



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 07:42 pm BST

PDB ID : 4UU0
Title : CRYSTAL STRUCTURE OF (SR) CALCIUM-ATPASE E2(TG) IN THE PRESENCE OF 14:1 PC
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Deposited on : 2014-07-24
Resolution : 2.50 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

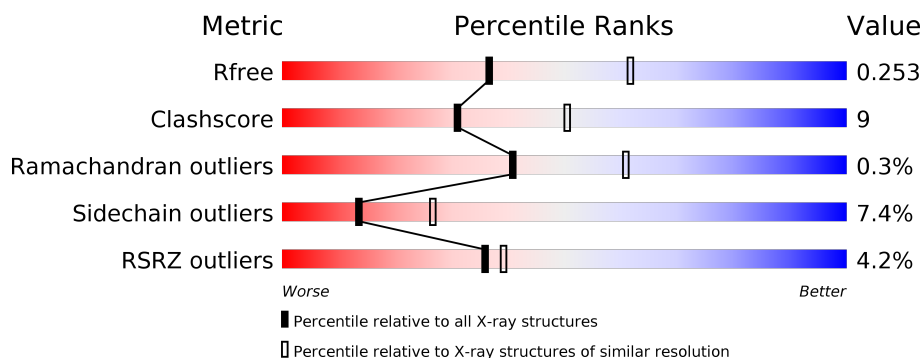
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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>4%</div> <div>76%</div> <div>21%</div> <div>.</div> </div>

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 7930 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.

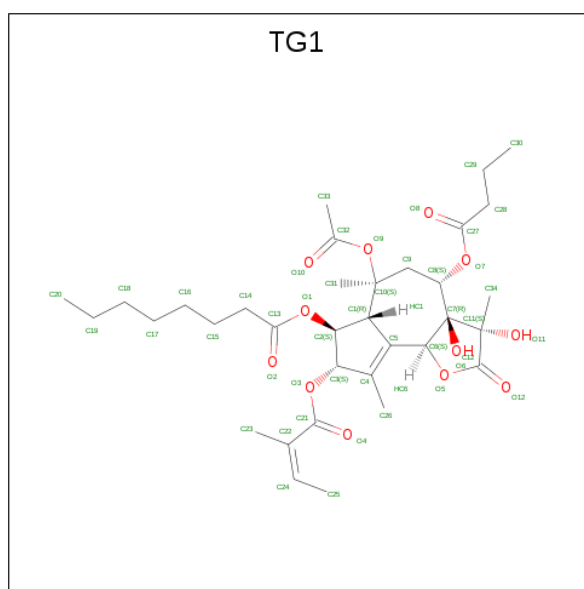
- Molecule 1 is a protein called SERCA1A.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ACE	-	acetylation	UNP B6CAM1

- 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
			Total	C	O		
2	A	1	46	34	12	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

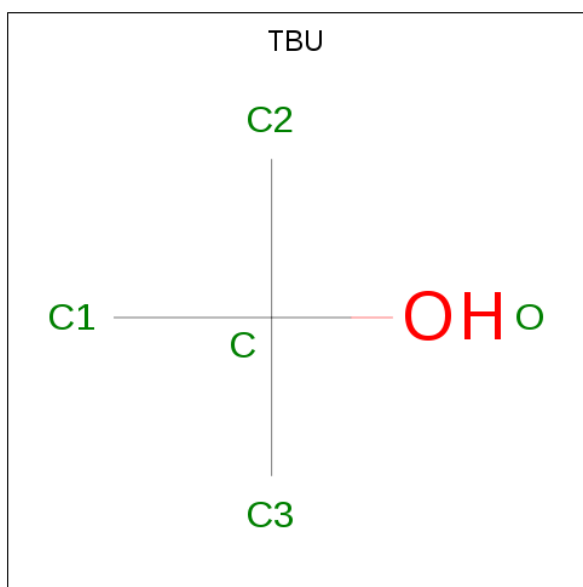
- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		

- Molecule 6 is TERTIARY-BUTYL ALCOHOL (three-letter code: TBU) (formula: $C_4H_{10}O$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			5	4	1		

