



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 08:48 am BST

PDB ID : 5A3S
Title : Crystal structure of the (SR) Calcium ATPase E2-vanadate complex bound to thapsigargin and TNP-ATP
Authors : Clausen, J.D.; Bublitz, M.; Arnou, B.; Olesen, C.; Andersen, J.P.; Moller, J.V.; Nissen, P.
Deposited on : 2015-06-03
Resolution : 3.30 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 following versions of software and data (see [references ⓘ](#)) 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 : 2.11
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) : 2.11

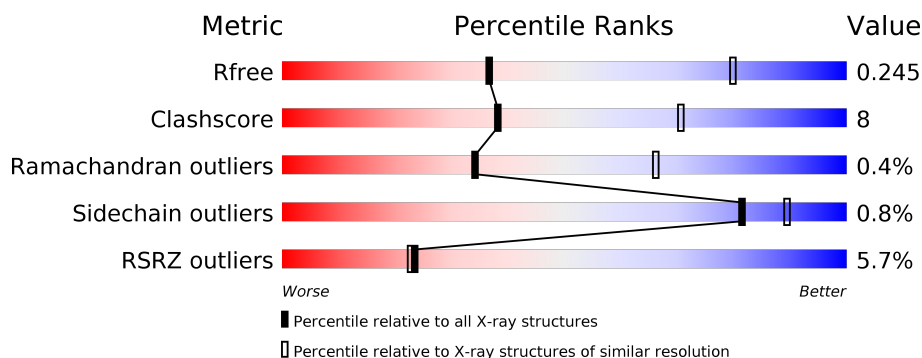
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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 on 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	995	<div> <div>6%</div> <div>83%</div> <div>16%</div> </div>
1	B	995	<div> <div>6%</div> <div>83%</div> <div>16%</div> </div>

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 15554 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.

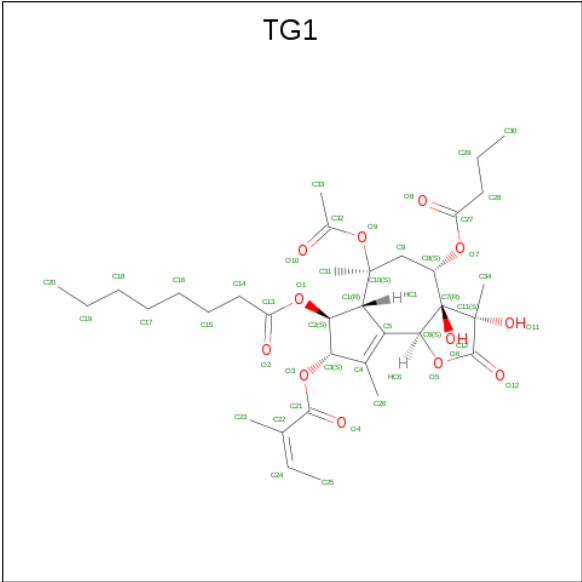
- Molecule 1 is a protein called SARCOPLASMIC RETICULUM CALCIUM ATPASE 1 MOLECULE SARCOPLASMIC/ENDOPLASMIC RETICULUM CALCIUM ATPASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	995	Total	C	N	O	S	0	0	0
			7672	4877	1287	1451	57			
1	B	995	Total	C	N	O	S	0	0	0
			7674	4878	1287	1452	57			

There are 2 discrepancies between the modelled and reference sequences:

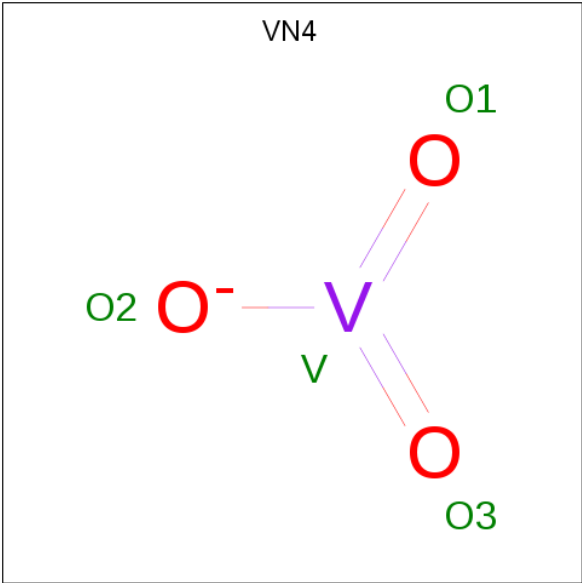
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ACE	-	acetylation	UNP PO4191
B	0	ACE	-	acetylation	UNP PO4191

- Molecule 2 is OCTANOIC ACID [3S-[3ALPHA, 3ABETA, 4ALPHA, 6BETA, 6ABETA, 7BETA, 8ALPHA(Z), 9BALPHA]]-6-(ACETYLOXY)-2,3,-3A,4,5,6,6A,7,8,9B-DECAHYDRO-3,3A-DIHYDROXY-3,6,9-TRIMETHYL-8-[(2-METHYL-1-OXO-2-BUTENYL)OXY]-2-OXO-4-(1-OXOBUTOXY)-AZULENO[4,5-B]FURAN-7-YL ESTER (three-letter code: TG1) (formula: C₃₄H₅₀O₁₂).



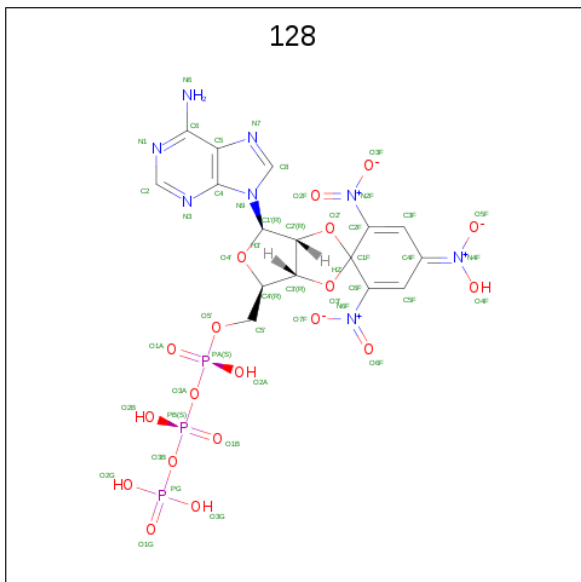
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			46	34	12		
2	B	1	Total	C	O	0	0
			46	34	12		

- Molecule 3 is oxido(dioxo)vanadium (three-letter code: VN4) (formula: O₃V).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	V	0	0
			4	3	1		
3	B	1	Total	O	V	0	0
			4	3	1		

- Molecule 4 is SPIRO(2,4,6-TRINITROBENZENE[1,2A]-2O',3O'-METHYLENE-ADENIN E-TRIPHOSPHATE (three-letter code: 128) (formula: $C_{16}H_{17}N_8O_{19}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			46	16	8	19	3		
4	B	1	Total	C	N	O	P	0	0
			46	16	8	19	3		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 6 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	K	0	0
			1	1		
6	A	1	Total	K	0	0
			1	1		

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total 1	Cl 1	0	0
7	A	1	Total 1	Cl 1	0	0

