



# Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 07:21 PM GMT

PDB ID : 2XO3  
Title : HUMAN ANNEXIN V WITH INCORPORATED METHIONINE ANALOGUE HOMOPROPARGYLGLYCINE  
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Deposited on : 2010-08-09  
Resolution : 2.30 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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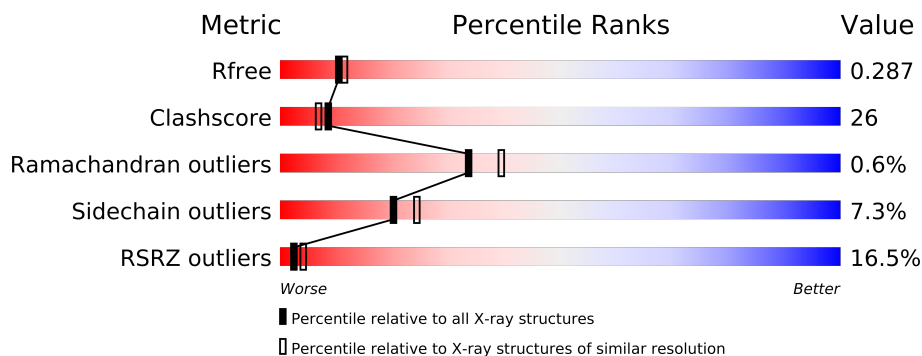
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.30 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))
$R_{free}$	66092	2929 (2.30-2.30)
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	320	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2780 atoms, of which 0 are hydrogen and 0 are deuterium.

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 ANNEXIN A5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	317	Total	C	N	O	S	72	0	1
			2497	1581	421	494	1			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	IZO	MET	ENGINEERED MUTATION	UNP P08758
A	28	IZO	MET	ENGINEERED MUTATION	UNP P08758
A	85	IZO	MET	ENGINEERED MUTATION	UNP P08758
A	152	IZO	MET	ENGINEERED MUTATION	UNP P08758
A	214	IZO	MET	ENGINEERED MUTATION	UNP P08758
A	259	IZO	MET	ENGINEERED MUTATION	UNP P08758
A	273	IZO	MET	ENGINEERED MUTATION	UNP P08758
A	299	IZO	MET	ENGINEERED MUTATION	UNP P08758

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Ca	0	0
			2	2		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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 water.

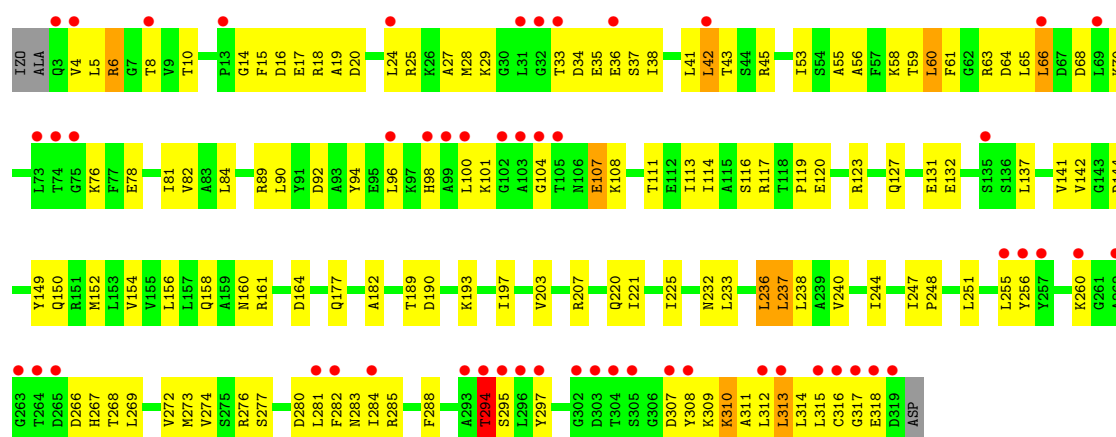
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	271	Total	O	0	0
			271	271		

### 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.

#### • Molecule 1: ANNEXIN A5

Chain A: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	154.97Å 154.97Å 35.58Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.96 – 2.30 19.96 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.96-2.30) 99.9 (19.96-2.30)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	9.89 (at 2.30Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, $R_{free}$	0.262 , 0.291 0.257 , 0.287	Depositor DCC
$R_{free}$ test set	693 reflections (5.16%)	DCC
Wilson B-factor (Å <sup>2</sup> )	27.7	Xtriage
Anisotropy	0.903	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 34.1	EDS
Estimated twinning fraction	0.023 for h,-h-k,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 14128 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	2780	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.20% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, SO4, IZO

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	0.38	0/2468	0.64	1/3316 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	104	GLY	N-CA-C	-5.12	100.29	113.10

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2497	0	2485	124	0
2	A	2	0	0	0	0
3	A	10	0	0	0	0
4	A	271	0	0	13	0
All	All	2780	0	2485	124	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 26.