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

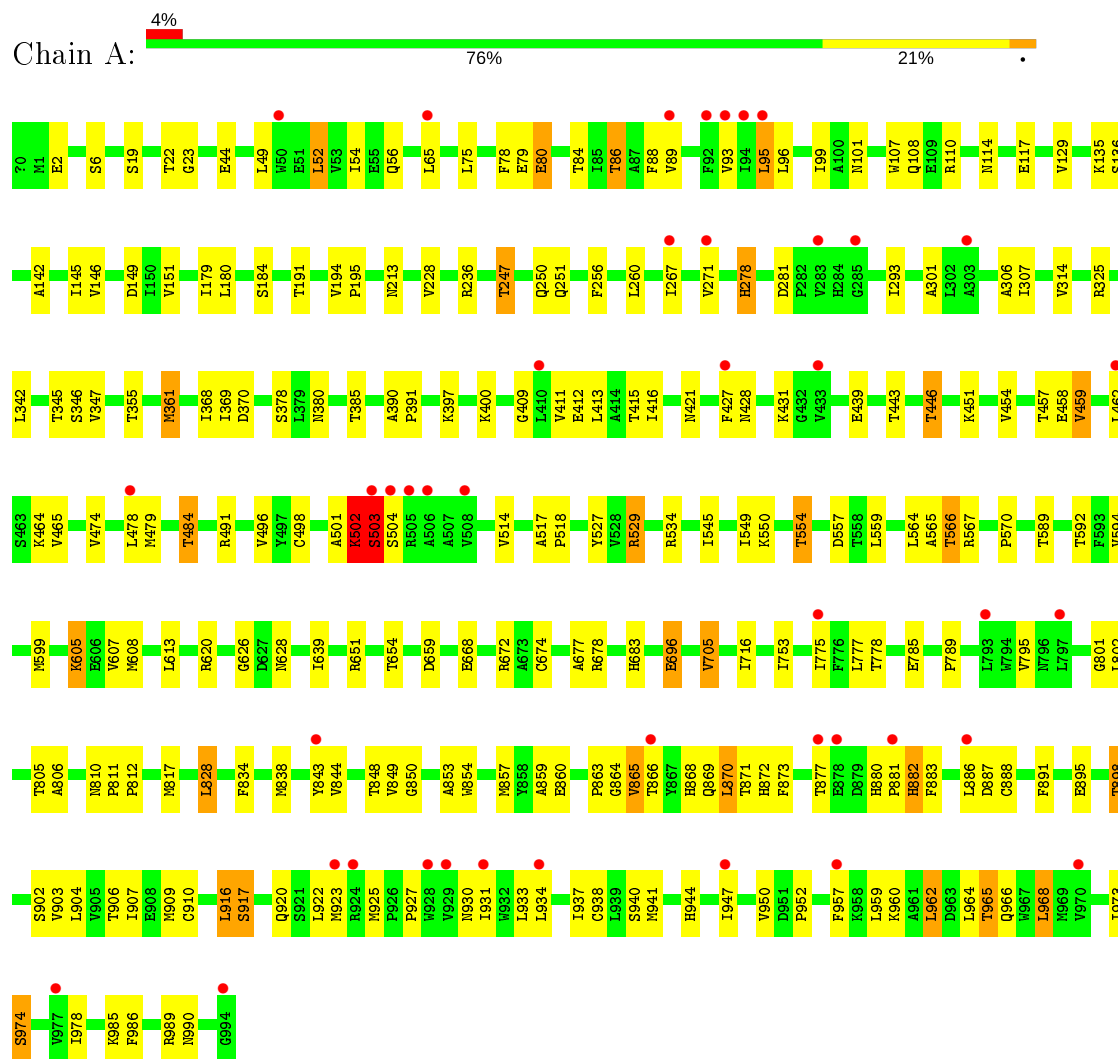
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	192	Total 192	O 192	0	0

3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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: SERCA1A



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	71.17Å 71.17Å 583.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	72.90 – 2.50 72.90 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (72.90-2.50) 97.0 (72.90-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 2.51Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.194 , 0.252 0.198 , 0.253	Depositor DCC
R_{free} test set	2703 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	63.9	Xtriage
Anisotropy	0.303	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 69.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7930	wwPDB-VP
Average B, all atoms (Å ²)	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.59% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MG, TG1, ACE, K, TBU, SO4

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	0.39	0/7813	0.54	0/10594

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	7674	0	7765	142	0
2	A	46	0	50	3	0
3	A	6	0	8	2	0
4	A	1	0	0	0	0
5	A	1	0	0	0	0
6	A	5	0	10	1	0
7	A	5	0	0	0	0
8	A	192	0	0	7	0
All	All	7930	0	7833	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 9.