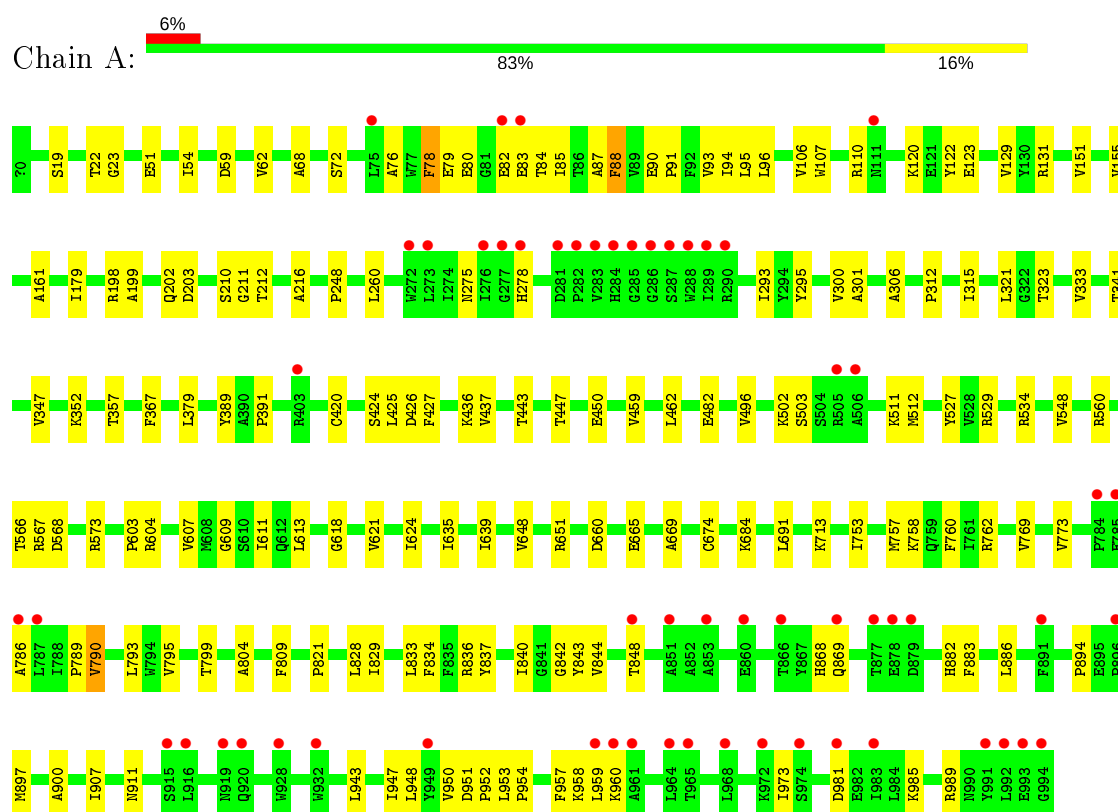
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	4	Total 4	O 4	0	0
8	B	4	Total 4	O 4	0	0

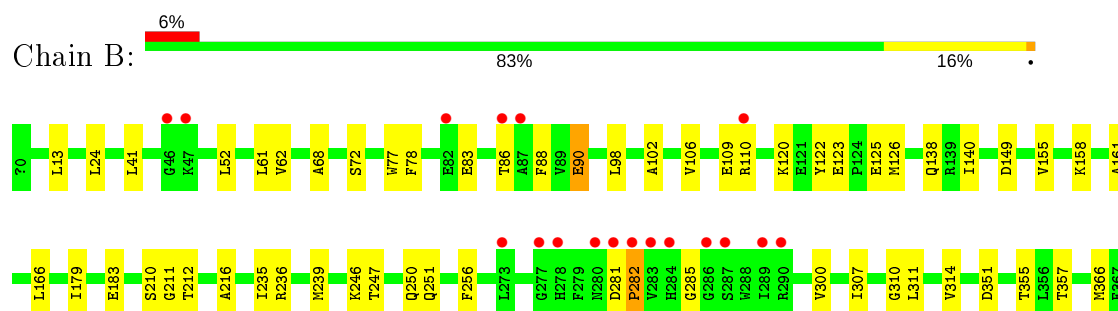
3 Residue-property plots

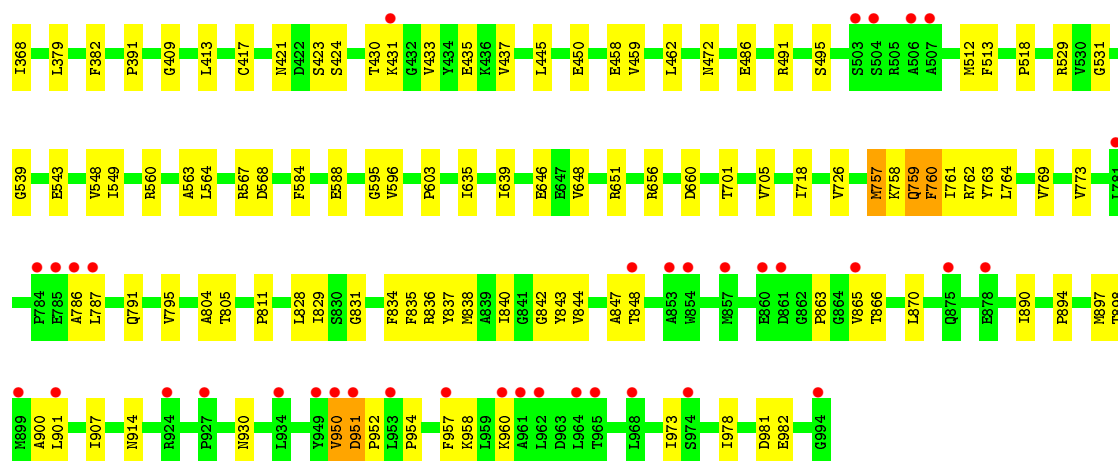
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: SARCOPLASMIC RETICULUM CALCIUM ATPASE 1 MOLECULE SARCOPLASMIC/ENDOPLASMIC RETICULUM CALCIUM ATPASE 1



- Molecule 1: SARCOPLASMIC RETICULUM CALCIUM ATPASE 1 MOLECULE SARCOPLASMIC/ENDOPLASMIC RETICULUM CALCIUM ATPASE 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	130.56 Å 93.78 Å 135.69 Å 90.00° 107.26° 90.00°	Depositor
Resolution (Å)	78.91 – 3.30 78.90 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (78.91-3.30) 99.8 (78.90-3.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 3.33 Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.210 , 0.245 0.210 , 0.245	Depositor DCC
R_{free} test set	783 reflections (1.65%)	wwPDB-VP
Wilson B-factor (Å ²)	97.1	Xtriage
Anisotropy	0.228	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 70.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.015 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15554	wwPDB-VP
Average B, all atoms (Å ²)	135.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.57% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, TG1, ACE, CL, K, VN4, 128

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	0.26	0/7810	0.43	0/10588
1	B	0.26	0/7813	0.43	0/10594
All	All	0.26	0/15623	0.43	0/21182

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

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	7672	0	7765	117	0
1	B	7674	0	7767	107	0
2	A	46	0	50	15	0
2	B	46	0	50	13	0
3	A	4	0	0	0	0
3	B	4	0	0	0	0
4	A	46	0	13	1	0
4	B	46	0	13	1	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	1	0	0	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	A	4	0	0	0	0
8	B	4	0	0	1	0
All	All	15554	0	15658	236	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 8.

