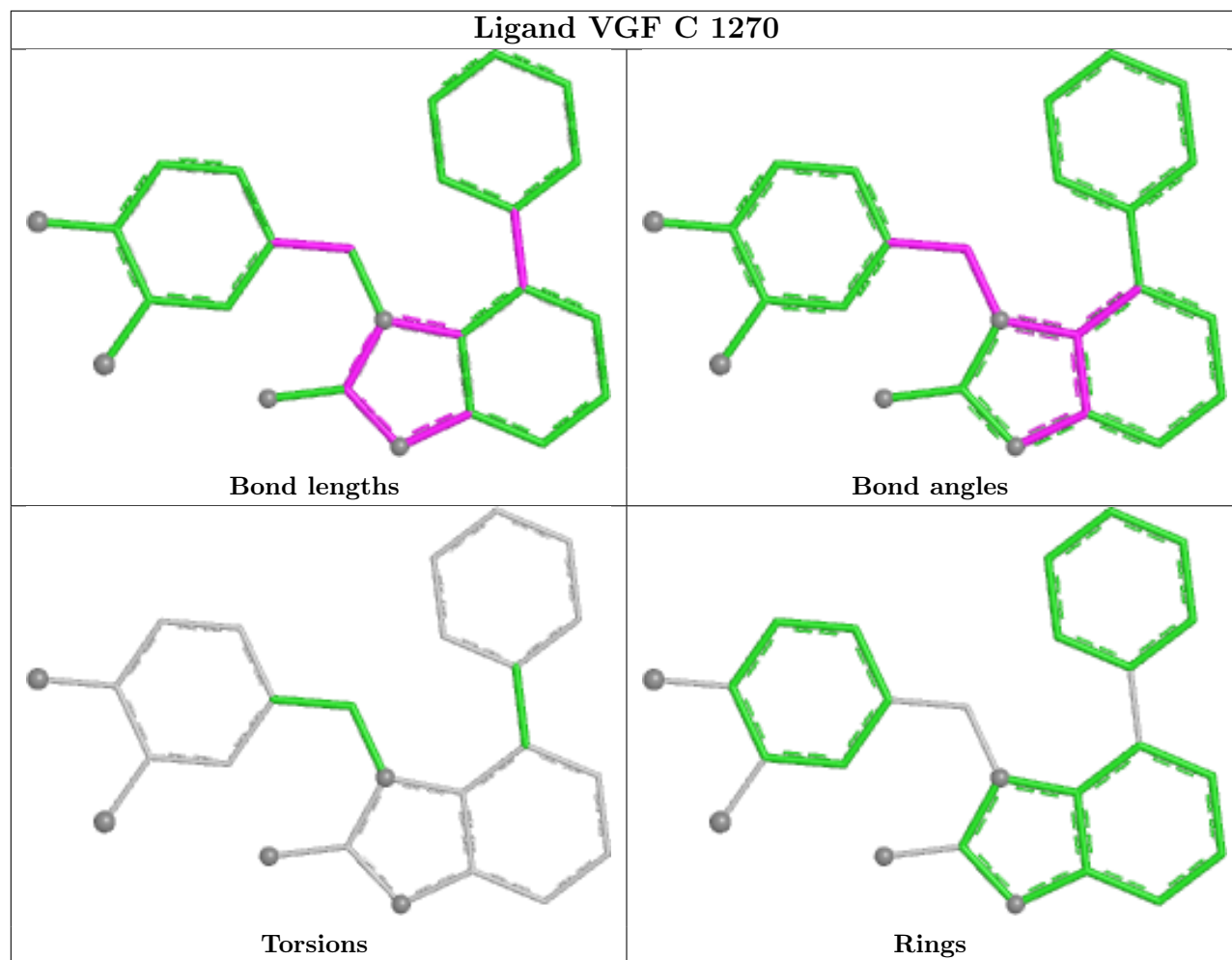












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [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	249/268 (92%)	0.02	2 (0%) 82 84	17, 30, 38, 45	11 (4%)
1	B	248/268 (92%)	0.04	1 (0%) 88 90	18, 30, 38, 43	5 (2%)
1	C	249/268 (92%)	0.50	11 (4%) 39 41	19, 30, 48, 64	3 (1%)
1	D	249/268 (92%)	0.27	0 100 100	19, 30, 41, 50	5 (2%)
All	All	995/1072 (92%)	0.21	14 (1%) 73 75	17, 30, 40, 64	24 (2%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	64	THR	5.4
1	C	212	ALA	3.7
1	C	66	SER	3.6
1	C	113	GLY	3.4
1	A	68	VAL	2.7
1	C	67	ASN	2.7
1	B	211	VAL	2.7
1	C	37	SER	2.6
1	C	211	VAL	2.5
1	C	249	ALA	2.4
1	A	113	GLY	2.3
1	C	35	HIS	2.2
1	C	152	SER	2.1
1	C	221	TRP	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](#)

