



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:13 PM GMT

PDB ID : 1ELV
Title : CRYSTAL STRUCTURE OF THE CATALYTIC DOMAIN OF HUMAN
COMPLEMENT C1S PROTEASE
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Deposited on : 2000-03-14
Resolution : 1.70 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

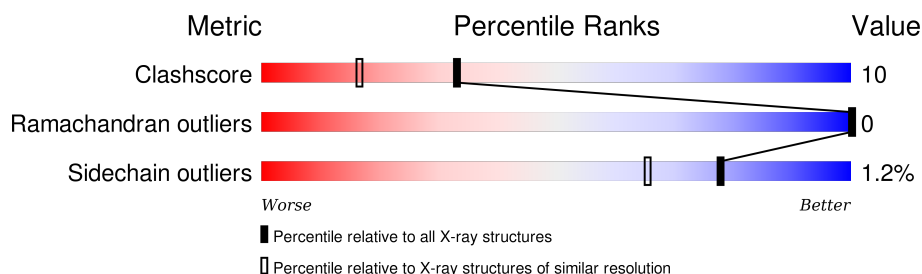
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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))
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	333	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	A	1001	-	X	X	-
2	FUC	A	1003	-	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2736 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 COMPLEMENT C1S COMPONENT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	47	10	0
			2357	1499	392	443	23			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	341	ASP	-	ENGINEERED	UNP P09871
A	342	LEU	-	ENGINEERED	UNP P09871

- Molecule 2 is a polymer of unknown type called SUGAR (3-MER).

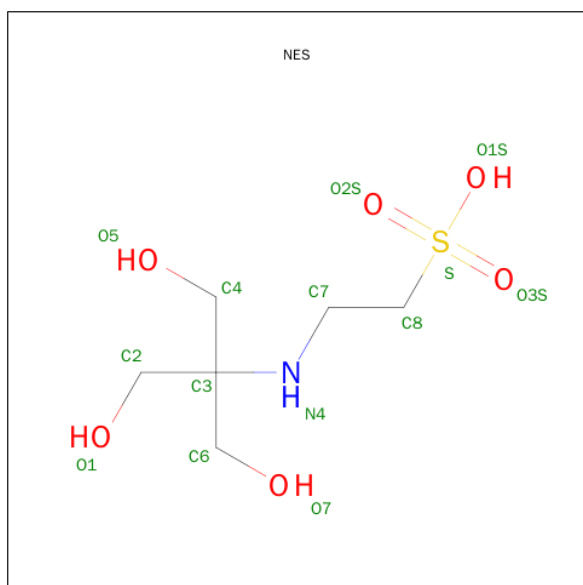
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 4 is 2-(2-HYDROXY-1,1-DIHYDROXYMETHYL-ETHYLAMINO)-ETHANESULFONIC ACID (three-letter code: NES) (formula: C₆H₁₅NO₆S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			14	6	1	6	1		

- Molecule 5 is water.


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	317	Total	O	0	0
			317	317		

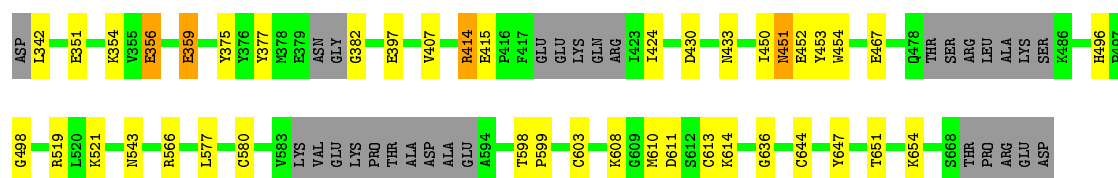
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

• Molecule 1: COMPLEMENT C1S COMPONENT

Chain A: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	39.08 Å 79.65 Å 60.21 Å 90.00° 91.24° 90.00°	Depositor
Resolution (Å)	15.00 – 1.70	Depositor
% Data completeness (in resolution range)	(Not available) (15.00-1.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.186 , 0.219	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2736	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FUC, NAG, SO4, NES