All (236) 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:848:THR:HG23	1:B:900:ALA:HB1	1.58	0.86
1:A:950:VAL:HG12	1:A:952:PRO:HD2	1.60	0.83
1:A:82:GLU:CA	1:A:83:GLU:N	2.43	0.82
1:A:260:LEU:HD13	2:A:1000:TG1:H232	1.61	0.80
2:A:1000:TG1:H313	2:A:1000:TG1:H332	1.63	0.80
1:B:769:VAL:HG21	2:B:1000:TG1:H333	1.62	0.80
1:A:894:PRO:HB3	1:A:959:LEU:H	1.50	0.76
1:B:646:GLU:OE2	1:B:651:ARG:NH1	2.19	0.74
1:B:786:ALA:HA	1:B:897:MET:HA	1.70	0.73
1:A:790:VAL:HB	1:A:957:PHE:HE1	1.54	0.72
1:A:848:THR:HG23	1:A:900:ALA:HB1	1.71	0.72
1:A:947:ILE:HD13	1:A:953:LEU:HD13	1.70	0.71
1:A:829:ILE:HG21	2:A:1000:TG1:H333	1.72	0.70
1:B:811:PRO:HD3	1:B:930:ASN:HD21	1.57	0.69
1:A:23:GLY:HA3	1:A:131:ARG:HA	1.74	0.69
1:A:85:ILE:O	1:A:88:PHE:HB3	1.91	0.69
1:A:829:ILE:HA	1:A:833:LEU:HD23	1.75	0.68
1:A:773:VAL:HG11	1:A:842:GLY:HA2	1.77	0.66
1:A:773:VAL:HG22	2:A:1000:TG1:H202	1.76	0.66
1:A:894:PRO:HA	1:A:958:LYS:HD2	1.75	0.66
1:A:260:LEU:HD11	1:A:306:ALA:HB1	1.77	0.66
1:A:651:ARG:NH2	1:A:674:CYS:SG	2.69	0.66
1:A:769:VAL:HA	2:A:1000:TG1:H251	1.79	0.65
1:A:897:MET:HB2	1:A:958:LYS:HG3	1.81	0.63
1:B:829:ILE:HD12	2:B:1000:TG1:HC91	1.80	0.62
1:B:835:PHE:HA	1:B:838:MET:HB3	1.81	0.62
1:B:125:GLU:HG3	1:B:126:MET:HG2	1.81	0.62
1:A:790:VAL:HB	1:A:957:PHE:CE1	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:19:SER:HB3	1:A:22:THR:HG22	1.82	0.62
2:B:1000:TG1:HC92	2:B:1000:TG1:O10	1.99	0.62
1:B:866:THR:CG2	1:B:870:LEU:HB2	2.29	0.61
1:A:76:ALA:HB1	1:A:88:PHE:CD2	2.35	0.61
1:A:786:ALA:HA	1:A:897:MET:HG2	1.83	0.61
1:A:155:VAL:HG12	1:A:216:ALA:HA	1.81	0.61
1:A:665:GLU:O	1:A:669:ALA:HB2	2.01	0.60
1:B:648:VAL:HG13	1:B:651:ARG:HB2	1.83	0.60
1:A:90:GLU:HG3	1:A:91:PRO:HD3	1.83	0.60
1:B:368:ILE:HG21	1:B:409:GLY:HA3	1.83	0.60
1:A:603:PRO:HB3	1:A:639:ILE:HD11	1.84	0.59
1:A:836:ARG:NH1	1:A:981:ASP:OD1	2.35	0.59
1:A:834:PHE:CZ	2:A:1000:TG1:H142	2.38	0.58
1:B:109:GLU:HG2	1:B:110:ARG:H	1.69	0.58
1:A:91:PRO:O	1:A:95:LEU:N	2.34	0.57
1:B:183:GLU:OE2	8:B:2002:HOH:O	2.16	0.57
1:B:155:VAL:HG12	1:B:216:ALA:HA	1.86	0.57
1:A:948:LEU:HD13	1:A:960:LYS:HG3	1.86	0.57
1:B:424:SER:O	1:B:437:VAL:HB	2.05	0.57
1:B:486:GLU:O	1:B:491:ARG:NH2	2.36	0.57
1:B:529:ARG:NH2	1:B:568:ASP:OD1	2.37	0.57
1:A:459:VAL:HA	1:A:462:LEU:HG	1.87	0.56
2:B:1000:TG1:C24	2:B:1000:TG1:H311	2.36	0.56
1:A:757:MET:HA	1:A:760:PHE:CE2	2.41	0.56
1:B:705:VAL:HG22	1:B:726:VAL:HG11	1.88	0.55
1:A:837:TYR:HA	1:A:840:ILE:HG22	1.89	0.55
2:B:1000:TG1:H262	2:B:1000:TG1:H233	1.88	0.55
1:A:529:ARG:NH2	1:A:568:ASP:OD1	2.40	0.55
1:A:758:LYS:HG2	1:A:828:LEU:HD23	1.89	0.55
1:B:491:ARG:NH1	1:B:588:GLU:OE2	2.40	0.55
1:A:512:MET:HB2	1:A:567:ARG:HB3	1.89	0.54
1:B:512:MET:HB2	1:B:567:ARG:HB3	1.88	0.54
1:A:611:ILE:HG13	1:A:639:ILE:HG22	1.90	0.54
1:B:41:LEU:HB3	1:B:236:ARG:HD2	1.90	0.54
1:A:301:ALA:HB2	1:A:789:PRO:HG3	1.88	0.54
1:A:762:ARG:NH2	1:A:828:LEU:O	2.39	0.54
1:A:828:LEU:HD13	2:A:1000:TG1:H303	1.89	0.54
1:A:107:TRP:HA	1:A:110:ARG:HG2	1.89	0.53
1:B:246:LYS:HE2	1:B:251:GLN:HG2	1.88	0.53
1:B:773:VAL:HG11	1:B:842:GLY:HA2	1.89	0.53
1:B:914:ASN:HD21	1:B:978:ILE:HA	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:837:TYR:HA	1:B:840:ILE:HG22	1.89	0.53
1:A:560:ARG:HG3	4:A:1002:128:C2	2.39	0.53
1:B:357:THR:HA	1:B:603:PRO:HA	1.91	0.53
1:B:256:PHE:CE1	2:B:1000:TG1:H24	2.45	0.52
1:B:701:THR:HA	1:B:718:ILE:O	2.09	0.52
1:A:829:ILE:HG12	2:A:1000:TG1:HC8	1.92	0.52
1:A:59:ASP:HB3	1:A:62:VAL:HG12	1.92	0.52
1:A:943:LEU:O	1:A:947:ILE:HG12	2.11	0.51
1:A:72:SER:HB3	1:A:91:PRO:HB3	1.91	0.51
1:A:527:TYR:CD1	1:A:534:ARG:HD3	2.46	0.51
1:A:834:PHE:HZ	2:A:1000:TG1:H142	1.74	0.51
1:A:179:ILE:HD13	1:A:212:THR:HA	1.91	0.51
1:A:120:LYS:O	1:A:123:GLU:HG2	2.10	0.51
1:A:68:ALA:HB1	1:A:300:VAL:HG23	1.93	0.51
1:B:256:PHE:HE1	2:B:1000:TG1:H24	1.77	0.50
1:B:656:ARG:NH1	1:B:660:ASP:OD1	2.45	0.50
1:B:836:ARG:NH1	1:B:981:ASP:OD1	2.45	0.50
1:B:68:ALA:HB1	1:B:300:VAL:HG23	1.93	0.50
1:B:844:VAL:HB	1:B:907:ILE:HG21	1.93	0.50
1:B:950:VAL:HG22	1:B:951:ASP:H	1.76	0.49
2:B:1000:TG1:C4	2:B:1000:TG1:H233	2.43	0.49
1:A:604:ARG:HB2	1:A:607:VAL:HG23	1.94	0.49
1:B:247:THR:O	1:B:250:GLN:HG2	2.13	0.49
1:B:68:ALA:O	1:B:72:SER:OG	2.24	0.49
1:B:757:MET:O	1:B:760:PHE:HD1	1.95	0.49
1:B:431:LYS:HG3	1:B:435:GLU:OE2	2.12	0.49
2:B:1000:TG1:H142	2:B:1000:TG1:H332	1.93	0.49
1:B:281:ASP:HB2	1:B:282:PRO:HD3	1.95	0.49
2:A:1000:TG1:H333	2:A:1000:TG1:HC91	1.94	0.48
1:A:795:VAL:HA	1:A:799:THR:HG22	1.95	0.48
1:B:866:THR:HG23	1:B:870:LEU:HB2	1.94	0.48
1:B:757:MET:O	1:B:758:LYS:C	2.52	0.48
1:B:950:VAL:HG13	1:B:954:PRO:HD3	1.95	0.48
1:B:847:ALA:HB2	1:B:973:ILE:HG21	1.95	0.48
1:B:901:LEU:HD23	1:B:957:PHE:CZ	2.48	0.48
1:B:539:GLY:O	1:B:543:GLU:HG2	2.13	0.48
1:B:898:THR:HG21	1:B:960:LYS:HB3	1.96	0.48
1:A:844:VAL:HB	1:A:907:ILE:HG21	1.95	0.48
1:A:907:ILE:O	1:A:911:ASN:HB2	2.13	0.48
1:A:323:THR:HG23	1:A:333:VAL:HB	1.95	0.47
1:A:436:LYS:HB2	1:A:443:THR:HG21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1000:TG1:C26	2:B:1000:TG1:H233	2.43	0.47
1:A:94:ILE:HG12	1:A:793:LEU:HD21	1.95	0.47
1:B:762:ARG:NH2	1:B:828:LEU:O	2.46	0.47
1:A:357:THR:HA	1:A:603:PRO:HA	1.96	0.47
1:A:829:ILE:HG12	2:A:1000:TG1:C9	2.45	0.47
1:B:179:ILE:HD13	1:B:212:THR:HA	1.96	0.47
1:B:282:PRO:HB2	1:B:285:GLY:HA3	1.97	0.47
1:B:795:VAL:HG21	1:B:901:LEU:HD11	1.96	0.47
1:B:72:SER:HB3	1:B:90:GLU:OE1	2.14	0.47
