



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:53 AM UTC

PDB ID : 4ECL / pdb\_00004ecl  
Title : Crystal structure of the cytoplasmic domain of vancomycin resistance serine racemase VanTg  
Authors : Stogios, P.J.; Wawrzak, Z.; Minasov, G.; Evdokimova, E.; Egorova, O.; Cosme, J.; Di Leo, R.; Krishnamoorthy, M.; Meziane-Cherif, D.; Courvalin, P.; Savchenko, A.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : 2012-03-26  
Resolution : 2.02 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](mailto: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>.

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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)

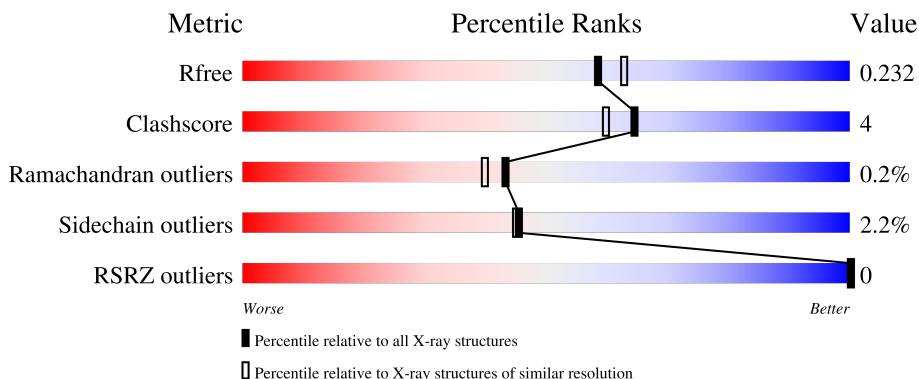
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*





The reported resolution of this entry is 2.02 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	13299 (2.04-2.00)
Clashscore	190562	1022 (2.02-2.02)
Ramachandran outliers	187476	1014 (2.02-2.02)
Sidechain outliers	187428	1014 (2.02-2.02)
RSRZ outliers	180081	13314 (2.04-2.00)

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  $\geq 3$ , 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	374	 89% 10% ..
1	B	374	 88% 11% .
1	C	374	 88% 10% ..
1	D	374	 91% 7% .

Validation Pipeline (wwPDB-VP) : 2.49

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 12319 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 Serine racemase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	372	2889	1836	492	548	6	7	0	0	0
1	B	369	2892	1842	493	545	5	7	0	3	0
1	C	370	2920	1858	499	550	5	8	0	7	0
1	D	369	2890	1839	488	550	6	7	0	4	0

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Cl	0	0
			2	2		
2	B	2	Total	Cl	0	0
			2	2		
2	C	1	Total	Cl	0	0
			1	1		
2	D	3	Total	Cl	0	0
			3	3		

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


- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	169	Total	O	0	3
			172	172		
4	B	162	Total	O	0	2
			164	164		
4	C	185	Total	O	0	3
			187	187		
4	D	177	Total	O	0	0
			177	177		

### 3 Residue-property plots [i](#)


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.

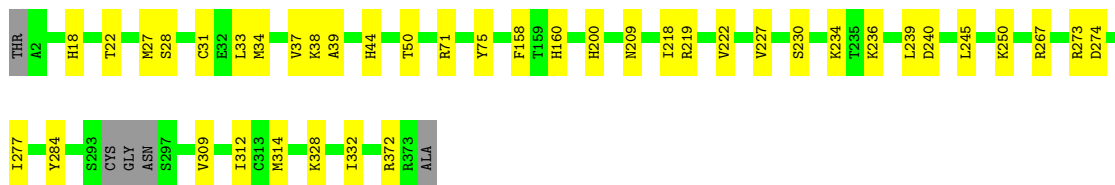
- Molecule 1: Serine racemase

Chain A:  89% 10% ..




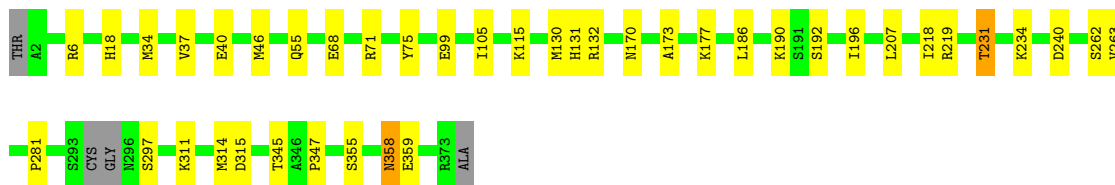
- Molecule 1: Serine racemase

Chain B:  88% 11% ..