All (124) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:255:LEU:HD11	1:A:288:PHE:CE1	1.72	1.24
1:A:6:ARG:H	1:A:283:ASN:HD21	1.06	1.01
1:A:309:LYS:O	1:A:313:LEU:HD13	1.68	0.94
1:A:255:LEU:HD11	1:A:288:PHE:HE1	1.35	0.91
1:A:309:LYS:HG3	1:A:313:LEU:HD11	1.53	0.90
1:A:6:ARG:N	1:A:283:ASN:HD21	1.77	0.81
1:A:309:LYS:C	1:A:313:LEU:HD13	2.04	0.79
1:A:6:ARG:H	1:A:283:ASN:ND2	1.79	0.78
1:A:255:LEU:HD12	1:A:256:TYR:N	2.01	0.76
1:A:41:LEU:O	1:A:45:ARG:HG2	1.86	0.75
1:A:5:LEU:HB3	1:A:280:ASP:HB3	1.71	0.73
1:A:240:VAL:O	1:A:244:ILE:HG12	1.89	0.72
1:A:288:PHE:HD2	1:A:294:THR:O	1.74	0.70
1:A:309:LYS:CG	1:A:313:LEU:HD11	2.23	0.69
1:A:96:LEU:O	1:A:100:LEU:HB2	1.95	0.66
1:A:313:LEU:N	1:A:313:LEU:HD12	2.10	0.66
1:A:149:TYR:CD1	1:A:232:ASN:HB3	2.31	0.65
1:A:119:PRO:O	1:A:123:ARG:HG3	1.97	0.65
1:A:127:GLN:O	1:A:131:GLU:HG3	1.97	0.65
1:A:78:GLU:O	1:A:82:VAL:HG23	1.96	0.64
1:A:193:LYS:O	1:A:197:ILE:HG12	1.97	0.64
1:A:308:TYR:CE1	1:A:312:LEU:HD11	2.33	0.64
1:A:288:PHE:CD2	1:A:294:THR:O	2.50	0.63
1:A:35:GLU:HG2	1:A:307:ASP:OD2	1.99	0.63
1:A:313:LEU:H	1:A:313:LEU:CD1	2.12	0.62
1:A:182:ALA:HB1	1:A:190:ASP:HB3	1.79	0.62
1:A:164:ASP:HA	4:A:2213:HOH:O	2.00	0.62
1:A:255:LEU:HD11	1:A:288:PHE:CZ	2.30	0.62
1:A:152:IZO:CG	1:A:236:LEU:HD13	2.30	0.62
1:A:84:LEU:HD12	1:A:274:VAL:HG22	1.83	0.60
1:A:313:LEU:N	1:A:313:LEU:CD1	2.65	0.59
1:A:24:LEU:O	1:A:28:IZO:HB2C	2.03	0.59
1:A:25:ARG:NH1	1:A:29:LYS:HG3	2.16	0.59
1:A:255:LEU:HD12	1:A:255:LEU:C	2.23	0.58
1:A:295:SER:HB3	4:A:2258:HOH:O	2.03	0.57
1:A:280:ASP:O	1:A:284:ILE:HG13	2.05	0.57
1:A:42:LEU:HD23	1:A:81:ILE:HG23	1.86	0.56
1:A:14:GLY:N	4:A:2023:HOH:O	2.38	0.56
1:A:37:SER:O	1:A:41:LEU:HB2	2.06	0.56
1:A:55:ALA:O	1:A:59:THR:HG23	2.06	0.55
1:A:297:TYR:CE2	1:A:318:GLU:HA	2.41	0.55
1:A:5:LEU:HD22	1:A:5:LEU:N	2.22	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:27:ALA:HB2	4:A:2050:HOH:O	2.06	0.54
1:A:255:LEU:CD1	1:A:288:PHE:HE1	2.16	0.54
1:A:221:ILE:O	1:A:225:ILE:HG13	2.07	0.54
1:A:5:LEU:HA	1:A:283:ASN:HD21	1.74	0.53
1:A:309:LYS:O	1:A:313:LEU:CD1	2.52	0.53
1:A:150:GLN:O	1:A:154:VAL:HG23	2.08	0.52
1:A:154:VAL:O	1:A:158:GLN:HG2	2.09	0.52
1:A:28:IZO:HA	1:A:33:THR:HG23	1.91	0.52
1:A:317:GLY:HA3	4:A:2256:HOH:O	2.09	0.52
1:A:15:PHE:HE1	1:A:53:ILE:HD11	1.75	0.52
1:A:107:GLU:HG2	1:A:149:TYR:CE2	2.45	0.52
1:A:90:LEU:HD22	1:A:132:GLU:HG3	1.91	0.52
1:A:267:HIS:CD2	4:A:2252:HOH:O	2.63	0.51
1:A:309:LYS:HG2	1:A:313:LEU:CD2	2.41	0.51
1:A:25:ARG:CZ	1:A:29:LYS:HG3	2.41	0.51
1:A:233:LEU:HG	1:A:237:LEU:HD22	1.92	0.51
1:A:6:ARG:O	1:A:280:ASP:HA	2.11	0.50
1:A:5:LEU:HD22	1:A:5:LEU:H	1.77	0.50
1:A:310:LYS:O	1:A:314:LEU:HD12	2.11	0.50
1:A:89:ARG:HG3	1:A:90:LEU:HG	1.91	0.50