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:A:898:THR:HG21	1:A:960:LYS:H	1.37	0.90
1:A:484:THR:HB	1:A:496:VAL:HG12	1.59	0.83
1:A:421:ASN:HD21	1:A:446:THR:HG22	1.52	0.75
1:A:651:ARG:NH2	1:A:674:CYS:SG	2.61	0.74
1:A:411:VAL:HA	1:A:454:VAL:HG21	1.71	0.73
1:A:325:ARG:HH12	1:A:753:ILE:HD11	1.54	0.70
1:A:950:VAL:HG12	1:A:952:PRO:HD2	1.74	0.69
1:A:927:PRO:HB2	1:A:934:LEU:HD21	1.74	0.68
1:A:626:GLY:HA3	6:A:1997:TBU:H32	1.77	0.67
1:A:416:ILE:HD11	1:A:566:THR:HG22	1.77	0.67
1:A:501:ALA:O	1:A:503:SER:N	2.27	0.66
1:A:659:ASP:OD1	1:A:683:HIS:NE2	2.27	0.66
1:A:527:TYR:HB2	1:A:592:THR:HG22	1.78	0.66
1:A:678:ARG:HH22	3:A:1301:GOL:H12	1.62	0.65
1:A:345:THR:HG22	1:A:716:ILE:HD13	1.79	0.64
1:A:412:GLU:OE1	1:A:529:ARG:HD2	1.97	0.63
1:A:628:ASN:HD22	3:A:1301:GOL:H2	1.64	0.62
1:A:342:LEU:O	1:A:345:THR:HG23	1.99	0.62
1:A:260:LEU:HD11	1:A:306:ALA:HB1	1.83	0.59
1:A:962:LEU:HB2	1:A:966:GLN:HB2	1.83	0.59
1:A:853:ALA:O	1:A:857:MET:N	2.34	0.58
1:A:865:VAL:HB	1:A:870:LEU:HD21	1.86	0.58
1:A:859:ALA:HB3	1:A:864:GLY:HA2	1.85	0.58
1:A:86:THR:OG1	1:A:86:THR:O	2.20	0.58
1:A:247:THR:HG21	8:A:2089:HOH:O	2.04	0.58
1:A:965:THR:HA	1:A:968:LEU:HD22	1.86	0.57
1:A:421:ASN:ND2	1:A:446:THR:HG22	2.19	0.57
1:A:370:ASP:OD2	1:A:380:ASN:ND2	2.37	0.57
1:A:895:GLU:HA	1:A:898:THR:HG23	1.87	0.56
1:A:907:ILE:HG13	1:A:974:SER:HB2	1.87	0.56
1:A:608:MET:HG2	8:A:2169:HOH:O	2.06	0.55
1:A:413:LEU:HG	1:A:564:LEU:HD12	1.87	0.55
1:A:869:GLN:HB2	1:A:872:HIS:ND1	2.22	0.54
1:A:778:THR:HG21	1:A:785:GLU:HA	1.90	0.54
1:A:443:THR:HA	1:A:446:THR:HG23	1.90	0.54
1:A:428:ASN:ND2	1:A:431:LYS:HE3	2.23	0.54
1:A:75:LEU:HD22	1:A:293:ILE:HG23	1.90	0.53
1:A:567:ARG:HD3	1:A:570:PRO:HA	1.91	0.53
1:A:557:ASP:HB3	1:A:559:LEU:HG	1.90	0.53
1:A:668:GLU:HG3	1:A:672:ARG:HH12	1.73	0.53
1:A:278:HIS:HA	1:A:281:ASP:OD2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:882:HIS:HB3	1:A:883:PHE:HD1	1.75	0.52
1:A:22:THR:HG22	1:A:23:GLY:O	2.09	0.51
1:A:347:VAL:HG22	1:A:620:ARG:HB3	1.92	0.51
1:A:501:ALA:C	1:A:503:SER:H	2.13	0.51
1:A:795:VAL:HG21	1:A:904:LEU:HD23	1.93	0.51
1:A:267:ILE:O	1:A:271:VAL:HG23	2.11	0.51