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	0.68	5/2459 (0.2%)	1.06	7/3337 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	359	GLU	CD-OE2	10.22	1.36	1.25
1	A	351	GLU	CG-CD	7.25	1.62	1.51
1	A	397	GLU	CG-CD	6.74	1.62	1.51
1	A	359	GLU	CD-OE1	-5.14	1.20	1.25
1	A	397	GLU	CD-OE1	-5.13	1.20	1.25

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	467	GLU	OE1-CD-OE2	9.03	134.13	123.30
1	A	566	ARG	NE-CZ-NH1	6.45	123.53	120.30
1	A	521	LYS	CD-CE-NZ	-6.18	97.49	111.70
1	A	519	ARG	NE-CZ-NH1	5.79	123.19	120.30
1	A	611	ASP	CB-CG-OD1	5.43	123.18	118.30
1	A	359	GLU	OE1-CD-OE2	-5.21	117.05	123.30
1	A	566	ARG	CD-NE-CZ	5.05	130.66	123.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	359	GLU	Sidechain
1	A	415	GLU	Sidechain

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	2357	0	2266	32	0
2	A	38	0	26	16	0
3	A	10	0	0	0	0
4	A	14	0	14	0	0
5	A	317	0	0	4	0
All	All	2736	0	2306	48	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 10.

All (48) 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:424:ILE:HG12	1:A:613[B]:CYS:SG	1.42	1.59
2:A:1001:NAG:C4	2:A:1001:NAG:C5	1.81	1.54
2:A:1001:NAG:C6	2:A:1001:NAG:O6	1.63	1.46
2:A:1003:FUC:C4	2:A:1003:FUC:C5	1.96	1.44
2:A:1002:NAG:C4	2:A:1002:NAG:O4	1.73	1.37
1:A:424:ILE:CG1	1:A:613[B]:CYS:SG	2.25	1.25
1:A:577:LEU:O	1:A:580[B]:CYS:SG	2.19	1.01
2:A:1001:NAG:O6	2:A:1001:NAG:C5	2.14	0.95
2:A:1001:NAG:C5	2:A:1001:NAG:C3	2.49	0.91
2:A:1001:NAG:O4	2:A:1001:NAG:C5	2.26	0.82
2:A:1001:NAG:C6	2:A:1003:FUC:C1	2.59	0.81
2:A:1003:FUC:C4	2:A:1003:FUC:C6	2.60	0.79
1:A:424:ILE:CD1	1:A:613[B]:CYS:SG	2.73	0.76
2:A:1003:FUC:C3	2:A:1003:FUC:C5	2.60	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1002:NAG:C3	2:A:1002:NAG:O4	2.36	0.74
1:A:496:HIS:HD2	1:A:498:GLY:H	1.36	0.73
1:A:496:HIS:CD2	1:A:498:GLY:H	2.07	0.72
2:A:1001:NAG:C6	2:A:1001:NAG:C4	2.67	0.71
2:A:1002:NAG:C5	2:A:1002:NAG:O4	2.38	0.71
1:A:608:LYS:HD2	1:A:610:MET:HE2	1.78	0.65
1:A:451:ASN:HD22	1:A:453:TYR:H	1.43	0.65
1:A:430:ASP:H	1:A:433:ASN:ND2	2.00	0.59
1:A:354:LYS:HE2	1:A:356:GLU:OE1	2.03	0.58
1:A:451:ASN:ND2	1:A:453:TYR:H	2.01	0.57
1:A:580[B]:CYS:HB3	1:A:603:CYS:SG	2.45	0.56
1:A:543:ASN:OD1	1:A:654:LYS:HE2	2.06	0.56
2:A:1001:NAG:C6	2:A:1001:NAG:O4	2.55	0.54
1:A:382:GLY:HA3	5:A:301:HOH:O	2.08	0.54
1:A:451:ASN:HD21	1:A:454:TRP:HD1	1.57	0.52
1:A:451:ASN:C	1:A:451:ASN:HD22	2.13	0.51
1:A:424:ILE:HD11	1:A:613[B]:CYS:SG	2.51	0.51
1:A:377:TYR:CE2	1:A:407:VAL:HG23	2.46	0.50
1:A:598:THR:HB	1:A:599:PRO:CD	2.42	0.49
2:A:1001:NAG:O6	2:A:1001:NAG:H5	2.10	0.48
1:A:598:THR:HB	1:A:599:PRO:HD2	1.95	0.47
1:A:613[B]:CYS:HB3	1:A:644:CYS:SG	2.55	0.47
1:A:375:TYR:OH	1:A:414:ARG:HD2	2.15	0.46
1:A:580[A]:CYS:SG	1:A:647:TYR:HB3	2.56	0.45
2:A:1003:FUC:O4	2:A:1003:FUC:C5	2.59	0.45
1:A:614[A]:LYS:HG2	5:A:178:HOH:O	2.17	0.44
1:A:636:GLY:HA2	1:A:651:THR:O	2.18	0.44
1:A:450:ILE:O	1:A:451:ASN:HB3	2.19	0.43
1:A:608:LYS:NZ	5:A:231:HOH:O	2.52	0.43
1:A:608:LYS:HB2	1:A:610:MET:CE	2.49	0.42
1:A:452:GLU:HG2	1:A:453:TYR:CD1	2.55	0.42
1:A:577:LEU:HD12	1:A:580[B]:CYS:SG	2.60	0.42
1:A:452:GLU:H	1:A:452:GLU:CD	2.22	0.42
1:A:342:LEU:HA	5:A:285:HOH:O	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	303/333 (91%)	297 (98%)	6 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	260/277 (94%)	257 (99%)	3 (1%)	78	65