1:A:950:VAL:HG12	1:A:951:ASP:N	2.29	0.47
1:A:950:VAL:O	1:A:954:PRO:HG2	2.14	0.47
1:A:84:THR:OG1	1:A:87:ALA:HB3	2.14	0.46
1:B:757:MET:O	1:B:760:PHE:CD1	2.69	0.46
1:A:837:TYR:HD2	2:A:1000:TG1:H331	1.81	0.46
1:A:611:ILE:HG13	1:A:639:ILE:CG2	2.46	0.46
1:B:391:PRO:HB3	1:B:450:GLU:HB3	1.96	0.46
1:A:950:VAL:CG1	1:A:952:PRO:HD2	2.39	0.46
1:B:366:MET:HG3	1:B:382:PHE:HB2	1.96	0.46
1:A:424:SER:O	1:A:437:VAL:HB	2.16	0.46
1:B:957:PHE:O	1:B:958:LYS:HB2	2.15	0.46
1:A:609:GLY:O	1:A:613:LEU:HG	2.16	0.46
1:A:951:ASP:HB3	1:A:952:PRO:HD3	1.98	0.46
1:B:459:VAL:HA	1:B:462:LEU:HG	1.97	0.46
1:B:61:LEU:HB2	1:B:307:ILE:HD12	1.96	0.46
1:A:78:PHE:CE2	1:A:293:ILE:HG21	2.50	0.46
1:B:758:LYS:HG2	1:B:828:LEU:HD22	1.97	0.46
1:A:76:ALA:HB1	1:A:88:PHE:HD2	1.78	0.46
1:A:512:MET:O	1:A:566:THR:HA	2.16	0.45
2:A:1000:TG1:C33	2:A:1000:TG1:HC91	2.46	0.45
1:A:352:LYS:HD2	1:A:635:ILE:HG13	1.97	0.45
1:A:868:HIS:ND1	1:A:869:GLN:HG3	2.32	0.45
1:A:129:VAL:HG12	1:A:151:VAL:HG22	1.98	0.45
1:A:312:PRO:HA	1:A:315:ILE:HG12	1.99	0.45
1:B:978:ILE:O	1:B:982:GLU:HB2	2.16	0.45
1:A:379:LEU:HD12	1:A:548:VAL:HG21	1.99	0.45
1:A:985:LYS:HG2	1:A:989:ARG:HH12	1.82	0.45
1:B:368:ILE:HD13	1:B:595:GLY:HA3	1.99	0.45
1:A:248:PRO:HD2	1:A:341:THR:HG22	1.99	0.44
1:A:78:PHE:CG	1:A:80:GLU:HG3	2.52	0.44
1:A:624:ILE:HG22	1:A:684:LYS:HE2	1.98	0.44
2:B:1000:TG1:C14	2:B:1000:TG1:H332	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:829:ILE:O	2:B:1000:TG1:H343	2.17	0.44
1:B:413:LEU:HD12	1:B:564:LEU:HD22	2.00	0.44
1:B:635:ILE:O	1:B:639:ILE:HG12	2.17	0.44
2:B:1000:TG1:O5	2:B:1000:TG1:H261	2.18	0.44
1:A:618:GLY:HA3	1:A:821:PRO:HD3	1.99	0.44
1:A:78:PHE:CZ	1:A:293:ILE:HG13	2.53	0.44
1:A:843:TYR:CE2	1:A:973:ILE:HG23	2.52	0.44
1:B:314:VAL:HG12	1:B:760:PHE:CE2	2.52	0.44
1:B:843:TYR:CE2	1:B:973:ILE:HG23	2.53	0.44
1:A:106:VAL:O	1:A:110:ARG:HG2	2.17	0.44
1:B:560:ARG:HG3	4:B:1002:128:N1	2.33	0.44
1:A:275:ASN:HB2	1:A:278:HIS:HB2	2.00	0.43
1:A:198:ARG:NH2	1:A:660:ASP:OD1	2.51	0.43
1:A:760:PHE:HB2	1:A:804:ALA:HB1	2.00	0.43
1:B:760:PHE:HD1	1:B:761:ILE:N	2.16	0.43
1:A:391:PRO:HB3	1:A:450:GLU:HB3	1.99	0.43
1:B:311:LEU:HD13	1:B:764:LEU:HD12	2.01	0.43
1:B:379:LEU:HD12	1:B:548:VAL:HG21	1.99	0.43
1:B:897:MET:HB2	1:B:958:LYS:HE3	2.00	0.43
1:A:753:ILE:O	1:A:757:MET:HG3	2.18	0.43
1:A:78:PHE:HE2	1:A:293:ILE:HG21	1.84	0.43
1:B:894:PRO:HA	1:B:958:LYS:HD2	2.01	0.43
1:A:502:LYS:HG3	1:A:503:SER:H	1.83	0.43
1:B:417:CYS:HB3	1:B:445:LEU:HB3	1.99	0.43
1:A:648:VAL:HG13	1:A:651:ARG:HB2	2.01	0.43
1:B:759:GLN:OE1	1:B:762:ARG:NH1	2.43	0.43
1:A:347:VAL:HG11	1:A:691:LEU:HD13	2.01	0.42
1:A:883:PHE:HB3	1:A:886:LEU:HD11	2.01	0.42
1:A:90:GLU:O	1:A:94:ILE:HG13	2.18	0.42
1:B:13:LEU:HD21	1:B:166:LEU:HD21	2.01	0.42
1:B:122:TYR:O	1:B:211:GLY:HA2	2.19	0.42
1:B:235:ILE:O	1:B:239:MET:HG3	2.19	0.42
1:B:549:ILE:HD11	1:B:596:VAL:HG21	1.99	0.42
1:B:62:VAL:HG23	1:B:98:LEU:HD22	2.01	0.42
1:A:426:ASP:OD1	1:A:427:PHE:N	2.52	0.42
1:A:51:GLU:HA	1:A:54:ILE:HG22	2.02	0.42
1:A:161:ALA:HA	1:A:210:SER:HB2	2.01	0.42
1:A:278:HIS:CE1	1:A:295:TYR:HH	2.27	0.42
1:A:511:LYS:CD	1:A:568:ASP:HA	2.50	0.42
1:B:310:GLY:O	1:B:314:VAL:HG23	2.20	0.42
1:A:199:ALA:HB1	1:A:203:ASP:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:83:GLU:HB2	1:B:86:THR:HB	2.02	0.42
1:A:611:ILE:HD12	1:A:621:VAL:HG11	2.02	0.42
1:B:52:LEU:HD23	1:B:52:LEU:O	2.20	0.42
1:B:760:PHE:CD1	1:B:761:ILE:N	2.88	0.42
1:B:760:PHE:O	1:B:763:TYR:HB3	2.20	0.42
1:B:760:PHE:HD2	1:B:804:ALA:O	2.01	0.42
1:B:865:VAL:O	1:B:866:THR:HB	2.20	0.42
2:A:1000:TG1:H203	2:A:1000:TG1:H172	1.77	0.42
1:A:122:TYR:O	1:A:211:GLY:HA2	2.20	0.42
1:A:950:VAL:HG12	1:A:951:ASP:H	1.85	0.42
1:B:495:SER:HA	1:B:513:PHE:O	2.19	0.42
1:B:950:VAL:CG1	1:B:954:PRO:HD3	2.50	0.42
1:A:93:VAL:HA	1:A:96:LEU:HG	2.02	0.42
1:A:389:TYR:HB3	1:A:425:LEU:HD11	2.01	0.41
1:A:88:PHE:O	1:A:91:PRO:HD2	2.20	0.41
1:B:138:GLN:HB3	1:B:140:ILE:HG23	2.02	0.41
1:A:90:GLU:OE1	1:A:789:PRO:HB2	2.18	0.41
1:B:834:PHE:O	1:B:838:MET:HB2	2.20	0.41
1:A:367:PHE:CD1	1:A:379:LEU:HD13	2.56	0.41
1:B:102:ALA:O	1:B:106:VAL:HG23	2.21	0.41
1:A:829:ILE:CG1	2:A:1000:TG1:HC8	2.50	0.41
1:A:713:LYS:HD2	1:A:713:LYS:HA	1.88	0.41
1:B:491:ARG:NH1	1:B:584:PHE:HB3	2.35	0.41
1:B:158:LYS:HB2	1:B:158:LYS:HE3	1.92	0.41
1:B:314:VAL:HG13	1:B:805:THR:OG1	2.21	0.41
1:A:202:GLN:OE1	1:A:202:GLN:N	2.53	0.41
1:A:420:CYS:HA	1:A:496:VAL:HG21	2.03	0.41
1:B:24:LEU:HG	1:B:149:ASP:HA	2.03	0.41
1:B:787:LEU:HD21	1:B:848:THR:HG21	2.03	0.41
1:A:321:LEU:HD13	1:A:809:PHE:HZ	1.85	0.41
1:B:120:LYS:O	1:B:123:GLU:HG2	2.21	0.41
1:B:907:ILE:HD11	1:B:973:ILE:HG22	2.03	0.41
1:A:443:THR:O	1:A:447:THR:HG22	2.21	0.41
1:B:351:ASP:O	1:B:355:THR:HB	2.21	0.41
1:B:314:VAL:HG12	1:B:760:PHE:HE2	1.85	0.40
1:B:77:TRP:HD1	1:B:78:PHE:CE1	2.38	0.40
1:B:791:GLN:HG2	1:B:957:PHE:CE1	2.56	0.40
1:A:482:GLU:OE2	1:A:573:ARG:NH1	2.54	0.40
1:B:423:SER:HB2	1:B:437:VAL:O	2.20	0.40
1:B:431:LYS:HB3	1:B:433:VAL:HG12	2.03	0.40
1:B:863:PRO:HG2	1:B:890:ILE:HG21	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:518:PRO:HA	1:B:563:ALA:HB2	2.03	0.40
1:B:161:ALA:HA	1:B:210:SER:HB2	2.04	0.40
1:B:958:LYS:HE2	1:B:958:LYS:HB2	1.89	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	991/995 (100%)	925 (93%)	66 (7%)	0	100	100
1	B	993/995 (100%)	931 (94%)	55 (6%)	7 (1%)	22	54
All	All	1984/1990 (100%)	1856 (94%)	121 (6%)	7 (0%)	34	66

