



# Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 01:28 am BST

PDB ID : 2NWQ  
Title : Short chain dehydrogenase from *Pseudomonas aeruginosa*  
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Deposited on : 2006-11-16  
Resolution : 2.30 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.

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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	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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

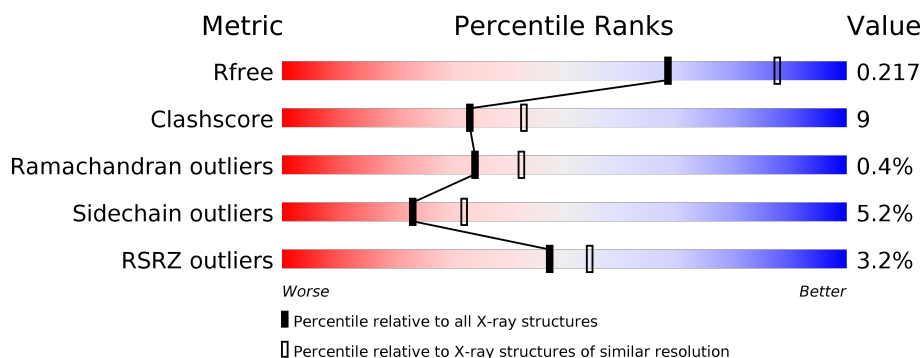
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (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 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	272	<div> <div>3%</div> <div> <div></div> <div>71%</div> <div>11%</div> <div>•</div> <div>16%</div> </div> </div>
1	B	272	<div> <div>2%</div> <div> <div></div> <div>72%</div> <div>10%</div> <div>•</div> <div>15%</div> </div> </div>
1	C	272	<div> <div>3%</div> <div> <div></div> <div>72%</div> <div>11%</div> <div>•</div> <div>15%</div> </div> </div>
1	D	272	<div> <div>2%</div> <div> <div></div> <div>68%</div> <div>14%</div> <div>•</div> <div>15%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7384 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 Probable short-chain dehydrogenase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	229	Total	C	N	O	S	Se	0	2	0
			1737	1097	304	327	5	4			
1	B	230	Total	C	N	O	S	Se	0	1	0
			1743	1098	308	328	5	4			
1	C	230	Total	C	N	O	S	Se	0	0	0
			1734	1093	305	328	4	4			
1	D	230	Total	C	N	O	S	Se	0	0	0
			1735	1093	305	329	4	4			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	GLY	-	CLONING ARTIFACT	UNP Q9HUQ6
A	-17	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
A	-16	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
A	-15	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
A	-14	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
A	-13	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
A	-12	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
A	-11	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
A	-10	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
A	-9	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
A	-8	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
A	-7	GLY	-	CLONING ARTIFACT	UNP Q9HUQ6
A	-6	LEU	-	CLONING ARTIFACT	UNP Q9HUQ6
A	-5	VAL	-	CLONING ARTIFACT	UNP Q9HUQ6
A	-4	PRO	-	CLONING ARTIFACT	UNP Q9HUQ6
A	-3	ARG	-	CLONING ARTIFACT	UNP Q9HUQ6
A	-2	GLY	-	CLONING ARTIFACT	UNP Q9HUQ6
A	-1	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
A	0	HIS	-	CLONING ARTIFACT	UNP Q9HUQ6
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
A	65	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	106	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
A	224	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
A	238	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
B	-18	GLY	-	CLONING ARTIFACT	UNP Q9HUQ6
B	-17	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
B	-16	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
B	-15	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
B	-14	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
B	-13	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
B	-12	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
B	-11	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
B	-10	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
B	-9	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
B	-8	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
B	-7	GLY	-	CLONING ARTIFACT	UNP Q9HUQ6
B	-6	LEU	-	CLONING ARTIFACT	UNP Q9HUQ6
B	-5	VAL	-	CLONING ARTIFACT	UNP Q9HUQ6
B	-4	PRO	-	CLONING ARTIFACT	UNP Q9HUQ6
B	-3	ARG	-	CLONING ARTIFACT	UNP Q9HUQ6
B	-2	GLY	-	CLONING ARTIFACT	UNP Q9HUQ6
B	-1	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
B	0	HIS	-	CLONING ARTIFACT	UNP Q9HUQ6
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
B	65	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
B	106	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
B	224	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
B	238	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
C	-18	GLY	-	CLONING ARTIFACT	UNP Q9HUQ6
C	-17	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
C	-16	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
C	-15	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
C	-14	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
C	-13	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
C	-12	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
C	-11	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
C	-10	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
C	-9	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
C	-8	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
C	-7	GLY	-	CLONING ARTIFACT	UNP Q9HUQ6
C	-6	LEU	-	CLONING ARTIFACT	UNP Q9HUQ6
C	-5	VAL	-	CLONING ARTIFACT	UNP Q9HUQ6
C	-4	PRO	-	CLONING ARTIFACT	UNP Q9HUQ6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	ARG	-	CLONING ARTIFACT	UNP Q9HUQ6
C	-2	GLY	-	CLONING ARTIFACT	UNP Q9HUQ6
C	-1	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
C	0	HIS	-	CLONING ARTIFACT	UNP Q9HUQ6
C	1	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
C	65	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
C	106	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
C	224	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
C	238	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
D	-18	GLY	-	CLONING ARTIFACT	UNP Q9HUQ6
D	-17	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
D	-16	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
D	-15	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
D	-14	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
D	-13	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
D	-12	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
D	-11	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
D	-10	HIS	-	EXPRESSION TAG	UNP Q9HUQ6
D	-9	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
D	-8	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
D	-7	GLY	-	CLONING ARTIFACT	UNP Q9HUQ6
D	-6	LEU	-	CLONING ARTIFACT	UNP Q9HUQ6
D	-5	VAL	-	CLONING ARTIFACT	UNP Q9HUQ6
D	-4	PRO	-	CLONING ARTIFACT	UNP Q9HUQ6
D	-3	ARG	-	CLONING ARTIFACT	UNP Q9HUQ6
D	-2	GLY	-	CLONING ARTIFACT	UNP Q9HUQ6
D	-1	SER	-	CLONING ARTIFACT	UNP Q9HUQ6
D	0	HIS	-	CLONING ARTIFACT	UNP Q9HUQ6
D	1	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
D	65	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
D	106	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
D	224	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6
D	238	MSE	MET	MODIFIED RESIDUE	UNP Q9HUQ6