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	356	GLU
1	A	414	ARG
1	A	451	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	433	ASN
1	A	437	GLN
1	A	451	ASN
1	A	496	HIS

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 ⓘ

3 carbohydrates are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	A	1001	1,2	14,14,15	7.88	13 (92%)	15,19,21	8.52	12 (80%)
2	NAG	A	1002	2	14,14,15	6.23	11 (78%)	15,19,21	6.95	10 (66%)
2	FUC	A	1003	2	10,10,11	7.71	8 (80%)	14,14,16	6.82	12 (85%)

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	NAG	A	1001	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1002	2	-	0/6/23/26	0/1/1/1
2	FUC	A	1003	2	-	0/0/17/20	0/1/1/1

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	NAG	O5-C1	-14.46	1.19	1.43
2	A	1002	NAG	C4-C5	-9.86	1.32	1.53
2	A	1001	NAG	C2-N2	-7.35	1.33	1.46
2	A	1001	NAG	C8-C7	-6.11	1.38	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1002	NAG	C1-C2	-5.80	1.44	1.52
2	A	1003	FUC	O5-C1	-5.33	1.34	1.43
2	A	1001	NAG	C4-C3	-4.61	1.40	1.52
2	A	1001	NAG	C3-C2	-3.93	1.43	1.52
2	A	1003	FUC	O5-C5	-3.65	1.16	1.41
2	A	1002	NAG	C7-N2	-3.12	1.22	1.34
2	A	1001	NAG	O4-C4	-2.97	1.35	1.43
2	A	1002	NAG	O6-C6	-2.82	1.30	1.42
2	A	1001	NAG	C7-N2	-2.75	1.23	1.34
2	A	1001	NAG	C6-C5	-2.68	1.42	1.51
2	A	1002	NAG	O3-C3	-2.41	1.37	1.43
2	A	1003	FUC	C1-C2	-2.11	1.47	1.52
2	A	1003	FUC	O4-C4	2.24	1.48	1.43
2	A	1002	NAG	C2-N2	2.61	1.50	1.46
2	A	1002	NAG	C6-C5	2.84	1.62	1.51
2	A	1003	FUC	C4-C3	3.33	1.61	1.52
2	A	1001	NAG	O6-C6	4.96	1.63	1.42
2	A	1001	NAG	O3-C3	6.36	1.58	1.43
2	A	1002	NAG	O5-C5	6.39	1.57	1.43
2	A	1003	FUC	C6-C5	6.65	1.67	1.51
2	A	1003	FUC	O3-C3	7.16	1.60	1.43
2	A	1002	NAG	C8-C7	8.04	1.66	1.50
2	A	1002	NAG	O7-C7	10.48	1.47	1.23
2	A	1001	NAG	C1-C2	11.07	1.67	1.52
2	A	1001	NAG	O7-C7	11.81	1.50	1.23
2	A	1002	NAG	O4-C4	12.53	1.73	1.43
2	A	1001	NAG	C4-C5	13.41	1.81	1.53
2	A	1003	FUC	C4-C5	20.80	1.96	1.52