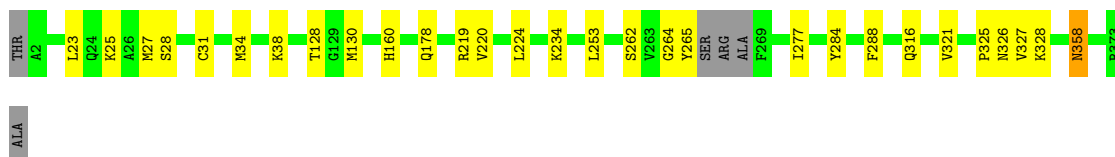
- Molecule 1: Serine racemase

Chain C:  88% 10% ..



- Molecule 1: Serine racemase

Chain D:  91% 7% ..



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.68Å 82.34Å 117.47Å 90.00° 90.14° 90.00°	Depositor
Resolution (Å)	19.91 – 2.02 19.91 – 2.02	Depositor EDS
% Data completeness (in resolution range)	98.2 (19.91-2.02) 90.7 (19.91-2.02)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.40 (at 2.02Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.181 , 0.233 0.184 , 0.232	Depositor DCC
$R_{free}$ test set	1992 reflections (2.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.6	Xtrriage
Anisotropy	1.595	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 40.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.010 for -k,-h,-l 0.009 for k,h,-l 0.135 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	12319	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.44% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, 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	0.44	0/2927	0.79	0/3943
1	B	0.44	0/2935	0.78	0/3951
1	C	0.44	0/2975	0.78	0/4004
1	D	0.45	0/2933	0.78	0/3951
All	All	0.44	0/11770	0.78	0/15849

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 [i](#)

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	2889	0	2965	34	0
1	B	2892	0	2984	29	0
1	C	2920	0	3019	25	0
1	D	2890	0	2966	18	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	1	0	0	0	0
2	D	3	0	0	0	0
3	A	5	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	5	0	0	1	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
4	A	172	0	0	2	0
4	B	164	0	0	1	0
4	C	187	0	0	2	0
4	D	177	0	0	1	0
All	All	12319	0	11934	91	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 4.