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

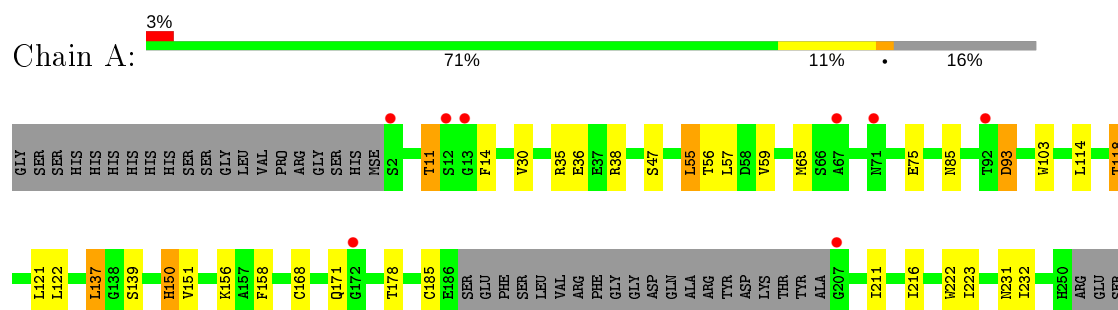
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	106	Total	O	0	0
			106	106		
3	B	112	Total	O	0	0
			112	112		
3	C	90	Total	O	0	0
			90	90		
3	D	107	Total	O	0	0
			107	107		

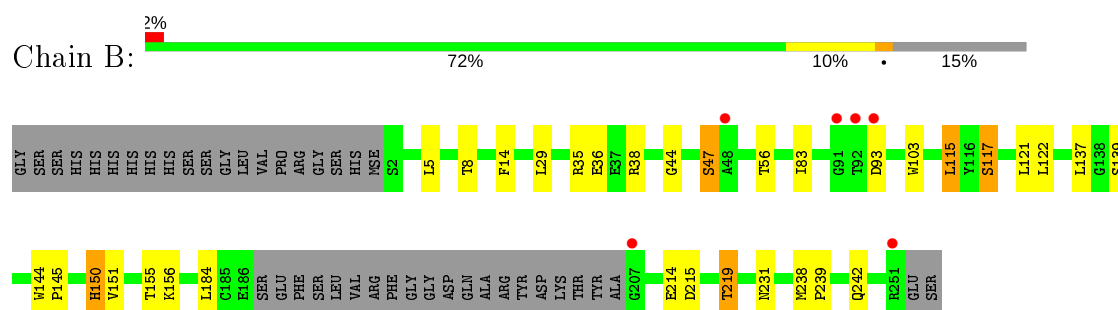
### 3 Residue-property plots [i](#)

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 ( $RSRZ > 2$ ). 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.