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	531	GLY
1	B	831	GLY
1	B	950	VAL
1	B	282	PRO
1	B	458	GLU
1	B	951	ASP
1	B	952	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	840/840 (100%)	835 (99%)	5 (1%)	86	91
1	B	840/840 (100%)	832 (99%)	8 (1%)	76	86
All	All	1680/1680 (100%)	1667 (99%)	13 (1%)	81	89

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	PHE
1	A	79	GLU
1	A	88	PHE
1	A	790	VAL
1	A	882	HIS
1	B	88	PHE
1	B	90	GLU
1	B	421	ASN
1	B	430	THR
1	B	472	ASN
1	B	757	MET
1	B	759	GLN
1	B	760	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	810	ASN
1	B	930	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 carbohydrates in this entry.

5.6 Ligand geometry

Of 14 ligands modelled in this entry, 8 are monoatomic - leaving 6 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
3	VN4	B	1001	1,8,5	0,3,3	0.00	-	-		
4	128	A	1002	5	33,50,50	1.47	6 (18%)	36,80,80	1.18	2 (5%)
4	128	B	1002	5	33,50,50	1.48	6 (18%)	36,80,80	1.32	6 (16%)
3	VN4	A	1001	1,8,5	0,3,3	0.00	-	-		
2	TG1	A	1000	-	43,48,48	0.93	1 (2%)	44,72,72	1.24	4 (9%)
2	TG1	B	1000	-	43,48,48	0.88	1 (2%)	44,72,72	0.86	1 (2%)

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
4	128	B	1002	5	-	5/22/80/80	0/5/5/5
4	128	A	1002	5	-	5/22/80/80	0/5/5/5
2	TG1	A	1000	-	-	18/33/99/99	0/3/3/3
2	TG1	B	1000	-	-	9/33/99/99	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1002	128	C5F-C6F	4.71	1.51	1.37
4	A	1002	128	C5F-C6F	4.60	1.50	1.37
4	B	1002	128	PG-O1G	3.03	1.60	1.50
4	A	1002	128	PG-O1G	3.00	1.60	1.50
4	A	1002	128	C8-N7	-2.45	1.30	1.34
4	B	1002	128	C8-N7	-2.40	1.30	1.34
4	B	1002	128	PG-O3G	-2.36	1.45	1.54
4	A	1002	128	PG-O3G	-2.30	1.46	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1002	128	C5F-C4F	-2.28	1.32	1.40
4	B	1002	128	PA-O1A	2.28	1.59	1.50
4	A	1002	128	PA-O1A	2.27	1.59	1.50
4	B	1002	128	C5F-C4F	-2.20	1.32	1.40
2	B	1000	TG1	C1-C5	2.02	1.54	1.51
2	A	1000	TG1	C1-C5	2.01	1.54	1.51

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1000	TG1	C10-O9-C32	4.09	131.25	121.53
4	B	1002	128	O3G-PG-O3B	3.42	116.12	104.64
4	A	1002	128	O3G-PG-O3B	3.27	115.62	104.64
4	B	1002	128	O2'-C1F-C2F	-3.12	106.20	110.47
4	B	1002	128	O2'-C1F-C6F	2.46	113.83	110.47
4	A	1002	128	O3'-C1F-C6F	-2.44	107.13	110.47
2	A	1000	TG1	O7-C8-C9	2.40	110.92	106.63
2	B	1000	TG1	C10-O9-C32	2.36	127.15	121.53
2	A	1000	TG1	O1-C13-C14	2.18	116.21	111.50
2	A	1000	TG1	O1-C13-O2	-2.17	118.47	123.70
4	B	1002	128	O3'-C1F-C6F	-2.15	107.53	110.47
4	B	1002	128	C5'-C4'-C3'	2.13	121.47	114.40
4	B	1002	128	O3'-C3'-C2'	2.03	106.83	103.58

There are no chirality outliers.

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1002	128	C5'-O5'-PA-O2A
4	A	1002	128	O4'-C4'-C5'-O5'
4	B	1002	128	C5'-O5'-PA-O1A
4	B	1002	128	C5'-O5'-PA-O2A
2	A	1000	TG1	O3-C21-C22-C23
2	A	1000	TG1	O3-C21-C22-C24
2	A	1000	TG1	O10-C32-O9-C10
2	A	1000	TG1	C33-C32-O9-C10
2	A	1000	TG1	O8-C27-O7-C8
2	A	1000	TG1	C28-C27-O7-C8
2	B	1000	TG1	C9-C10-O9-C32
2	B	1000	TG1	C1-C10-O9-C32
2	B	1000	TG1	C14-C13-O1-C2
2	B	1000	TG1	C2-C3-O3-C21

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Mol	Chain	Res	Type	Atoms
2	B	1000	TG1	C22-C21-O3-C3
2	B	1000	TG1	O2-C13-O1-C2
4	A	1002	128	C3'-C4'-C5'-O5'
2	A	1000	TG1	C13-C14-C15-C16
2	B	1000	TG1	O4-C21-O3-C3
4	B	1002	128	O4'-C4'-C5'-O5'
4	B	1002	128	C3'-C4'-C5'-O5'
2	A	1000	TG1	O4-C21-C22-C23
2	B	1000	TG1	C14-C15-C16-C17
2	A	1000	TG1	C16-C17-C18-C19
2	A	1000	TG1	C17-C18-C19-C20
2	A	1000	TG1	O4-C21-C22-C24
2	A	1000	TG1	C14-C13-O1-C2
2	B	1000	TG1	C15-C16-C17-C18
2	A	1000	TG1	O2-C13-O1-C2
4	A	1002	128	C5'-O5'-PA-O3A
4	B	1002	128	C5'-O5'-PA-O3A
4	A	1002	128	C5'-O5'-PA-O1A
2	A	1000	TG1	C21-C22-C24-C25
2	A	1000	TG1	C14-C15-C16-C17
2	A	1000	TG1	O7-C27-C28-C29
2	A	1000	TG1	O8-C27-C28-C29
2	A	1000	TG1	C27-C28-C29-C30

