



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 2Q3Z / pdb_00002q3z
Title : Transglutaminase 2 undergoes large conformational change upon activation
Authors : Strop, P.; Pinkas, D.M.; Brunger, A.T.; Khosla, C.
Deposited on : 2007-05-30
Resolution : 2.00 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
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

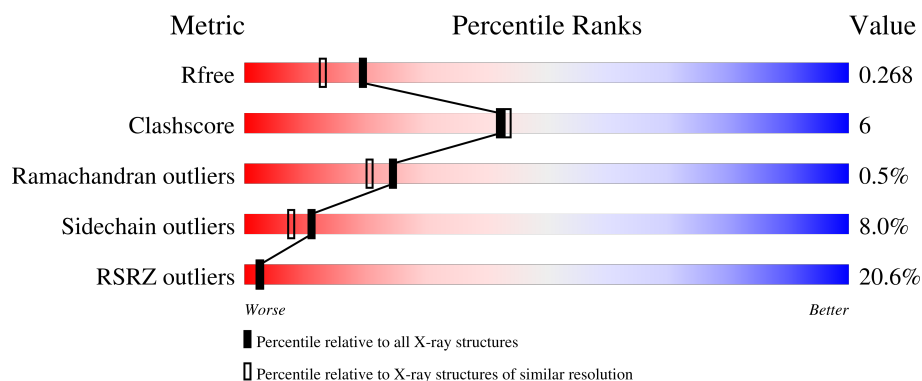
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	687	
2	X	7	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5519 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 Transglutaminase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	655	Total	C	N	O	S	66	0	0
			5186	3282	894	979	31			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	51	GLN	GLU	conflict	UNP P21980
A	186	GLN	GLU	conflict	UNP P21980
A	224	GLY	VAL	conflict	UNP P21980
A	533	THR	ASN	conflict	UNP P21980
A	655	VAL	LEU	conflict	UNP P21980

- Molecule 2 is a protein called Polypeptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	X	7	Total	C	N	O	0	0	1
			46	33	6	7			

- Molecule 3 is SULFATE ION (CCD ID: 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		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		

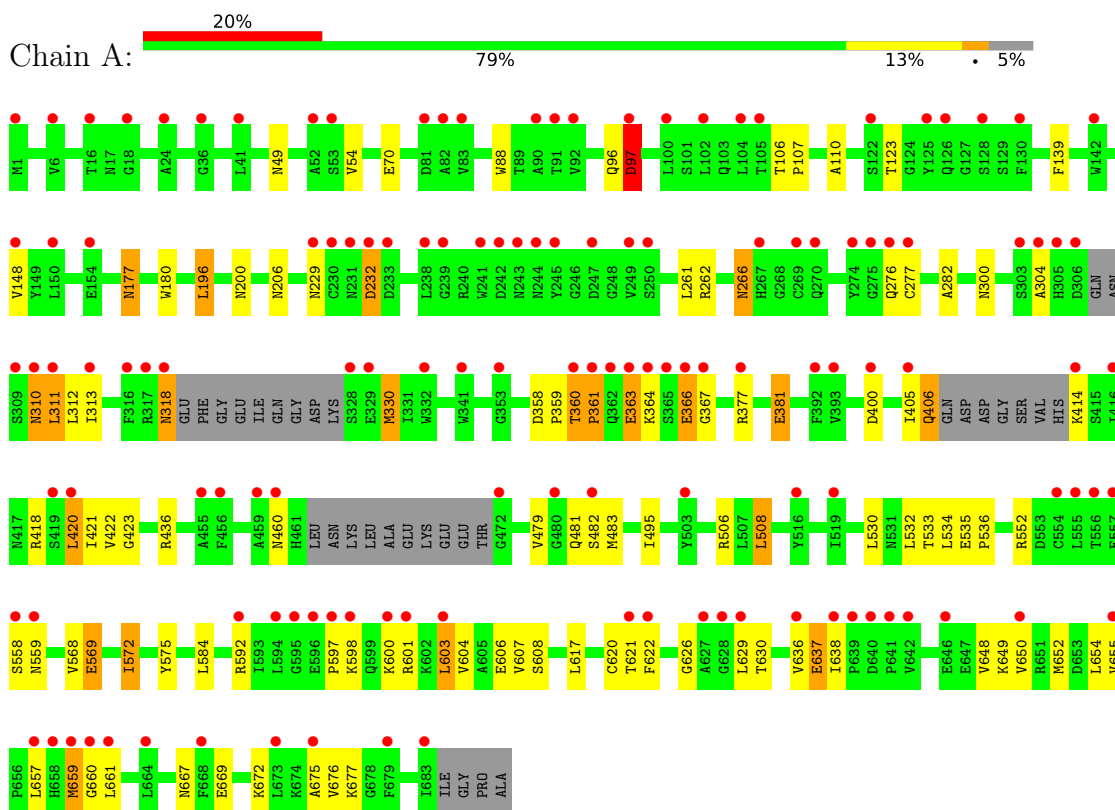
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	262	Total	O	0	0
			262	262		