1:A:314:VAL:HG13	1:A:805:THR:HG22	1.92	0.51
1:A:870:LEU:HD22	1:A:870:LEU:H	1.75	0.50
1:A:247:THR:CG2	1:A:250:GLN:H	2.25	0.50
1:A:880:HIS:CG	1:A:881:PRO:HD3	2.47	0.50
1:A:898:THR:HB	1:A:959:LEU:HD22	1.94	0.49
1:A:806:ALA:HB1	1:A:933:LEU:HA	1.94	0.49
1:A:986:PHE:O	1:A:990:ASN:ND2	2.39	0.49
1:A:427:PHE:HB3	1:A:465:VAL:HA	1.95	0.49
1:A:301:ALA:HA	1:A:789:PRO:HG3	1.95	0.49
1:A:142:ALA:HA	1:A:145:ILE:HD12	1.94	0.49
1:A:411:VAL:O	1:A:415:THR:HG23	2.12	0.48
1:A:654:THR:HA	1:A:677:ALA:O	2.12	0.48
1:A:869:GLN:C	1:A:871:THR:H	2.17	0.48
1:A:873:PHE:HB2	1:A:891:PHE:CD2	2.48	0.48
1:A:346:SER:OG	1:A:696:GLU:HG3	2.14	0.48
1:A:457:THR:O	1:A:459:VAL:N	2.47	0.48
1:A:95:LEU:O	1:A:99:ILE:HG12	2.14	0.48
1:A:369:ILE:HD11	1:A:545:ILE:HD11	1.95	0.48
1:A:347:VAL:HG23	1:A:696:GLU:HG2	1.96	0.48
1:A:964:LEU:HD22	1:A:964:LEU:H	1.79	0.47
1:A:906:THR:HA	1:A:941:MET:HE1	1.95	0.47
1:A:922:LEU:HA	1:A:925:MET:O	2.15	0.47
1:A:135:LYS:HG3	1:A:136:SER:N	2.29	0.47
1:A:550:LYS:O	1:A:554:THR:HB	2.16	0.46
1:A:834:PHE:HE2	2:A:1003:TG1:HC1	1.81	0.46
1:A:565:ALA:HA	1:A:594:VAL:HG13	1.98	0.46
1:A:501:ALA:O	1:A:502:LYS:HD3	2.15	0.46
1:A:877:THR:O	1:A:880:HIS:HD2	1.99	0.46
1:A:848:THR:HG22	1:A:903:VAL:HG13	1.97	0.46
1:A:909:MET:HE2	1:A:940:SER:HB2	1.98	0.46
1:A:361:MET:HE2	1:A:599:MET:HG3	1.96	0.46
1:A:247:THR:O	1:A:251:GLN:HG3	2.16	0.45
1:A:247:THR:HG22	1:A:250:GLN:HB2	1.97	0.45
1:A:863:PRO:HB2	1:A:865:VAL:HG22	1.99	0.45
1:A:887:ASP:CG	1:A:888:CYS:H	2.20	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:534:ARG:HD2	1:A:592:THR:HG21	1.99	0.45
1:A:902:SER:HA	1:A:944:HIS:CE1	2.51	0.45
1:A:44:GLU:O	8:A:2027:HOH:O	2.21	0.45
1:A:179:ILE:HG13	1:A:180:LEU:HD13	1.99	0.44
1:A:6:SER:HA	1:A:194:VAL:O	2.18	0.44
1:A:910:CYS:HB3	1:A:978:ILE:HG13	2.00	0.44
1:A:843:TYR:OH	1:A:973:ILE:O	2.32	0.44
1:A:368:ILE:HD12	1:A:409:GLY:HA3	2.00	0.44
1:A:247:THR:HG22	1:A:250:GLN:H	1.83	0.44
1:A:80:GLU:CD	1:A:80:GLU:H	2.20	0.44
1:A:865:VAL:HG11	1:A:870:LEU:HD11	1.99	0.43
1:A:801:GLY:O	1:A:805:THR:HG23	2.19	0.43
1:A:909:MET:HE3	1:A:937:ILE:HG23	2.00	0.43
1:A:868:HIS:HB3	1:A:870:LEU:HD21	2.00	0.43