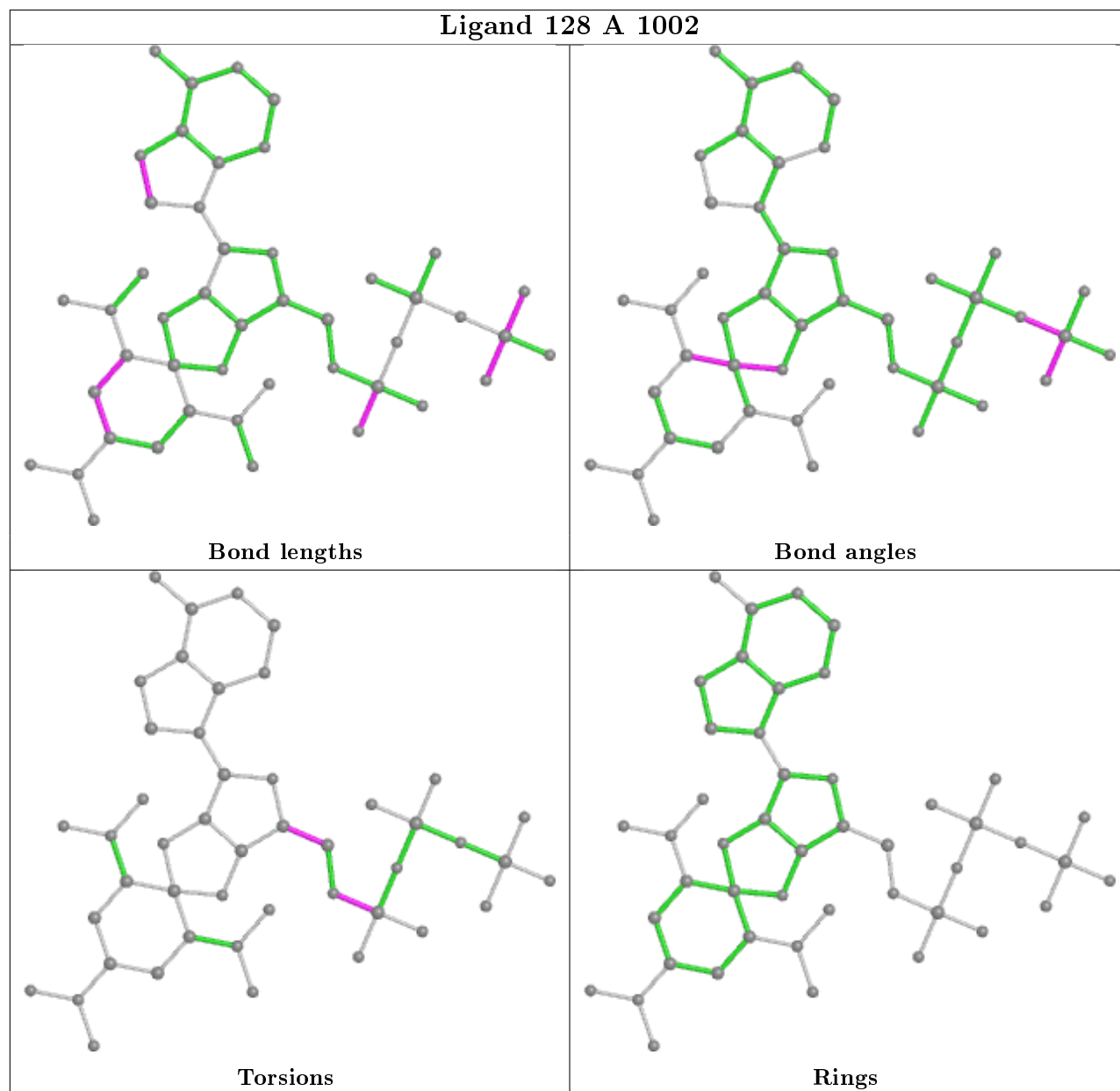
There are no ring outliers.

4 monomers are involved in 30 short contacts:

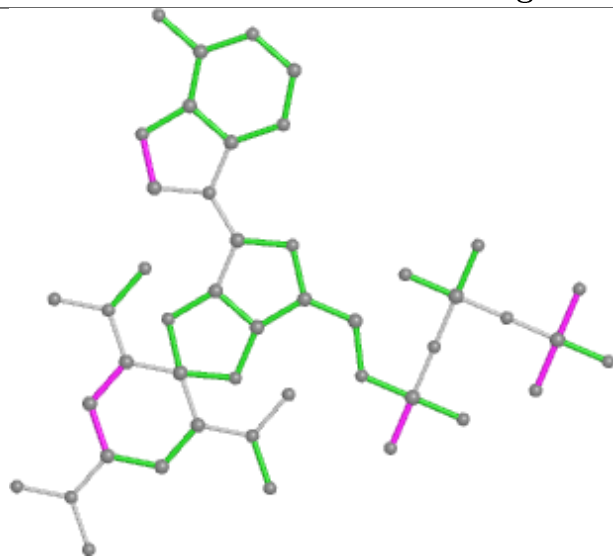
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1002	128	1	0
4	B	1002	128	1	0
2	A	1000	TG1	15	0
2	B	1000	TG1	13	0

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

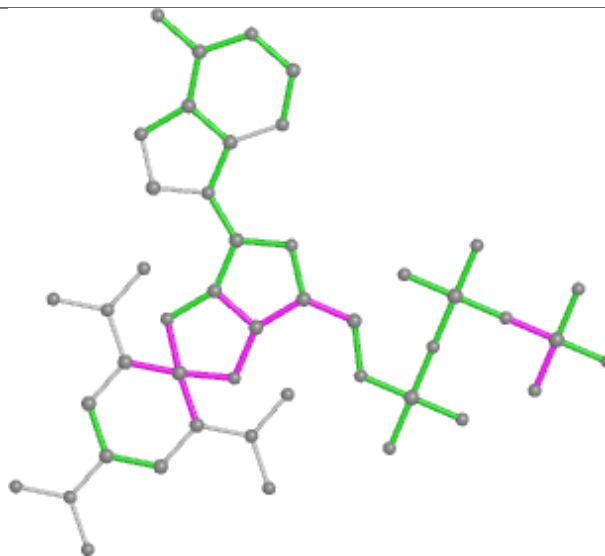
any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