1:A:5:LEU:HA	1:A:283:ASN:ND2	2.27	0.50
1:A:25:ARG:O	1:A:29:LYS:HB2	2.12	0.50
1:A:255:LEU:CD1	1:A:288:PHE:CE1	2.68	0.49
1:A:41:LEU:HD22	1:A:45:ARG:NH1	2.28	0.49
1:A:28:IZO:HE	1:A:65:LEU:HD12	1.95	0.49
1:A:14:GLY:CA	4:A:2023:HOH:O	2.59	0.49
1:A:247:ILE:N	1:A:248:PRO:CD	2.75	0.49
1:A:15:PHE:HA	4:A:2025:HOH:O	2.12	0.49
1:A:66:LEU:HD13	1:A:70:LYS:HE2	1.94	0.49
1:A:107:GLU:HG2	1:A:149:TYR:CZ	2.48	0.49
1:A:267:HIS:HD2	4:A:2252:HOH:O	1.97	0.48
1:A:58:LYS:HE2	1:A:64:ASP:HA	1.97	0.47
1:A:309:LYS:CG	1:A:313:LEU:CD1	2.93	0.47
1:A:268:THR:O	1:A:272:VAL:HG23	2.14	0.47
1:A:220:GLN:HA	1:A:220:GLN:HE21	1.80	0.47
1:A:203:VAL:O	1:A:207:ARG:HG3	2.14	0.46
1:A:27:ALA:HB1	1:A:34:ASP:HB3	1.96	0.46
1:A:76:LYS:HD3	1:A:266:ASP:OD2	2.15	0.46
1:A:309:LYS:HG2	1:A:313:LEU:HD21	1.96	0.46
1:A:63:ARG:HD3	1:A:68:ASP:OD2	2.15	0.46
1:A:273:IZO:O	1:A:277:SER:HB3	2.16	0.46
1:A:315:LEU:O	1:A:315:LEU:HD23	2.16	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:177:GLN:NE2	1:A:177:GLN:HA	2.31	0.46
1:A:113:ILE:O	1:A:117:ARG:HD3	2.16	0.45
1:A:309:LYS:O	1:A:311:ALA:N	2.49	0.45
1:A:111:THR:HG23	1:A:236:LEU:HA	1.97	0.45
1:A:61:PHE:HA	4:A:2093:HOH:O	2.17	0.45
1:A:309:LYS:CG	1:A:313:LEU:HD21	2.46	0.44
1:A:5:LEU:CA	1:A:283:ASN:HD21	2.29	0.44
1:A:20:ASP:OD2	1:A:45:ARG:HD2	2.18	0.44
1:A:17:GLU:HG2	1:A:18:ARG:N	2.32	0.44
1:A:114:ILE:O	1:A:114:ILE:HG22	2.18	0.44
1:A:8:THR:HG21	1:A:316:CYS:O	2.17	0.44
1:A:94:TYR:CE1	1:A:98:HIS:CE1	3.05	0.44
1:A:160:ASN:O	1:A:161:ARG:C	2.56	0.44
1:A:100:LEU:HD12	1:A:100:LEU:HA	1.86	0.43
1:A:149:TYR:CG	1:A:232:ASN:HB3	2.53	0.43
1:A:15:PHE:HZ	1:A:53:ILE:HG13	1.83	0.43
1:A:92:ASP:O	1:A:96:LEU:HG	2.19	0.43
1:A:36:GLU:HB3	4:A:2061:HOH:O	2.18	0.43
1:A:56:ALA:O	1:A:60:LEU:HB2	2.19	0.43
1:A:308:TYR:CE1	1:A:312:LEU:CD1	3.00	0.43
1:A:84:LEU:CD1	1:A:274:VAL:HG22	2.48	0.43
1:A:120:GLU:HA	1:A:123:ARG:HH11	1.83	0.42
1:A:189:THR:HG22	1:A:190:ASP:N	2.33	0.42
1:A:272:VAL:O	1:A:276:ARG:HG2	2.19	0.42
1:A:116:SER:O	1:A:247:ILE:HD13	2.20	0.42
1:A:142:VAL:HG12	1:A:142:VAL:O	2.18	0.42
1:A:309:LYS:O	1:A:310:LYS:C	2.58	0.41
1:A:137:LEU:O	1:A:141:VAL:HG23	2.20	0.41
1:A:10:THR:HG22	4:A:2020:HOH:O	2.20	0.41
1:A:152:IZO:HG1C	1:A:236:LEU:HD13	1.99	0.41
1:A:285:ARG:NH1	1:A:317:GLY:O	2.53	0.41
1:A:41:LEU:HD12	1:A:42:LEU:HD12	2.01	0.41
1:A:313:LEU:HD13	1:A:313:LEU:H	1.85	0.41
1:A:158:GLN:O	1:A:160:ASN:ND2	2.54	0.41
1:A:152:IZO:O	1:A:156:LEU:HG	2.21	0.41
1:A:6:ARG:NH2	1:A:282:PHE:HE2	2.19	0.41
1:A:38:ILE:HG22	1:A:42:LEU:HD22	2.01	0.41
1:A:25:ARG:NH2	1:A:63:ARG:NH1	2.68	0.41
1:A:16:ASP:HB3	1:A:19:ALA:HB3	2.03	0.41
1:A:317:GLY:HA2	4:A:2268:HOH:O	2.22	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	308/320 (96%)	284 (92%)	22 (7%)	2 (1%)	33	39