3 Residue-property plots

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: Transglutaminase 2



• Molecule 2: Polypeptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	71.67Å 71.67Å 309.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.00 25.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (25.00-2.00) 98.4 (25.00-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 1.85Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.228 , 0.266 0.228 , 0.268	Depositor DCC
R_{free} test set	4103 reflections (6.10%)	wwPDB-VP
Wilson B-factor (Å ²)	30.3	Xtriage
Anisotropy	0.641	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 53.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5519	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% 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: ACE, NH2, SO4, ONL

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	0.78	2/5297 (0.0%)	0.86	5/7186 (0.1%)
2	X	1.63	1/35 (2.9%)	1.45	0/47
All	All	0.79	3/5332 (0.1%)	0.86	5/7233 (0.1%)

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	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	X	1	ACE	C-N	-8.82	1.34	1.43
1	A	672	LYS	CG-CD	-5.44	1.36	1.52
1	A	661	LEU	CB-CG	-5.10	1.43	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	360	THR	CA-C-N	7.67	129.42	119.84
1	A	360	THR	C-N-CA	7.67	129.42	119.84
1	A	358	ASP	CA-C-N	5.33	126.27	120.83
1	A	358	ASP	C-N-CA	5.33	126.27	120.83
1	A	97	ASP	CB-CG-OD1	-5.04	106.82	118.40

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	363	GLU	Peptide
1	A	600	LYS	Peptide
1	A	659	MET	Peptide
1	A	97	ASP	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	5186	0	5097	64	0
2	X	46	0	43	4	0
3	A	25	0	0	0	0
4	A	262	0	0	0	0
All	All	5519	0	5140	64	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 6.