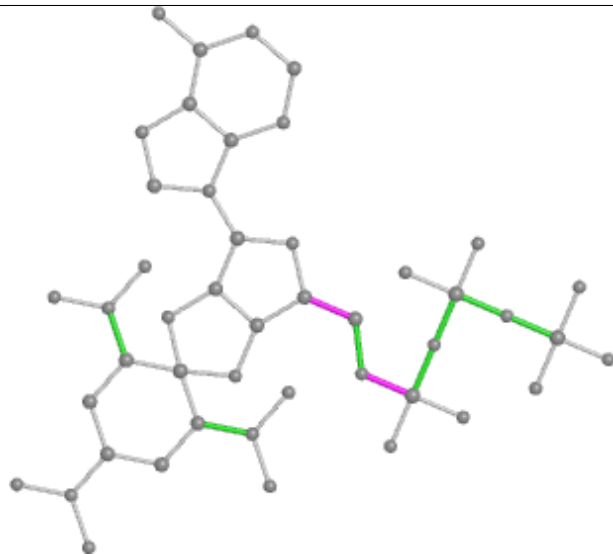
Ligand 128 B 1002



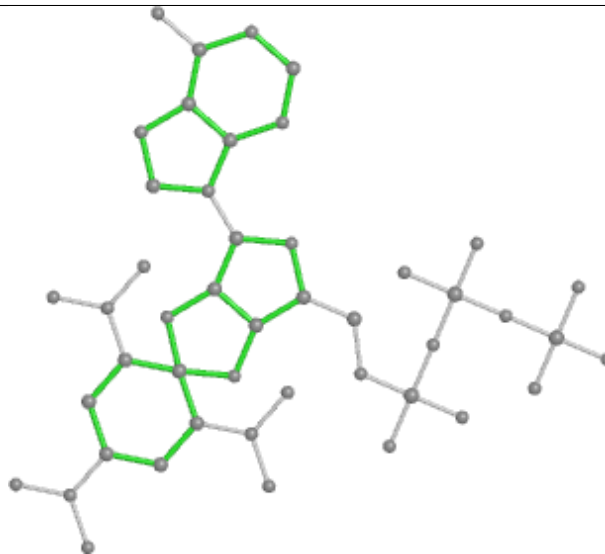
Bond lengths



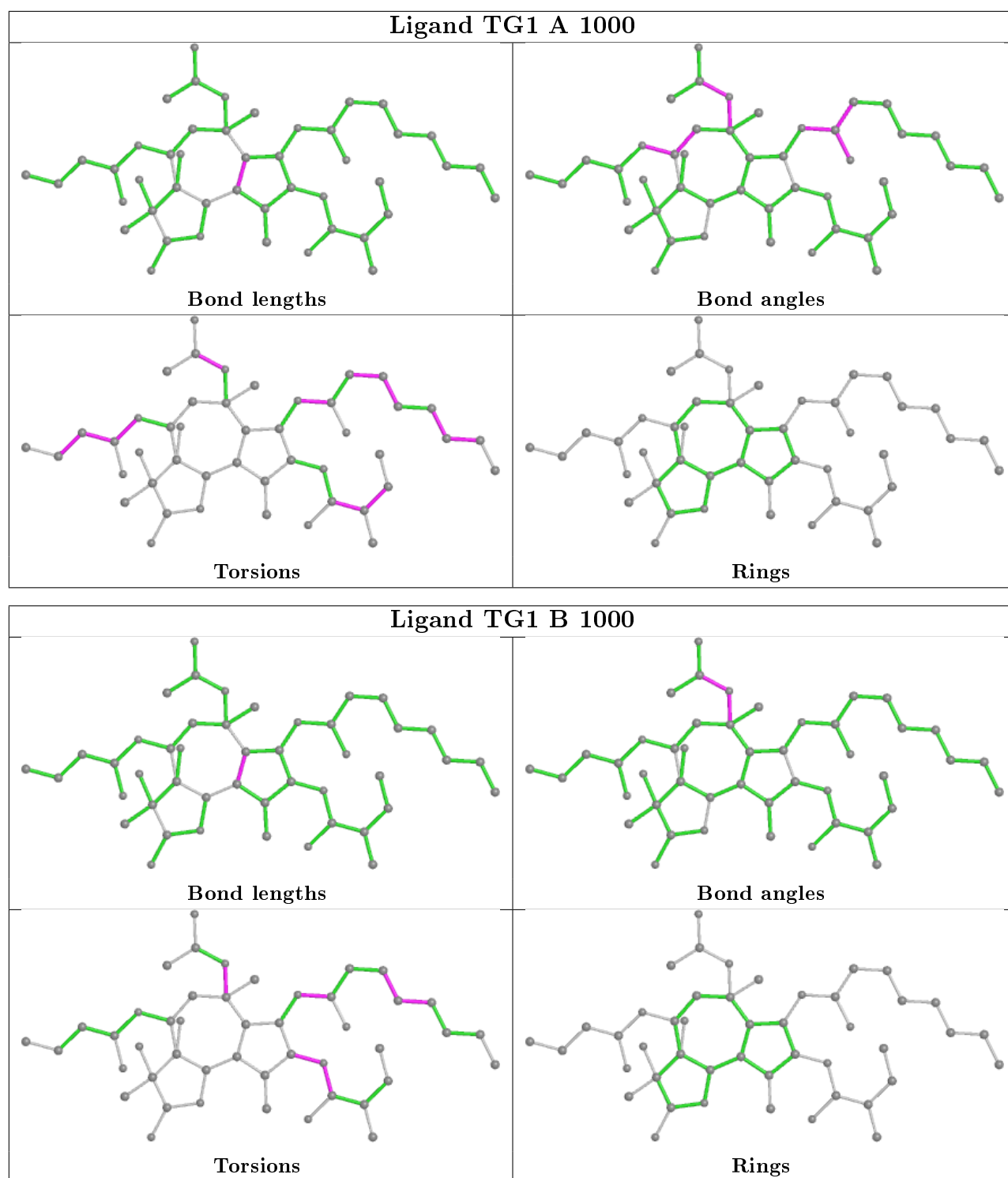
Bond angles



Torsions



Rings



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	994/995 (99%)	0.25	58 (5%)	23	22	51, 110, 250, 425	0
1	B	994/995 (99%)	0.20	55 (5%)	25	23	50, 126, 250, 377	0
All	All	1988/1990 (99%)	0.23	113 (5%)	23	23	50, 119, 250, 425	0

All (113) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	961	ALA	12.9
1	A	284	HIS	10.1
1	A	878	GLU	9.7
1	B	281	ASP	8.8
1	A	283	VAL	8.8
1	A	994	GLY	8.3
1	B	282	PRO	8.3
1	B	283	VAL	8.0
1	A	505	ARG	7.5
1	A	993	GLU	7.0
1	A	285	GLY	6.9
1	A	965	THR	6.6
1	B	47	LYS	6.6
1	B	962	LEU	6.6
1	B	46	GLY	6.4
1	B	278	HIS	5.5
1	B	280	ASN	5.4
1	A	286	GLY	5.2
1	B	957	PHE	5.0
1	A	287	SER	5.0
1	A	992	LEU	4.9
1	A	282	PRO	4.8
1	B	110	ARG	4.6
1	A	281	ASP	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	853	ALA	4.5
1	A	289	ILE	4.5
1	B	878	GLU	4.4
1	B	960	LYS	4.4
1	A	877	THR	4.3
1	A	277	GLY	4.1
1	B	284	HIS	4.1
1	A	276	ILE	4.0
1	B	860	GLU	3.9
1	A	961	ALA	3.9
1	B	289	ILE	3.8
1	B	875	GLN	3.7
1	A	972	LYS	3.7
1	B	286	GLY	3.6
1	A	278	HIS	3.6
1	A	964	LEU	3.5
1	B	949	TYR	3.5
1	B	507	ALA	3.5
1	B	974	SER	3.4
1	A	949	TYR	3.4
1	B	854	TRP	3.3
1	A	82	GLU	3.3
1	B	86	THR	3.3
1	B	431	LYS	3.3
1	A	506	ALA	3.3
1	A	932	TRP	3.2
1	A	915	SER	3.2
1	A	879	ASP	3.2
1	B	861	ASP	3.1
1	B	87	ALA	3.1
1	A	960	LYS	3.0
1	B	924	ARG	3.0
1	A	111	ASN	3.0
1	B	287	SER	3.0
1	A	981	ASP	2.9
1	B	901	LEU	2.9
1	A	272	TRP	2.8
1	B	277	GLY	2.8
1	A	786	ALA	2.8
1	A	974	SER	2.8
1	B	785	GLU	2.8
1	B	950	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	928	TRP	2.7
1	A	991	TYR	2.7
1	A	959	LEU	2.7
1	B	968	LEU	2.7
1	A	866	THR	2.7
1	B	273	LEU	2.7
1	B	784	PRO	2.7
1	A	290	ARG	2.6
1	B	994	GLY	2.6
1	B	865	VAL	2.6
1	B	853	ALA	2.6
1	B	506	ALA	2.5
1	B	290	ARG	2.5
1	B	965	THR	2.5
1	A	784	PRO	2.4
1	B	503	SER	2.4
1	A	916	LEU	2.4
1	B	82	GLU	2.4
1	B	781	LEU	2.4
1	A	787	LEU	2.4
1	A	851	ALA	2.4
1	A	860	GLU	2.4
1	A	848	THR	2.3
1	A	919	ASN	2.3
1	B	787	LEU	2.3
1	A	896	PRO	2.3
1	A	968	LEU	2.3
1	A	983	ILE	2.2
1	B	953	LEU	2.2
1	A	403	ARG	2.2
1	A	75	LEU	2.1
1	A	83	GLU	2.1
1	A	920	GLN	2.1
1	B	857	MET	2.1
1	A	273	LEU	2.1
1	A	891	PHE	2.1
1	A	785	GLU	2.1
1	B	786	ALA	2.1
1	B	848	THR	2.0
1	B	934	LEU	2.0
1	B	964	LEU	2.0
1	B	899	MET	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	951	ASP	2.0
1	B	927	PRO	2.0
1	A	288	TRP	2.0
1	B	504	SER	2.0
1	A	869	GLN	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 carbohydrates in this entry.