1:A:347:VAL:CG2	1:A:696:GLU:HG2	2.48	0.43
1:A:65:LEU:HD23	1:A:65:LEU:HA	1.77	0.43
1:A:65:LEU:HG	1:A:307:ILE:HD12	2.00	0.43
1:A:518:PRO:HB3	1:A:549:ILE:HD13	2.01	0.43
1:A:194:VAL:HA	1:A:195:PRO:HD3	1.81	0.43
1:A:256:PHE:CE2	1:A:260:LEU:HD22	2.54	0.43
1:A:479:MET:HB3	1:A:498:CYS:HB3	2.01	0.43
1:A:957:PHE:HB3	1:A:959:LEU:HG	2.01	0.43
1:A:361:MET:HE2	1:A:361:MET:HB3	1.87	0.42
1:A:114:ASN:HB3	1:A:117:GLU:HG2	2.02	0.42
1:A:213:ASN:ND2	8:A:2075:HOH:O	2.52	0.42
1:A:909:MET:CE	1:A:940:SER:HB2	2.49	0.42
1:A:474:VAL:O	1:A:478:LEU:HD13	2.19	0.42
1:A:810:ASN:HD21	1:A:916:LEU:HA	1.84	0.42
1:A:985:LYS:O	1:A:989:ARG:HG3	2.20	0.42
1:A:802:LEU:HD12	1:A:940:SER:OG	2.19	0.42
1:A:811:PRO:HA	1:A:812:PRO:HD3	1.81	0.41
1:A:412:GLU:OE2	1:A:566:THR:HG21	2.19	0.41
1:A:459:VAL:HA	1:A:462:LEU:HD12	2.02	0.41
1:A:777:LEU:HB2	1:A:849:VAL:HG21	2.02	0.41
1:A:180:LEU:HA	1:A:180:LEU:HD12	1.88	0.41
1:A:2:GLU:HG3	8:A:2081:HOH:O	2.20	0.41
1:A:385:THR:O	1:A:451:LYS:NZ	2.37	0.41
1:A:850:GLY:O	1:A:854:TRP:N	2.42	0.41
1:A:592:THR:HG23	8:A:2160:HOH:O	2.21	0.41
1:A:129:VAL:HG12	1:A:151:VAL:HG22	2.02	0.41
1:A:301:ALA:HB1	1:A:775:ILE:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:ALA:HA	1:A:391:PRO:HD3	1.90	0.41
1:A:917:SER:OG	1:A:920:GLN:HB2	2.21	0.41
1:A:397:LYS:N	1:A:400:LYS:O	2.41	0.41
1:A:838:MET:SD	2:A:1003:TG1:H141	2.61	0.41
1:A:668:GLU:HG3	1:A:672:ARG:NH1	2.35	0.41
1:A:828:LEU:HD13	2:A:1003:TG1:H302	2.03	0.41
1:A:930:ASN:HB3	1:A:933:LEU:HB3	2.03	0.41
1:A:491:ARG:NH1	8:A:2133:HOH:O	2.46	0.40
1:A:608:MET:SD	1:A:639:ILE:HA	2.61	0.40
1:A:179:ILE:HB	1:A:705:VAL:HG13	2.03	0.40
1:A:903:VAL:HG23	1:A:974:SER:HB3	2.02	0.40
1:A:517:ALA:HA	1:A:518:PRO:HD3	1.80	0.40
1:A:605:LYS:H	1:A:605:LYS:HG2	1.53	0.40
1:A:89:VAL:O	1:A:93:VAL:HG23	2.22	0.40
1:A:944:HIS:O	1:A:947:ILE:HG12	2.21	0.40
1:A:52:LEU:O	1:A:56:GLN:HG2	2.21	0.40
1:A:613:LEU:HA	1:A:613:LEU:HD23	1.90	0.40
1:A:427:PHE:CE1	1:A:464:LYS:HD3	2.56	0.40
1:A:880:HIS:CD2	1:A:881:PRO:HD3	2.56	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	993/995 (100%)	946 (95%)	44 (4%)	3 (0%)	41 61