All (64) 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:636:VAL:HG21	1:A:650:VAL:HG11	1.49	0.95
1:A:360:THR:HG23	1:A:361:PRO:HD2	1.52	0.92
1:A:360:THR:CG2	1:A:361:PRO:HD2	2.10	0.81
1:A:603:LEU:HD12	1:A:654:LEU:HD12	1.64	0.77
1:A:638:ILE:HD13	1:A:648:VAL:HG21	1.66	0.76
1:A:622:PHE:HB2	1:A:636:VAL:HG22	1.74	0.68
1:A:318:ASN:HD22	1:A:318:ASN:H	1.43	0.64
1:A:54:VAL:HG12	1:A:123:THR:HG23	1.82	0.62
1:A:318:ASN:HD22	1:A:318:ASN:N	1.99	0.60
1:A:569:GLU:CG	1:A:572:ILE:HD12	2.32	0.60
1:A:659:MET:HE2	1:A:660:GLY:HA3	1.84	0.58
1:A:420:LEU:HD23	2:X:6:PHE:CD2	2.38	0.58
1:A:232:ASP:OD2	1:A:232:ASP:N	2.37	0.57
1:A:569:GLU:HG3	1:A:572:ILE:HD12	1.87	0.57
1:A:304:ALA:HB2	2:X:6:PHE:CD2	2.40	0.57
1:A:568:VAL:HG13	1:A:575:TYR:CE2	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:PHE:HB3	1:A:148:VAL:HG21	1.89	0.55
1:A:659:MET:HG3	1:A:660:GLY:N	2.22	0.54
1:A:406:GLN:HE21	1:A:406:GLN:HA	1.71	0.54
1:A:266:ASN:HD22	1:A:266:ASN:N	2.06	0.53
1:A:377:ARG:O	1:A:381:GLU:HB2	2.08	0.53
1:A:420:LEU:HD11	1:A:422:VAL:HG13	1.89	0.53
1:A:311:LEU:HD22	1:A:508:LEU:HD13	1.92	0.52
1:A:667:ASN:HD21	1:A:675:ALA:HA	1.75	0.51
1:A:366:GLU:HG3	1:A:367:GLY:N	2.25	0.51
1:A:318:ASN:N	1:A:318:ASN:ND2	2.59	0.51
1:A:421:ILE:N	1:A:421:ILE:HD12	2.27	0.50
1:A:310:ASN:HB3	1:A:313:ILE:HD12	1.94	0.50
1:A:420:LEU:HD23	2:X:6:PHE:CE2	2.47	0.49
1:A:621:THR:HG22	1:A:637:GLU:HA	1.93	0.49
1:A:506:ARG:HD3	1:A:530:LEU:HD22	1.95	0.49
1:A:229:ASN:OD1	1:A:361:PRO:HD3	2.12	0.49
1:A:276:GLN:O	1:A:277:CYS:C	2.56	0.48
1:A:420:LEU:CD1	1:A:422:VAL:HG13	2.43	0.48
1:A:229:ASN:C	1:A:229:ASN:HD22	2.21	0.48
1:A:300:ASN:OD1	1:A:423:GLY:HA2	2.13	0.47
1:A:196:LEU:C	1:A:196:LEU:HD23	2.39	0.47
1:A:206:ASN:C	1:A:206:ASN:HD22	2.22	0.47
1:A:495:ILE:HG21	1:A:534:LEU:HD11	1.95	0.47
1:A:88:TRP:CZ3	1:A:106:THR:HG22	2.50	0.47
1:A:481:GLN:HG2	1:A:482:SER:N	2.30	0.47
1:A:535:GLU:HG3	1:A:536:PRO:HD2	1.96	0.47
1:A:304:ALA:HB2	2:X:6:PHE:HD2	1.78	0.47
1:A:262:ARG:O	1:A:266:ASN:ND2	2.48	0.46
1:A:620:CYS:HB2	1:A:638:ILE:HB	1.97	0.45
1:A:107:PRO:HD2	1:A:110:ALA:HB2	1.99	0.45
1:A:406:GLN:HE21	1:A:406:GLN:CA	2.30	0.44
1:A:420:LEU:HD11	1:A:422:VAL:CG1	2.48	0.43
1:A:608:SER:HB3	1:A:649:LYS:HG2	2.01	0.43
1:A:506:ARG:NH1	1:A:530:LEU:HD13	2.33	0.42
1:A:49:ASN:ND2	1:A:96:GLN:O	2.51	0.42
1:A:311:LEU:CD2	1:A:508:LEU:HD13	2.49	0.42
1:A:420:LEU:HD22	1:A:421:ILE:N	2.35	0.42
1:A:569:GLU:HG2	1:A:572:ILE:HD12	2.02	0.42
1:A:558:SER:O	1:A:559:ASN:HB2	2.19	0.42
1:A:96:GLN:O	1:A:97:ASP:C	2.62	0.41
1:A:54:VAL:CG1	1:A:123:THR:HG23	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:MET:HE3	1:A:330:MET:HB2	1.92	0.41
1:A:667:ASN:ND2	1:A:677:LYS:HD3	2.35	0.41
1:A:483:MET:HE3	1:A:483:MET:HB2	1.97	0.41
1:A:180:TRP:CE2	1:A:282:ALA:HB1	2.56	0.40
1:A:229:ASN:HB3	1:A:359:PRO:O	2.20	0.40
1:A:592:ARG:HB2	1:A:606:GLU:HB3	2.03	0.40
1:A:177:ASN:ND2	1:A:177:ASN:N	2.69	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	645/687 (94%)	610 (95%)	32 (5%)	3 (0%)	24	21
2	X	4/7 (57%)	4 (100%)	0	0	100	100
All	All	649/694 (94%)	614 (95%)	32 (5%)	3 (0%)	24	21