6.4 Ligands [i](#)

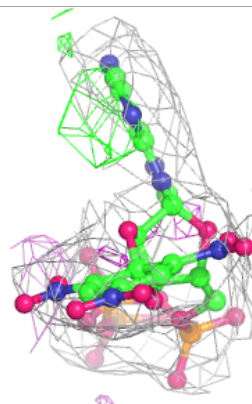
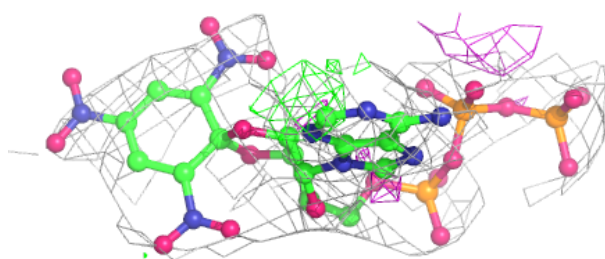
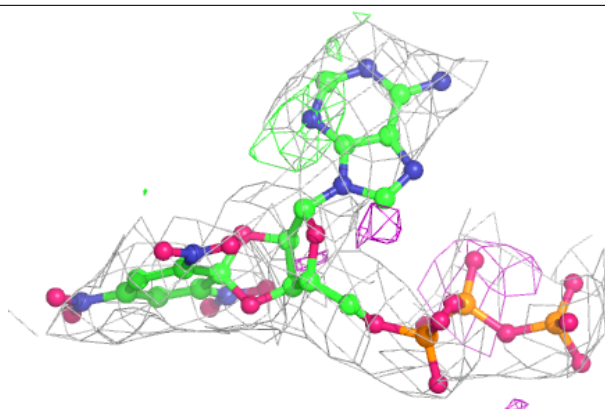
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	128	B	1002	46/46	0.84	0.23	153,187,205,208	0
2	TG1	B	1000	46/46	0.85	0.41	157,200,218,226	0
5	MG	A	1004	1/1	0.87	0.15	142,142,142,142	0
7	CL	B	1009	1/1	0.89	0.10	74,74,74,74	0
4	128	A	1002	46/46	0.90	0.20	107,144,157,169	0
6	K	B	1008	1/1	0.90	0.08	106,106,106,106	0
2	TG1	A	1000	46/46	0.91	0.47	122,165,182,193	0
5	MG	B	1004	1/1	0.92	0.11	195,195,195,195	0
7	CL	A	1009	1/1	0.96	0.14	74,74,74,74	0
5	MG	A	1003	1/1	0.96	0.28	92,92,92,92	0
6	K	A	1008	1/1	0.97	0.12	94,94,94,94	0
5	MG	B	1003	1/1	0.98	0.12	102,102,102,102	0
3	VN4	A	1001	4/4	0.99	0.26	85,95,118,119	0
3	VN4	B	1001	4/4	0.99	0.23	88,92,121,134	0

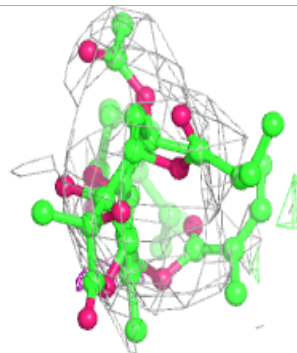
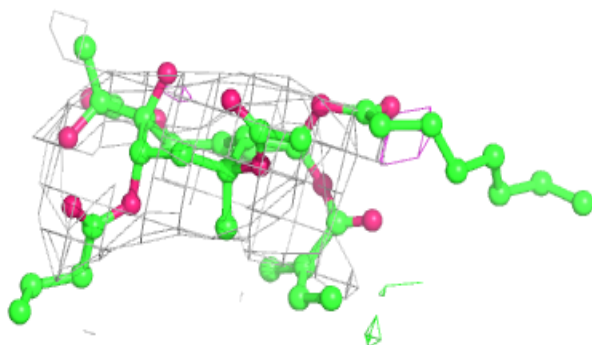
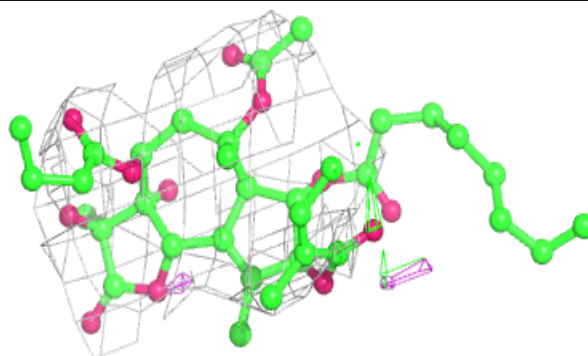
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 128 B 1002:

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

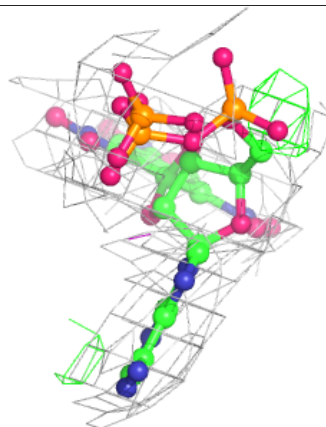
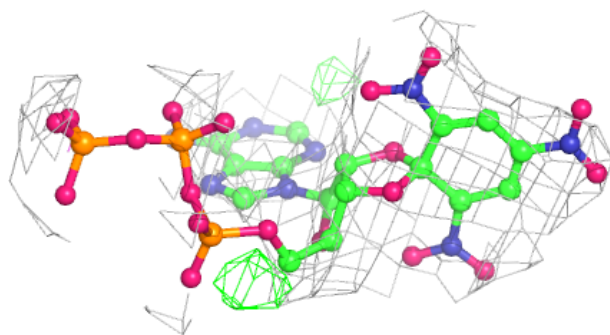
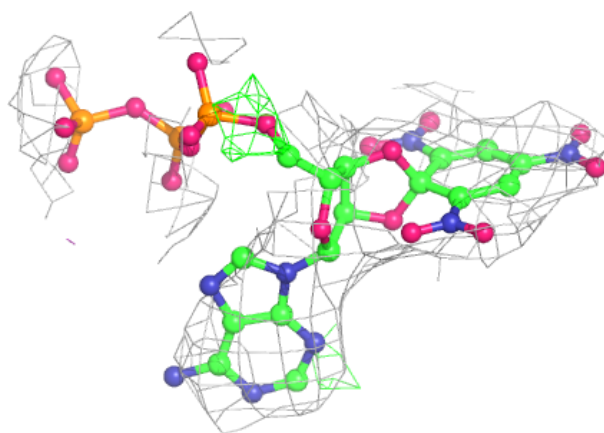
**Electron density around TG1 B 1000:**

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

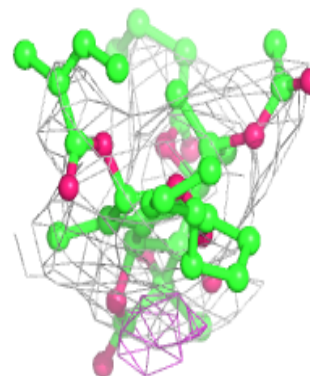
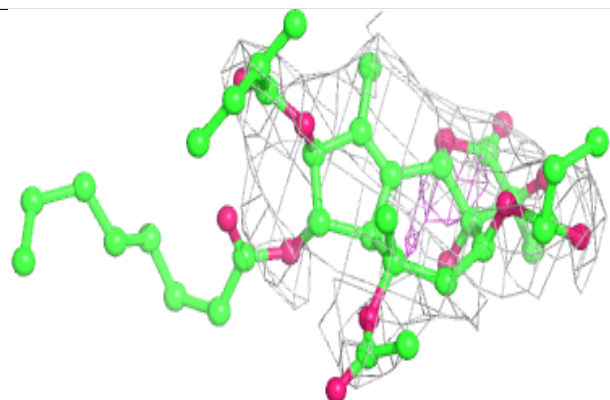
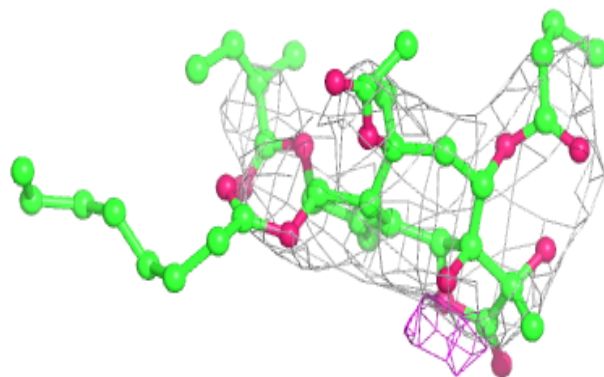


Electron density around 128 A 1002:

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

**Electron density around TG1 A 1000:**

$2mF_o-DF_c$ (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.