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1002	NAG	O7-C7-C8	-16.90	91.04	122.06
2	A	1002	NAG	C4-C3-C2	-11.96	92.63	111.23
2	A	1001	NAG	O7-C7-C8	-11.15	101.60	122.06
2	A	1003	FUC	C6-C5-C4	-11.04	91.35	113.08
2	A	1003	FUC	C3-C4-C5	-9.64	93.46	109.72
2	A	1002	NAG	O4-C4-C3	-7.99	92.34	110.34
2	A	1001	NAG	O4-C4-C5	-7.30	89.89	109.24
2	A	1001	NAG	O6-C6-C5	-6.77	88.97	111.33
2	A	1002	NAG	O3-C3-C2	-6.34	96.56	109.11
2	A	1002	NAG	C1-O5-C5	-5.66	105.06	112.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	NAG	O3-C3-C4	-5.65	97.62	110.34
2	A	1003	FUC	O4-C4-C5	-5.39	97.18	109.84
2	A	1001	NAG	C3-C4-C5	-5.19	101.14	110.20
2	A	1003	FUC	O3-C3-C4	-4.78	99.58	110.34
2	A	1003	FUC	O2-C2-C3	-3.93	102.21	110.12
2	A	1003	FUC	O5-C1-C2	-3.12	105.80	110.86
2	A	1002	NAG	O4-C4-C5	-2.67	102.17	109.24
2	A	1003	FUC	O2-C2-C1	-2.59	104.01	109.21
2	A	1002	NAG	C3-C2-N2	-2.44	104.72	110.56
2	A	1001	NAG	C2-N2-C7	3.45	127.47	123.04
2	A	1003	FUC	O3-C3-C2	4.19	117.57	110.00
2	A	1001	NAG	C3-C2-N2	4.67	121.74	110.56
2	A	1001	NAG	O5-C5-C6	4.67	117.46	107.35
2	A	1003	FUC	C1-C2-C3	4.78	115.20	109.54
2	A	1003	FUC	O5-C5-C4	5.69	119.39	109.53
2	A	1002	NAG	C3-C4-C5	6.28	121.14	110.20
2	A	1002	NAG	C2-N2-C7	6.59	131.51	123.04
2	A	1002	NAG	C8-C7-N2	7.60	130.66	116.11
2	A	1003	FUC	C1-O5-C5	7.97	124.68	112.38
2	A	1001	NAG	C8-C7-N2	11.32	137.77	116.11
2	A	1001	NAG	C4-C3-C2	13.59	132.36	111.23
2	A	1001	NAG	O4-C4-C3	13.98	141.82	110.34
2	A	1003	FUC	O5-C5-C6	14.64	130.34	106.13
2	A	1001	NAG	C1-O5-C5	15.51	131.93	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	NAG	9	0
2	A	1002	NAG	3	0
2	A	1003	FUC	5	0

5.6 Ligand geometry ⓘ

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	A	2001	-	4,4,4	0.83	0	6,6,6	0.39	0
3	SO4	A	2002	-	4,4,4	0.81	0	6,6,6	0.19	0
4	NES	A	2003	-	12,13,13	1.66	2 (16%)	17,18,18	1.75	5 (29%)

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	SO4	A	2001	-	-	0/0/0/0	0/0/0/0
3	SO4	A	2002	-	-	0/0/0/0	0/0/0/0
4	NES	A	2003	-	-	0/17/17/17	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	2003	NES	C6-C3	2.78	1.56	1.53
4	A	2003	NES	C4-C3	4.38	1.58	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2003	NES	O3S-S-C8	-3.65	103.79	106.91
4	A	2003	NES	C4-C3-N4	-2.48	101.97	109.19
4	A	2003	NES	C7-C8-S	-2.07	108.14	113.73
4	A	2003	NES	O7-C6-C3	2.57	116.77	111.42
4	A	2003	NES	C4-C3-C2	3.17	116.77	110.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.