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	361	PRO
1	A	597	PRO
1	A	626	GLY

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	570/596 (96%)	524 (92%)	46 (8%)	11	7
2	X	4/4 (100%)	4 (100%)	0	100	100
All	All	574/600 (96%)	528 (92%)	46 (8%)	11	8

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	GLU
1	A	177	ASN
1	A	196	LEU
1	A	200	ASN
1	A	232	ASP
1	A	261	LEU
1	A	266	ASN
1	A	310	ASN
1	A	311	LEU
1	A	312	LEU
1	A	318	ASN
1	A	330	MET
1	A	363	GLU
1	A	364	LYS
1	A	366	GLU
1	A	381	GLU
1	A	400	ASP
1	A	405	ILE
1	A	406	GLN
1	A	414	LYS
1	A	418	ARG
1	A	420	LEU
1	A	436	ARG
1	A	460	ASN
1	A	479	VAL
1	A	508	LEU
1	A	532	LEU
1	A	533	THR
1	A	552	ARG
1	A	569	GLU
1	A	572	ILE
1	A	584	LEU
1	A	598	LYS
1	A	601	ARG

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Mol	Chain	Res	Type
1	A	603	LEU
1	A	604	VAL
1	A	607	VAL
1	A	617	LEU
1	A	629	LEU
1	A	630	THR
1	A	637	GLU
1	A	652	MET
1	A	655	VAL
1	A	657	LEU
1	A	669	GLU
1	A	676	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	HIS
1	A	51	GLN
1	A	126	GLN
1	A	169	GLN
1	A	206	ASN
1	A	266	ASN
1	A	267	HIS
1	A	310	ASN
1	A	318	ASN
1	A	406	GLN
1	A	531	ASN
1	A	573	ASN
1	A	610	GLN
1	A	662	HIS
1	A	667	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	ONL	X	3	2,1	7,8,9	0.60	0	4,9,11	1.49	1 (25%)

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	ONL	X	3	2,1	-	2/6/7/9	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X	3	ONL	CB-CG-CD	-2.90	110.25	114.77

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	X	3	ONL	C-CA-CB-CG
2	X	3	ONL	OD-CD-CG-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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	688	-	4,4,4	0.18	0	6,6,6	0.37	0
3	SO4	A	690	-	4,4,4	0.26	0	6,6,6	0.11	0
3	SO4	A	691	-	4,4,4	0.27	0	6,6,6	0.60	0
3	SO4	A	689	-	4,4,4	0.27	0	6,6,6	0.31	0
3	SO4	A	692	-	4,4,4	0.23	0	6,6,6	0.10	0

There are no bond length outliers.

There are no bond angle outliers.

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 [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	655/687 (95%)	1.28	134 (20%) 2 2	27, 47, 60, 70	21 (3%)
2	X	4/7 (57%)	2.86	2 (50%) 0 1	62, 63, 66, 71	0
All	All	659/694 (94%)	1.29	136 (20%) 2 2	27, 47, 60, 71	21 (3%)