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	502	LYS
1	A	503	SER

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Mol	Chain	Res	Type
1	A	458	GLU

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	840/840 (100%)	778 (93%)	62 (7%)	13	27

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	SER
1	A	49	LEU
1	A	52	LEU
1	A	54	ILE
1	A	78	PHE
1	A	79	GLU
1	A	80	GLU
1	A	84	THR
1	A	86	THR
1	A	88	PHE
1	A	95	LEU
1	A	96	LEU
1	A	101	ASN
1	A	107	TRP
1	A	108	GLN
1	A	110	ARG
1	A	146	VAL
1	A	149	ASP
1	A	184	SER
1	A	191	THR
1	A	228	VAL
1	A	236	ARG
1	A	247	THR
1	A	278	HIS
1	A	355	THR

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Mol	Chain	Res	Type
1	A	361	MET
1	A	378	SER
1	A	439	GLU
1	A	446	THR
1	A	459	VAL
1	A	484	THR
1	A	502	LYS
1	A	503	SER
1	A	504	SER
1	A	514	VAL
1	A	529	ARG
1	A	554	THR
1	A	566	THR
1	A	589	THR
1	A	605	LYS
1	A	607	VAL
1	A	696	GLU
1	A	705	VAL
1	A	817	MET
1	A	828	LEU
1	A	844	VAL
1	A	860	GLU
1	A	865	VAL
1	A	866	THR
1	A	870	LEU
1	A	882	HIS
1	A	886	LEU
1	A	898	THR
1	A	916	LEU
1	A	917	SER
1	A	923	MET
1	A	931	ILE
1	A	938	CYS
1	A	962	LEU
1	A	965	THR
1	A	968	LEU
1	A	974	SER

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

Mol	Chain	Res	Type
1	A	108	GLN

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Mol	Chain	Res	Type
1	A	880	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	$\# Z > 2$
7	SO4	A	1998	-	4,4,4	0.12	0	6,6,6	0.10	0
3	GOL	A	1301	-	5,5,5	0.46	0	5,5,5	0.77	0
6	TBU	A	1997	-	4,4,4	0.79	0	6,6,6	0.51	0
2	TG1	A	1003	-	43,48,48	4.31	8 (18%)	44,72,72	3.70	15 (34%)

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	GOL	A	1301	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	TG1	A	1003	-	-	14/33/99/99	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1003	TG1	C4-C5	25.48	1.55	1.34
2	A	1003	TG1	O12-C12	7.68	1.38	1.20
2	A	1003	TG1	O5-C12	3.63	1.40	1.35
2	A	1003	TG1	C24-C22	3.52	1.53	1.31
2	A	1003	TG1	C3-C4	3.05	1.54	1.50
2	A	1003	TG1	O9-C10	-2.88	1.43	1.48
2	A	1003	TG1	O7-C8	-2.63	1.41	1.46
2	A	1003	TG1	C1-C5	2.24	1.54	1.51

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1003	TG1	O12-C12-C11	-15.28	112.92	128.28
2	A	1003	TG1	O5-C12-O12	-12.07	105.63	121.62
2	A	1003	TG1	C10-C1-C5	6.67	123.24	115.26
2	A	1003	TG1	C26-C4-C3	-6.39	110.92	121.27
2	A	1003	TG1	C10-O9-C32	4.36	131.89	121.53
2	A	1003	TG1	O3-C21-O4	-4.30	115.12	123.32
2	A	1003	TG1	O7-C8-C9	4.12	113.99	106.63
2	A	1003	TG1	C23-C22-C24	-4.04	106.58	123.20
2	A	1003	TG1	C23-C22-C21	-2.87	108.91	116.09
2	A	1003	TG1	C2-O1-C13	-2.68	113.07	117.53
2	A	1003	TG1	O9-C32-C33	-2.64	105.88	110.68
2	A	1003	TG1	C26-C4-C5	-2.35	123.95	129.82
2	A	1003	TG1	O3-C21-C22	2.21	117.07	111.52
2	A	1003	TG1	O11-C11-C12	2.19	113.72	106.32
2	A	1003	TG1	O1-C13-O2	-2.17	118.45	123.70

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1301	GOL	C1-C2-C3-O3
3	A	1301	GOL	O2-C2-C3-O3
2	A	1003	TG1	C22-C21-O3-C3
2	A	1003	TG1	O3-C21-C22-C24