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	294	THR
1	A	310	LYS

### 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	262/264 (99%)	243 (93%)	19 (7%)	20	24

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	VAL
1	A	6	ARG
1	A	42	LEU
1	A	43	THR
1	A	60	LEU
1	A	66	LEU
1	A	101	LYS
1	A	107	GLU
1	A	108	LYS
1	A	144	ASP
1	A	236	LEU
1	A	237	LEU

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Mol	Chain	Res	Type
1	A	238	LEU
1	A	251	LEU
1	A	260	LYS
1	A	269	LEU
1	A	281	LEU
1	A	294	THR
1	A	313	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	127	GLN
1	A	160	ASN
1	A	177	GLN
1	A	181	GLN
1	A	220	GLN
1	A	267	HIS
1	A	283	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

7 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	IZO	A	152	1	7,7,8	7.30	2 (28%)	5,7,9	2.77	1 (20%)
1	IZO	A	214	1	7,7,8	7.11	2 (28%)	5,7,9	2.35	1 (20%)
1	IZO	A	259	1	7,7,8	7.62	3 (42%)	5,7,9	1.26	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	IZO	A	273	1	7,7,8	7.11	2 (28%)	5,7,9	0.52	0
1	IZO	A	28	1	7,7,8	7.07	3 (42%)	5,7,9	1.92	1 (20%)
1	IZO	A	299	1	7,7,8	7.39	2 (28%)	5,7,9	1.87	2 (40%)
1	IZO	A	85	1	7,7,8	6.79	2 (28%)	5,7,9	0.73	0

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
1	IZO	A	152	1	-	0/4/6/8	0/0/0/0
1	IZO	A	214	1	-	0/4/6/8	0/0/0/0
1	IZO	A	259	1	-	0/4/6/8	0/0/0/0
1	IZO	A	273	1	-	0/4/6/8	0/0/0/0
1	IZO	A	28	1	-	0/4/6/8	0/0/0/0
1	IZO	A	299	1	-	0/4/6/8	0/0/0/0
1	IZO	A	85	1	-	0/4/6/8	0/0/0/0