All (136) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	275	GLY	5.1
1	A	683	ILE	4.8
1	A	365	SER	4.6
1	A	558	SER	4.6
1	A	269	CYS	4.6
1	A	554	CYS	4.3
1	A	243	ASN	4.2
1	A	661	LEU	4.2
1	A	97	ASP	4.0
2	X	5	PRO	3.9
1	A	366	GLU	3.9
1	A	459	ALA	3.8
1	A	233	ASP	3.8
1	A	657	LEU	3.8
2	X	6	PHE	3.8
1	A	420	LEU	3.6
1	A	16	THR	3.6
1	A	519	ILE	3.6
1	A	363	GLU	3.6
1	A	241	TRP	3.6
1	A	305	HIS	3.5
1	A	679	PHE	3.5
1	A	419	SER	3.5
1	A	361	PRO	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	244	ASN	3.4
1	A	636	VAL	3.4
1	A	405	ILE	3.4
1	A	640	ASP	3.3
1	A	627	ALA	3.2
1	A	277	CYS	3.2
1	A	329	GLU	3.2
1	A	480	GLY	3.2
1	A	642	VAL	3.1
1	A	456	PHE	3.1
1	A	360	THR	3.1
1	A	392	PHE	3.1
1	A	629	LEU	3.1
1	A	332	TRP	3.1
1	A	239	GLY	3.0
1	A	362	GLN	3.0
1	A	328	SER	3.0
1	A	105	THR	3.0
1	A	597	PRO	3.0
1	A	655	VAL	3.0
1	A	664	LEU	3.0
1	A	231	ASN	2.9
1	A	1	MET	2.9
1	A	250	SER	2.9
1	A	229	ASN	2.9
1	A	317	ARG	2.8
1	A	82	ALA	2.8
1	A	594	LEU	2.8
1	A	306	ASP	2.8
1	A	660	GLY	2.8
1	A	675	ALA	2.8
1	A	100	LEU	2.8
1	A	557	GLU	2.8
1	A	603	LEU	2.8
1	A	668	PHE	2.7
1	A	472	GLY	2.7
1	A	621	THR	2.7
1	A	125	TYR	2.7
1	A	36	GLY	2.7
1	A	41	LEU	2.7
1	A	658	HIS	2.7
1	A	303	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	313	ILE	2.6
1	A	638	ILE	2.6
1	A	367	GLY	2.6
1	A	267	HIS	2.6
1	A	92	VAL	2.6
1	A	142	TRP	2.6
1	A	304	ALA	2.6
1	A	400	ASP	2.6
1	A	249	VAL	2.5
1	A	556	THR	2.5
1	A	659	MET	2.5
1	A	150	LEU	2.5
1	A	310	ASN	2.5
1	A	455	ALA	2.4
1	A	102	LEU	2.4
1	A	309	SER	2.4
1	A	628	GLY	2.4
1	A	318	ASN	2.3
1	A	18	GLY	2.3
1	A	81	ASP	2.3
1	A	91	THR	2.3
1	A	126	GLN	2.3
1	A	242	ASP	2.3
1	A	364	LYS	2.3
1	A	600	LYS	2.3
1	A	83	VAL	2.3
1	A	559	ASN	2.3
1	A	482	SER	2.3
1	A	646	GLU	2.3
1	A	6	VAL	2.3
1	A	641	PRO	2.3
1	A	90	ALA	2.3
1	A	673	LEU	2.3
1	A	238	LEU	2.2
1	A	122	SER	2.2
1	A	148	VAL	2.2
1	A	247	ASP	2.2
1	A	595	GLY	2.2
1	A	154	GLU	2.2
1	A	128	SER	2.2
1	A	650	VAL	2.2
1	A	596	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	104	LEU	2.2
1	A	274	TYR	2.2
1	A	393	VAL	2.1
1	A	24	ALA	2.1
1	A	592	ARG	2.1
1	A	601	ARG	2.1
1	A	53	SER	2.1
1	A	245	TYR	2.1
1	A	232	ASP	2.1
1	A	230	CYS	2.1
1	A	460	ASN	2.1
1	A	503	TYR	2.1
1	A	130	PHE	2.1
1	A	341	TRP	2.1
1	A	414	LYS	2.1
1	A	270	GLN	2.1
1	A	377	ARG	2.1
1	A	416	ILE	2.1
1	A	622	PHE	2.1
1	A	276	GLN	2.0
1	A	639	PRO	2.0
1	A	598	LYS	2.0
1	A	353	GLY	2.0
1	A	316	PHE	2.0
1	A	52	ALA	2.0
1	A	311	LEU	2.0
1	A	555	LEU	2.0
1	A	516	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ONL	X	3	9/10	0.87	0.14	55,57,62,63	0

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	SO4	A	690	5/5	0.54	0.12	107,108,108,108	0
3	SO4	A	692	5/5	0.75	0.12	78,78,79,80	0
3	SO4	A	689	5/5	0.83	0.22	56,58,60,60	0
3	SO4	A	688	5/5	0.95	0.15	45,49,50,50	0
3	SO4	A	691	5/5	0.96	0.13	46,49,49,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.