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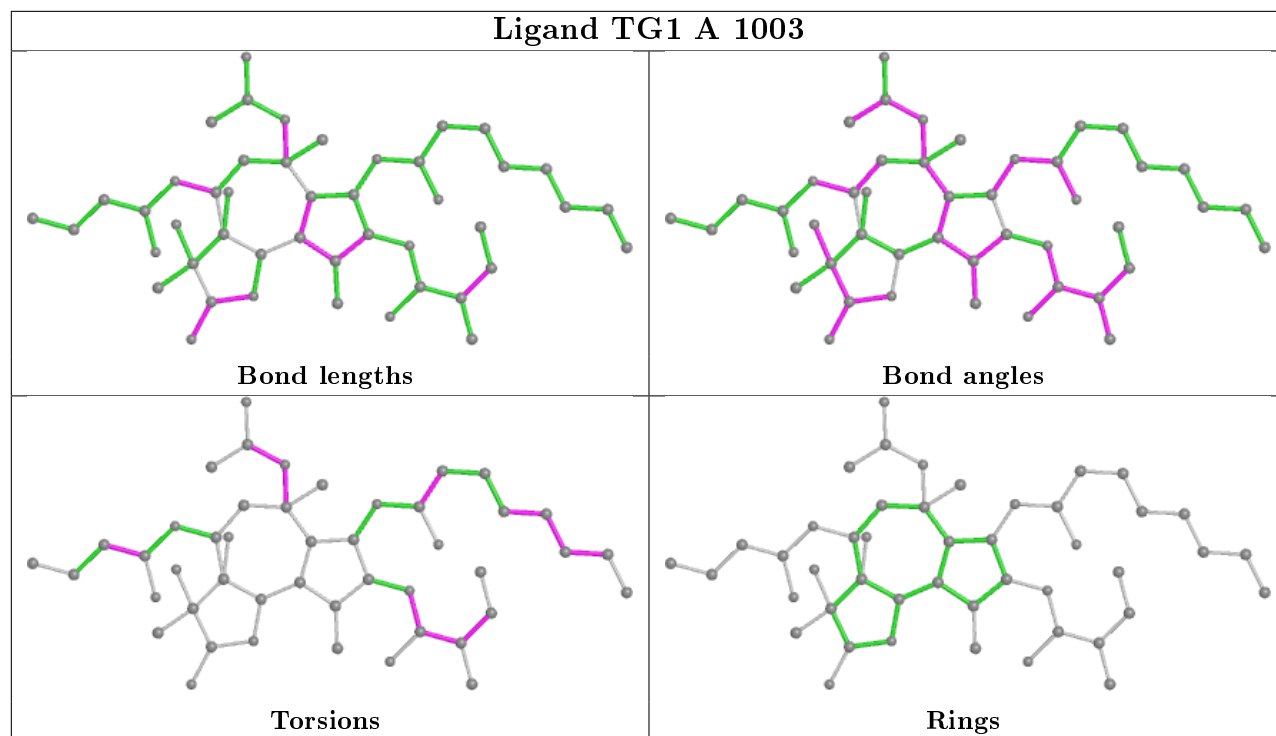
Mol	Chain	Res	Type	Atoms
2	A	1003	TG1	C21-C22-C24-C25
2	A	1003	TG1	O4-C21-O3-C3
2	A	1003	TG1	O4-C21-C22-C24
2	A	1003	TG1	O10-C32-O9-C10
2	A	1003	TG1	C16-C17-C18-C19
2	A	1003	TG1	C17-C18-C19-C20
2	A	1003	TG1	C9-C10-O9-C32
2	A	1003	TG1	O1-C13-C14-C15
2	A	1003	TG1	C15-C16-C17-C18
2	A	1003	TG1	O2-C13-C14-C15
2	A	1003	TG1	O8-C27-C28-C29
2	A	1003	TG1	O7-C27-C28-C29

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1301	GOL	2	0
6	A	1997	TBU	1	0
2	A	1003	TG1	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 ⓘ

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%)	0.34	42 (4%) 36 39	44, 88, 164, 259	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	506	ALA	13.7
1	A	504	SER	10.0
1	A	503	SER	5.6
1	A	924	ARG	4.8
1	A	508	VAL	4.7
1	A	878	GLU	4.7
1	A	505	ARG	3.9
1	A	271	VAL	3.7
1	A	877	THR	3.7
1	A	947	ILE	3.6
1	A	283	VAL	3.6
1	A	957	PHE	3.0
1	A	95	LEU	3.0
1	A	267	ILE	2.9
1	A	433	VAL	2.8
1	A	866	THR	2.8
1	A	410	LEU	2.7
1	A	934	LEU	2.7
1	A	285	GLY	2.7
1	A	427	PHE	2.7
1	A	462	LEU	2.7
1	A	303	ALA	2.6
1	A	977	VAL	2.6
1	A	923	MET	2.6
1	A	970	VAL	2.6
1	A	928	TRP	2.5
1	A	994	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	65	LEU	2.4
1	A	89	VAL	2.4
1	A	92	PHE	2.4
1	A	886	LEU	2.4
1	A	797	LEU	2.3
1	A	931	ILE	2.3
1	A	881	PRO	2.2
1	A	93	VAL	2.2
1	A	478	LEU	2.2
1	A	929	VAL	2.1
1	A	94	ILE	2.1
1	A	793	LEU	2.1
1	A	50	TRP	2.1
1	A	843	TYR	2.0
1	A	775	ILE	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.