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	259	IZO	O-C	19.31	1.24	1.11
1	A	299	IZO	O-C	19.13	1.24	1.11
1	A	152	IZO	O-C	19.08	1.24	1.11
1	A	273	IZO	O-C	18.66	1.24	1.11
1	A	214	IZO	O-C	18.61	1.24	1.11
1	A	28	IZO	O-C	18.05	1.23	1.11
1	A	85	IZO	O-C	17.78	1.23	1.11
1	A	259	IZO	CA-C	4.04	1.56	1.48
1	A	299	IZO	CA-C	3.84	1.55	1.48
1	A	28	IZO	CA-C	3.69	1.55	1.48
1	A	259	IZO	CB-CA	3.64	1.56	1.53
1	A	28	IZO	CB-CA	3.02	1.55	1.53
1	A	152	IZO	CA-C	2.76	1.53	1.48
1	A	214	IZO	CA-C	2.66	1.53	1.48
1	A	85	IZO	CA-C	2.42	1.52	1.48
1	A	273	IZO	CA-C	2.37	1.52	1.48

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	152	IZO	C-CA-N	-5.98	107.86	113.83
1	A	214	IZO	C-CA-N	-4.96	108.87	113.83
1	A	28	IZO	C-CA-N	-4.05	109.78	113.83
1	A	299	IZO	C-CA-N	-3.36	110.47	113.83
1	A	259	IZO	C-CA-N	-2.37	111.46	113.83
1	A	299	IZO	CG-CB-CA	2.26	117.03	112.67

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	SO4	A	1322	2	4,4,4	0.23	0	6,6,6	0.20	0
3	SO4	A	1323	-	4,4,4	0.15	0	6,6,6	0.07	0

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	1322	2	-	0/0/0/0	0/0/0/0
3	SO4	A	1323	-	-	0/0/0/0	0/0/0/0

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.

## 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 ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	317/320 (99%)	0.90	53 (16%) 2 4	14, 38, 91, 96	23 (7%)

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	294	THR	7.7
1	A	305	SER	6.6
1	A	102	GLY	6.3
1	A	262	ALA	6.2
1	A	103	ALA	5.9
1	A	263	GLY	5.2
1	A	297	TYR	5.1
1	A	264	THR	5.1
1	A	293	ALA	5.0
1	A	304	THR	4.9
1	A	303	ASP	4.8
1	A	4	VAL	4.4
1	A	296	LEU	4.4
1	A	316	CYS	4.0
1	A	73	LEU	3.9
1	A	32	GLY	3.8
1	A	74	THR	3.8
1	A	105	THR	3.7
1	A	308	TYR	3.7
1	A	265	ASP	3.7
1	A	318	GLU	3.5
1	A	69	LEU	3.4
1	A	75	GLY	3.4
1	A	3	GLN	3.3
1	A	24	LEU	3.3
1	A	319	ASP	3.3
1	A	31	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	255	LEU	3.1
1	A	104	GLY	3.1
1	A	33	THR	3.0
1	A	98	HIS	2.9
1	A	36	GLU	2.9
1	A	135	SER	2.9
1	A	317	GLY	2.9
1	A	313	LEU	2.8
1	A	295	SER	2.8
1	A	302	GLY	2.8
1	A	312	LEU	2.7
1	A	284	ILE	2.7
1	A	256	TYR	2.6
1	A	13	PRO	2.6
1	A	99	ALA	2.5
1	A	257	TYR	2.4
1	A	100	LEU	2.4
1	A	282	PHE	2.4
1	A	315	LEU	2.3
1	A	307	ASP	2.3
1	A	96	LEU	2.3
1	A	42	LEU	2.2
1	A	281	LEU	2.2
1	A	260	LYS	2.1
1	A	8	THR	2.1
1	A	66	LEU	2.0

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	IZO	A	259	8/9	0.29	0.02	78,79,80,81	3
1	IZO	A	152	8/9	0.15	0.01	22,23,27,28	0
1	IZO	A	85	8/9	0.18	-0.06	33,35,36,38	0
1	IZO	A	214	8/9	0.13	-0.24	20,23,25,26	0
1	IZO	A	28	8/9	0.23	-0.43	63,64,67,68	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
1	IZO	A	299	8/9	0.27	-0.55	91,92,92,93	3
1	IZO	A	273	8/9	0.16	-1.08	30,32,32,34	0

### 6.3 Carbohydrates

There are no carbohydrates in this entry.

### 6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	SO4	A	1322	5/5	0.10	-0.81	31,32,34,34	0
3	SO4	A	1323	5/5	0.17	-0.90	80,80,81,81	0
2	CA	A	1320	1/1	0.06	-2.54	25,25,25,25	0
2	CA	A	1321	1/1	0.11	-3.59	71,71,71,71	0

### 6.5 Other polymers

There are no such residues in this entry.