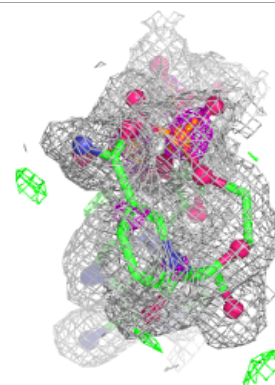
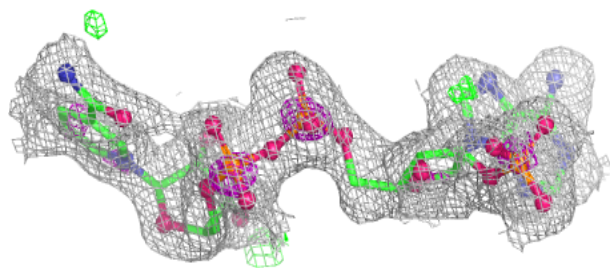
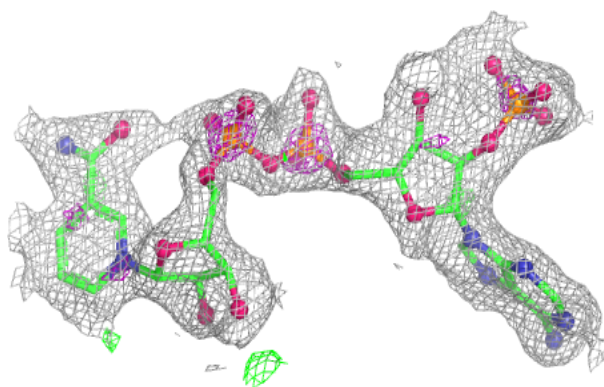
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	CL	C	1269	1/1	0.84	0.12	61,61,61,61	0
2	NAP	D	269	48/48	0.93	0.09	22,30,37,39	48
2	NAP	B	269	48/48	0.93	0.09	18,27,32,33	48
2	NAP	A	269	48/48	0.94	0.09	25,30,34,35	0
3	CL	A	1269	1/1	0.95	0.07	52,52,52,52	0
4	VGF	A	1270	25/25	0.96	0.08	25,27,29,30	0
4	VGF	B	1269	25/25	0.96	0.08	24,26,29,30	0
4	VGF	C	1270	25/25	0.97	0.08	29,31,33,34	0
4	VGF	D	1269	25/25	0.97	0.08	23,25,27,29	0

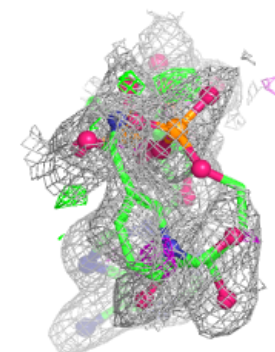
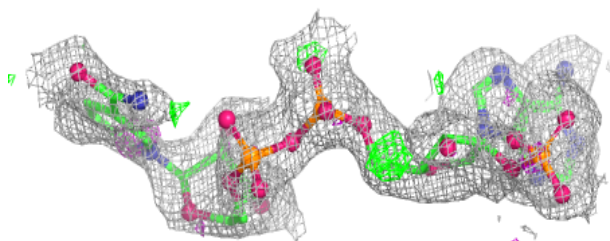
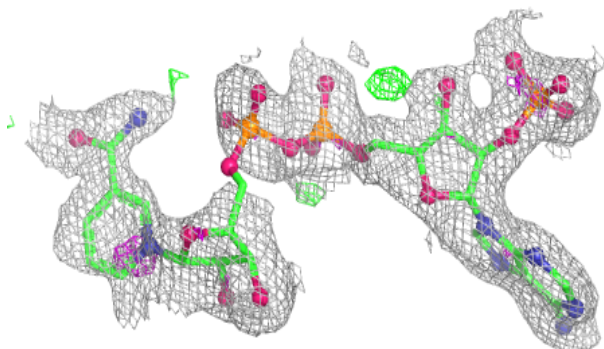
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAP D 269:

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

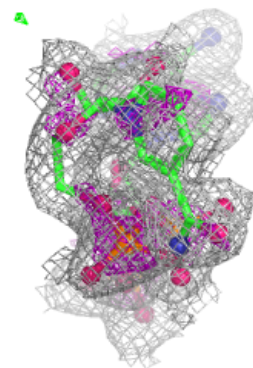
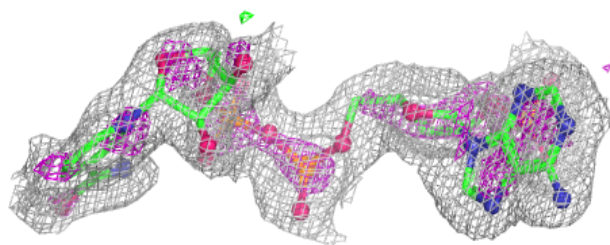
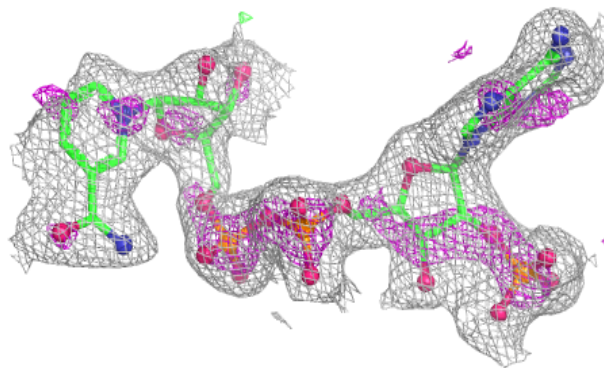
**Electron density around NAP B 269:**

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



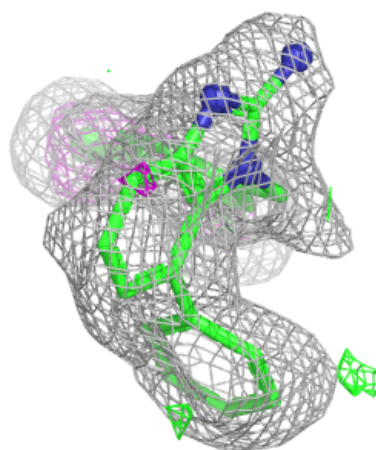
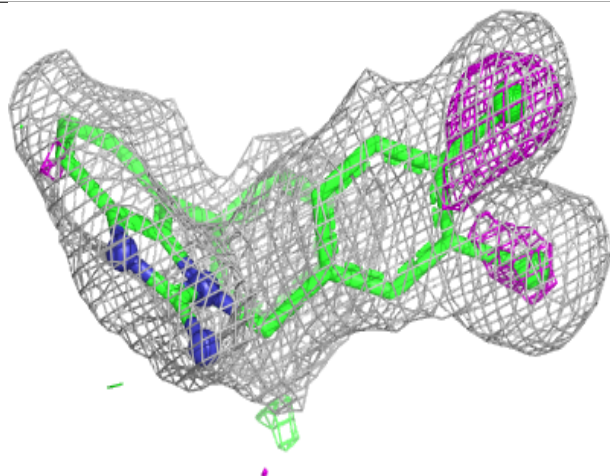
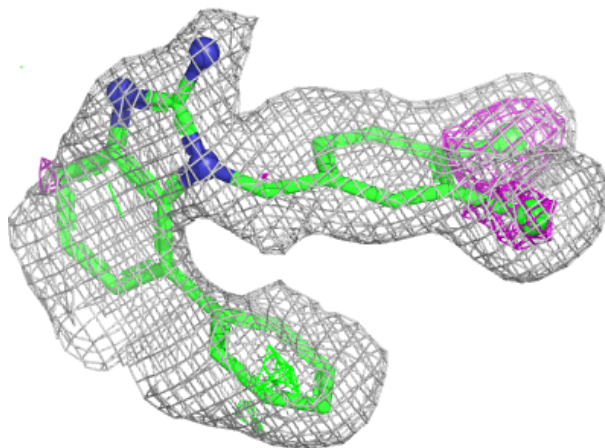
Electron density around NAP A 269:

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



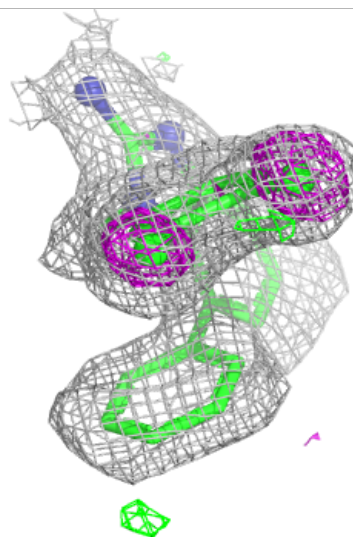
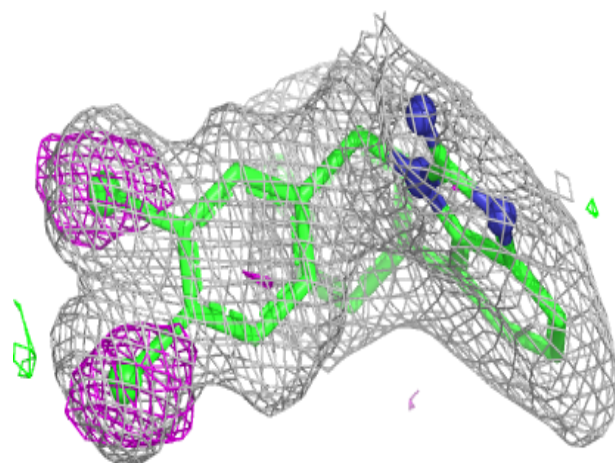
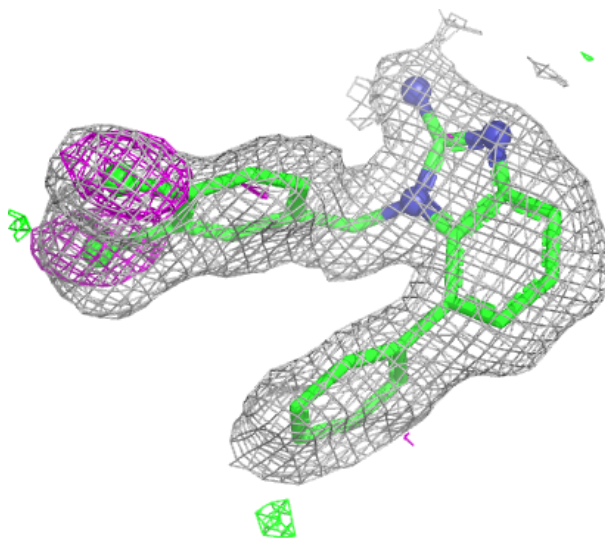
Electron density around VGF A 1270:

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



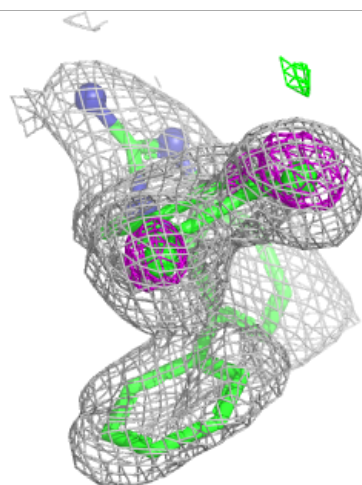
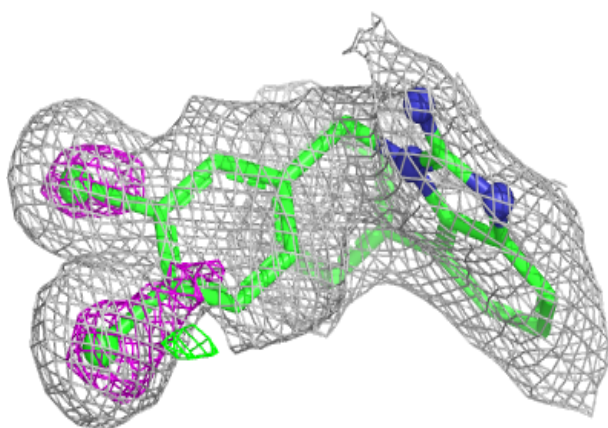
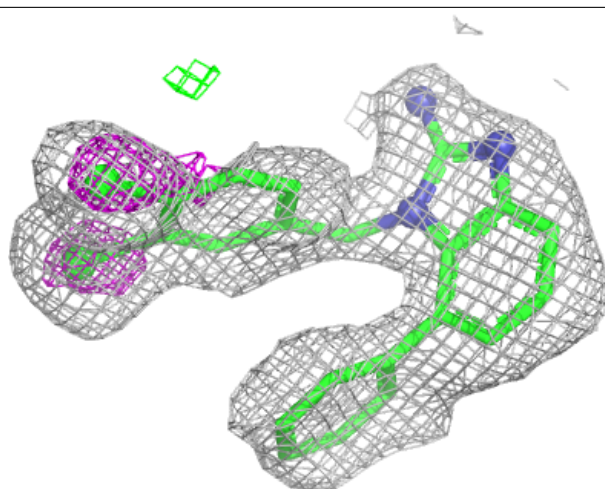
Electron density around VGF B 1269:

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



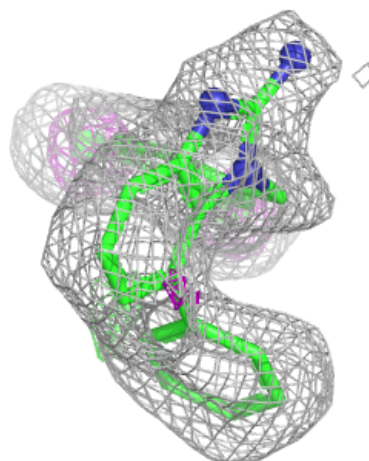
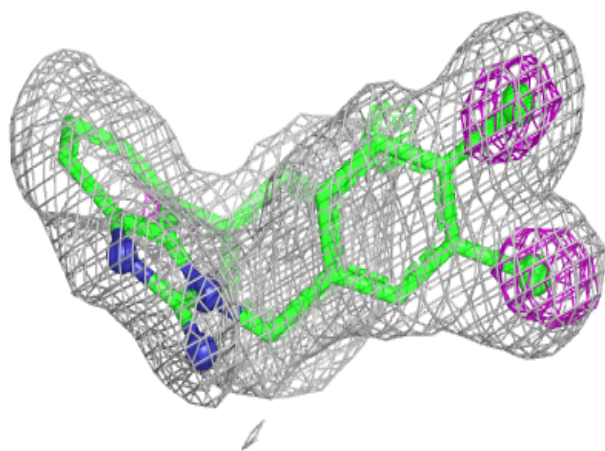
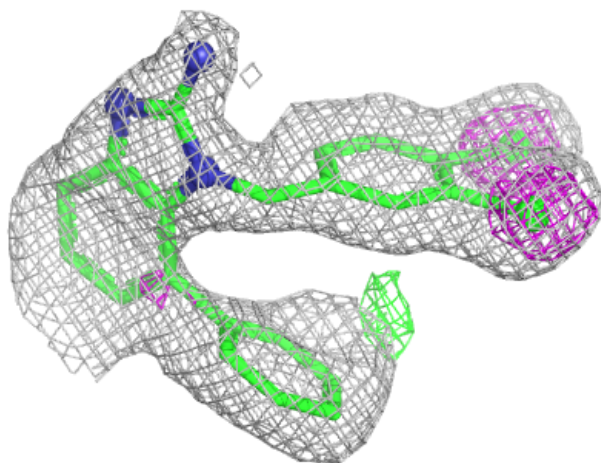
Electron density around VGF C 1270:

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



Electron density around VGF D 1269:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.