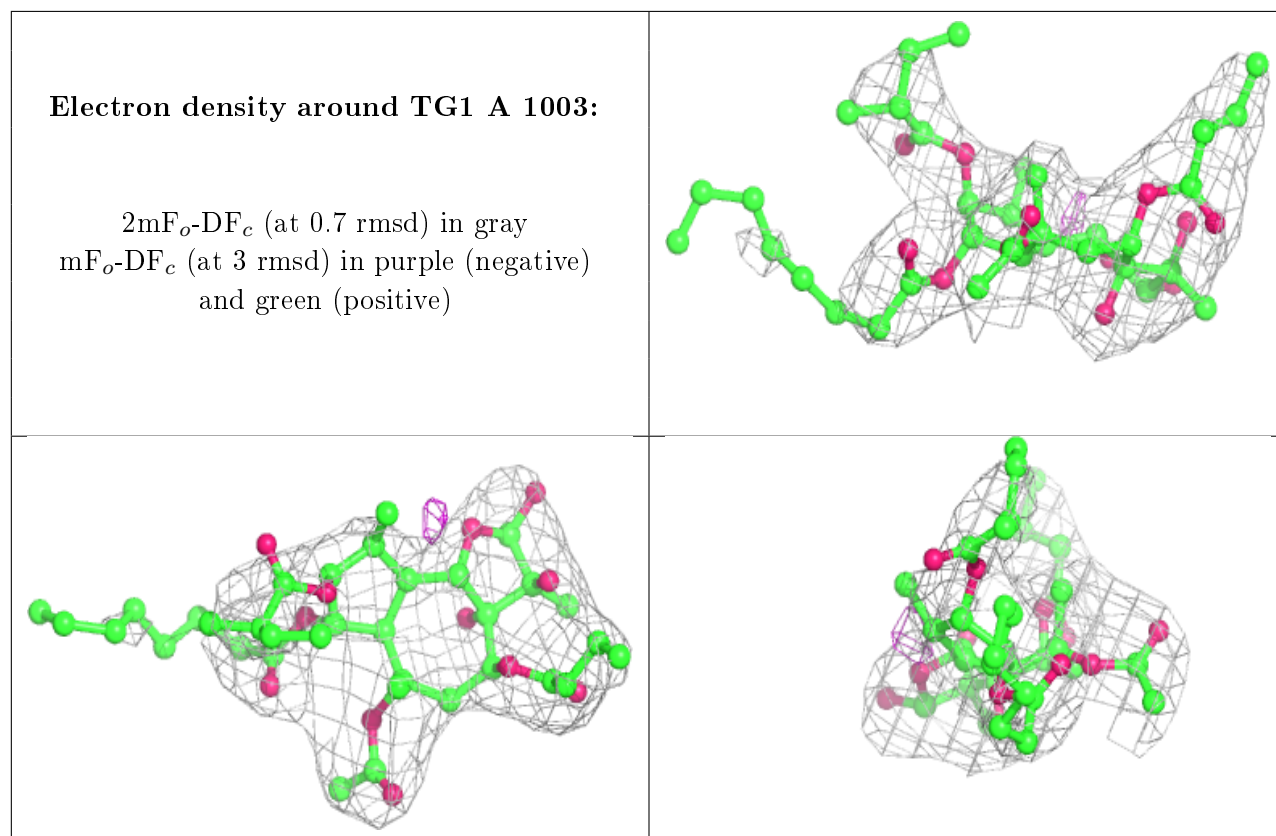
6.4 Ligands [i](#)

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
7	SO4	A	1998	5/5	0.86	0.18	135,144,147,147	0
3	GOL	A	1301	6/6	0.90	0.22	83,91,96,111	0
5	MG	A	1996	1/1	0.95	0.15	97,97,97,97	0
2	TG1	A	1003	46/46	0.96	0.24	70,98,125,130	0
4	K	A	1995	1/1	0.99	0.07	52,52,52,52	1
6	TBU	A	1997	5/5	0.99	0.20	50,52,56,63	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.