All (91) 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:314:MSE:HE2	1:B:38:LYS:HG3	1.49	0.92
1:A:314:MSE:HE3	1:B:39:ALA:HB3	1.54	0.88
1:D:358:ASN:HD22	1:D:358:ASN:H	1.39	0.69
1:A:358:ASN:HD22	1:A:358:ASN:H	1.39	0.69
3:B:403:SO4:O3	4:B:656:HOH:O	2.11	0.68
3:A:403:SO4:O1	4:A:638:HOH:O	2.12	0.67
1:A:40:GLU:OE2	1:A:71:ARG:NH2	2.27	0.64
1:B:27:MSE:HG2	1:B:218:ILE:HD12	1.80	0.62
1:C:132:ARG:HD3	1:D:316:GLN:HE21	1.64	0.61
1:B:71:ARG:NH2	1:B:75:TYR:OH	2.30	0.60
1:D:321:VAL:HG21	1:D:327:VAL:HG11	1.86	0.58
1:C:55:GLN:NE2	4:C:659:HOH:O	2.26	0.57
1:D:358:ASN:H	1:D:358:ASN:ND2	2.02	0.57
1:C:18:HIS:HE1	1:C:240:ASP:O	1.87	0.56
1:A:39:ALA:CB	1:B:314:MSE:HE3	2.35	0.56
1:C:358:ASN:H	1:C:358:ASN:HD22	1.52	0.56
1:C:231:THR:HG22	1:C:347:PRO:HB2	1.87	0.56
1:C:355:SER:OG	1:C:359:GLU:OE1	2.21	0.56
1:C:311:LYS:NZ	4:C:507:HOH:O	2.38	0.56
1:D:34:MSE:CE	1:D:219:ARG:HG2	2.36	0.56
1:D:23:LEU:HD13	1:D:220[A]:VAL:HG21	1.89	0.55
1:D:27:MSE:HG2	1:D:31:CYS:HB3	1.88	0.55
1:D:34:MSE:HE2	1:D:219:ARG:HG2	1.88	0.55
1:A:266:SER:C	1:A:268:ALA:H	2.13	0.55
1:B:222[A]:VAL:HG22	1:B:227:VAL:HG23	1.88	0.55
1:C:71[A]:ARG:NE	1:C:75:TYR:OH	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:314:MSE:SE	1:D:38:LYS:HE3	2.58	0.54
1:A:314:MSE:CE	1:B:38:LYS:HG3	2.30	0.54
1:B:34:MSE:CE	1:B:219:ARG:HG2	2.39	0.53
1:A:268:ALA:HB1	1:A:294:CYS:SG	2.48	0.53
1:B:160:HIS:HD2	1:B:219:ARG:HH21	1.57	0.52
1:B:18:HIS:HE1	1:B:240:ASP:O	1.94	0.51
1:C:46:MSE:HE1	1:C:68:GLU:HG2	1.92	0.51
1:A:267:ARG:H	1:A:267:ARG:HE	1.57	0.51
1:A:290:ARG:NH1	4:A:658:HOH:O	2.44	0.51
1:A:358:ASN:HD22	1:A:358:ASN:N	2.09	0.50
1:A:174:PHE:HA	1:A:177:LYS:HE3	1.94	0.50
1:A:38:LYS:HG3	1:B:314:MSE:HE1	1.91	0.50
1:B:37:VAL:HG11	1:B:50:THR:HG22	1.94	0.49
1:B:273:ARG:HG3	1:B:274:ASP:O	2.13	0.49
1:A:39:ALA:HB3	1:B:314:MSE:HE3	1.93	0.49
1:A:266:SER:C	1:A:268:ALA:N	2.70	0.49
1:A:200:HIS:HB3	1:A:217:TYR:HB2	1.96	0.48
1:D:316:GLN:NE2	4:D:501:HOH:O	2.45	0.47
1:A:47:TYR:HD1	1:A:75:TYR:CG	2.33	0.47
1:A:314:MSE:CE	1:B:39:ALA:HB3	2.36	0.46
1:A:171:ASP:OD2	1:B:267:ARG:NH2	2.49	0.46
1:C:131:HIS:HD2	1:D:262:SER:O	1.98	0.46
1:C:345:THR:HB	1:C:347:PRO:HD2	1.97	0.46
1:B:209:ASN:O	1:B:236:LYS:HD2	2.16	0.46
1:C:34:MSE:CE	1:C:219:ARG:HG2	2.46	0.45
1:A:38:LYS:HG3	1:B:314:MSE:CE	2.46	0.45
1:D:128:THR:O	1:D:178:GLN:HG2	2.17	0.45
1:D:220[A]:VAL:HG22	1:D:224:LEU:H	1.82	0.45
1:A:97:LYS:HB3	1:A:97:LYS:HE2	1.89	0.45
1:B:158:PHE:HB2	1:B:200:HIS:O	2.17	0.45
1:B:284:TYR:CE1	1:B:314:MSE:HG3	2.53	0.44
1:C:6:ARG:HG3	1:C:281:PRO:HB2	1.99	0.44
1:C:105:ILE:HD12	1:D:253:LEU:HD12	1.99	0.44
1:A:264:GLY:C	1:A:266:SER:H	2.25	0.44
1:C:130[B]:MSE:SE	1:D:264:GLY:HA2	2.68	0.44
1:B:34:MSE:HE2	1:B:219:ARG:HG2	2.00	0.44
1:A:13:LEU:HD13	1:A:52:TYR:CD1	2.53	0.44
1:A:231:THR:HA	1:A:232:ASN:HA	1.67	0.43
1:A:253:LEU:HG	1:A:254:ILE:N	2.33	0.43
1:C:37:VAL:O	1:C:46:MSE:HE2	2.19	0.43
1:C:130[B]:MSE:HE3	1:C:132:ARG:HD2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:LYS:HD2	1:A:188:TRP:CG	2.54	0.42
1:C:40:GLU:OE2	1:C:71[A]:ARG:NH2	2.32	0.42
1:C:207:LEU:HB2	1:C:218:ILE:HD13	2.02	0.42
1:A:104:LEU:HB2	1:A:124:ILE:HA	2.02	0.42
1:C:186:LEU:HD13	1:C:196:ILE:HG21	2.00	0.42
1:A:314:MSE:HE3	1:B:39:ALA:CB	2.36	0.42
1:B:31:CYS:SG	1:B:218:ILE:HG13	2.60	0.42
1:A:355:SER:OG	1:A:356:ILE:N	2.51	0.42
1:B:250:LYS:HE2	1:B:332:ILE:HG12	2.01	0.42
1:B:44:HIS:CD2	1:B:245:LEU:HB2	2.54	0.41
1:B:22:THR:HG22	1:B:239:LEU:HD13	2.02	0.41
1:B:277:ILE:HD12	1:B:309:VAL:HG21	2.02	0.41
1:C:132:ARG:HD3	1:D:316:GLN:NE2	2.32	0.41
1:D:325:PRO:HA	1:D:326:ASN:HA	1.58	0.41
1:C:173:ALA:O	1:C:177:LYS:HG2	2.20	0.41
1:D:284:TYR:HA	1:D:288:PHE:O	2.21	0.41
1:C:190:LYS:C	1:C:192:SER:H	2.28	0.41
1:A:39:ALA:HB2	1:B:314:MSE:HE3	2.01	0.41
1:C:262:SER:OG	1:C:263:VAL:N	2.53	0.41
1:A:229:SER:HA	1:A:357:THR:HB	2.02	0.41
1:A:236:LYS:HA	1:A:236:LYS:HD3	1.87	0.41
1:A:265:TYR:O	1:A:265:TYR:CG	2.74	0.41
1:B:27:MSE:HE1	1:B:33:LEU:HA	2.03	0.41
1:A:264:GLY:O	1:A:266:SER:N	2.54	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	370/374 (99%)	357 (96%)	10 (3%)	3 (1%)	16 8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	368/374 (98%)	357 (97%)	11 (3%)	0	100	100
1	C	373/374 (100%)	364 (98%)	9 (2%)	0	100	100
1	D	369/374 (99%)	353 (96%)	16 (4%)	0	100	100
All	All	1480/1496 (99%)	1431 (97%)	46 (3%)	3 (0%)	43	40

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	265	TYR
1	A	229	SER
1	A	267	ARG

### 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	317/311 (102%)	312 (98%)	5 (2%)	55	56
1	B	318/311 (102%)	312 (98%)	6 (2%)	50	50
1	C	323/311 (104%)	314 (97%)	9 (3%)	38	35
1	D	319/311 (103%)	310 (97%)	9 (3%)	38	35
All	All	1277/1244 (103%)	1248 (98%)	29 (2%)	45	43

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	130	MSE
1	A	138	GLU
1	A	315	ASP
1	A	358	ASN
1	A	371	ILE
1	B	28	SER
1	B	230	SER
1	B	234	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	312	ILE
1	B	328	LYS
1	B	372	ARG
1	C	99	GLU
1	C	115	LYS
1	C	170[A]	ASN
1	C	170[B]	ASN
1	C	231	THR
1	C	234	LYS
1	C	297	SER
1	C	315	ASP
1	C	358	ASN
1	D	25	LYS
1	D	28	SER
1	D	130	MSE
1	D	160	HIS
1	D	234	LYS
1	D	265	TYR
1	D	277	ILE
1	D	328	LYS
1	D	358	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	358	ASN
1	B	18	HIS
1	B	24	GLN
1	C	18	HIS
1	C	24	GLN
1	C	55	GLN
1	C	102	GLN
1	C	131	HIS
1	C	232	ASN
1	C	358	ASN
1	D	291	ASN
1	D	316	GLN
1	D	358	ASN
1	D	366	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 8 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	$\# Z  > 2$
3	SO4	C	402	-	4,4,4	0.19	0	6,6,6	0.39	0
3	SO4	D	404	-	4,4,4	0.27	0	6,6,6	0.22	0
3	SO4	B	403	-	4,4,4	0.32	0	6,6,6	0.12	0
3	SO4	A	403	-	4,4,4	0.29	0	6,6,6	0.17	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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	403	SO4	1	0
3	A	403	SO4	1	0

## 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	365/374 (97%)	-1.78	0 100 100	19, 32, 59, 103	0
1	B	362/374 (96%)	-1.76	0 100 100	17, 33, 59, 100	3 (0%)
1	C	363/374 (97%)	-1.77	0 100 100	16, 31, 57, 103	6 (1%)
1	D	362/374 (96%)	-1.82	0 100 100	13, 29, 62, 101	4 (1%)
All	All	1452/1496 (97%)	-1.78	0 100 100	13, 31, 60, 103	13 (0%)

There are no RSRZ outliers to report.

### 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 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, 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	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	CL	A	401	1/1	1.00	0.01	24,24,24,24	1
2	CL	A	402	1/1	1.00	0.02	20,20,20,20	1
2	CL	B	401	1/1	1.00	0.03	33,33,33,33	1
2	CL	B	402	1/1	1.00	0.04	13,13,13,13	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	CL	C	401	1/1	1.00	0.02	33,33,33,33	1
2	CL	D	401	1/1	1.00	0.02	53,53,53,53	0
2	CL	D	402	1/1	1.00	0.01	36,36,36,36	0
2	CL	D	403	1/1	1.00	0.01	39,39,39,39	0
3	SO4	A	403	5/5	1.00	0.02	23,26,31,35	0
3	SO4	B	403	5/5	1.00	0.01	22,22,26,27	5
3	SO4	C	402	5/5	1.00	0.02	23,26,30,30	0
3	SO4	D	404	5/5	1.00	0.02	24,26,31,34	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.