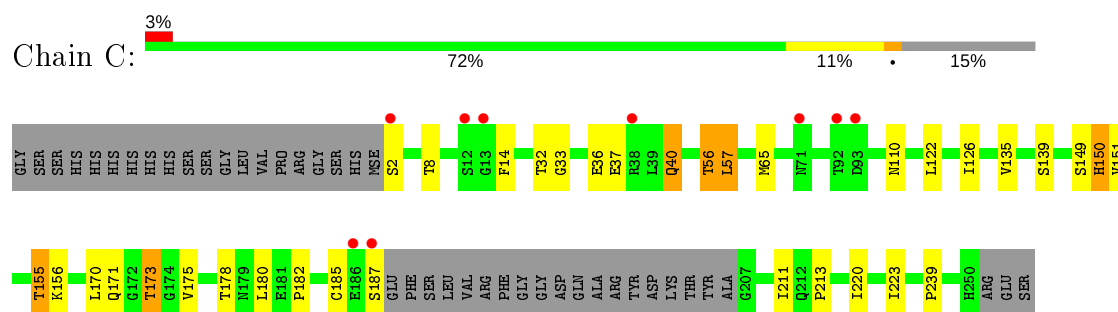
- Molecule 1: Probable short-chain dehydrogenase



- Molecule 1: Probable short-chain dehydrogenase

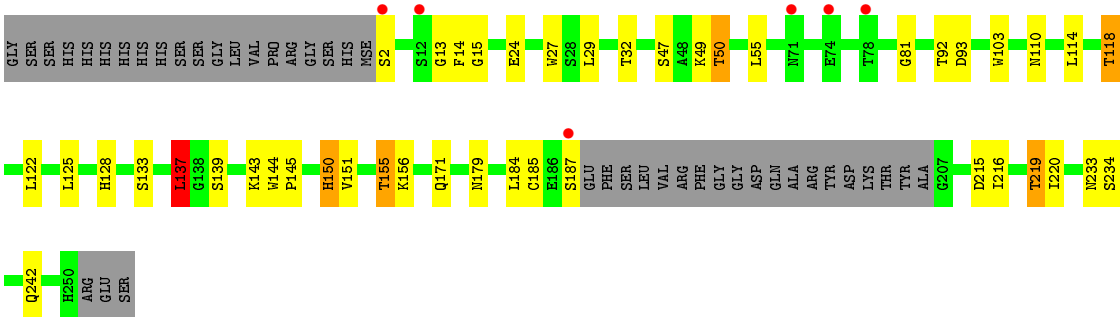


- Molecule 1: Probable short-chain dehydrogenase



- Molecule 1: Probable short-chain dehydrogenase







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.98 Å 107.92 Å 71.46 Å 90.00° 102.92° 90.00°	Depositor
Resolution (Å)	23.00 – 2.30 23.02 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.0 (23.00-2.30) 96.1 (23.02-2.30)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.84 (at 2.31 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.164 , 0.219 0.163 , 0.217	Depositor DCC
$R_{free}$ test set	2071 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.1	Xtriage
Anisotropy	0.108	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 38.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7384	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.51% 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: 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	0.52	0/1774	0.67	0/2407
1	B	0.53	0/1777	0.68	0/2410
1	C	0.51	0/1765	0.65	1/2395 (0.0%)
1	D	0.49	0/1766	0.69	1/2396 (0.0%)
All	All	0.51	0/7082	0.67	2/9608 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	137	LEU	CA-CB-CG	-5.56	102.52	115.30
1	C	57	LEU	CA-CB-CG	5.48	127.91	115.30

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	1737	0	1725	35	0
1	B	1743	0	1727	25	0
1	C	1734	0	1711	28	0
1	D	1735	0	1714	33	0
2	A	5	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
3	A	106	0	0	1	1
3	B	112	0	0	1	0
3	C	90	0	0	5	0
3	D	107	0	0	3	1
All	All	7384	0	6877	119	1

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 (119) 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:C:110:ASN:HD22	1:C:155:THR:HG21	1.21	1.04
1:D:110:ASN:HD22	1:D:155:THR:HG21	1.29	0.98
1:A:57:LEU:HD13	1:A:65:MSE:HE1	1.48	0.94
1:A:85:ASN:HD22	1:A:137[B]:LEU:HD22	1.37	0.90
1:A:211:ILE:HG21	1:A:216:ILE:HD11	1.52	0.90
1:C:173:THR:HG22	1:C:175:VAL:H	1.39	0.86
1:B:35:ARG:HH21	1:B:35:ARG:HG3	1.42	0.85
1:A:57:LEU:HD13	1:A:65:MSE:CE	2.09	0.81
1:C:170:LEU:O	1:C:173:THR:HB	1.84	0.77
1:A:57:LEU:CD1	1:A:65:MSE:HE1	2.15	0.76
1:C:36:GLU:OE1	1:C:56:THR:HG21	1.83	0.76
1:D:150:HIS:CD2	1:D:151:VAL:H	2.03	0.76
1:B:150:HIS:CD2	1:B:151:VAL:H	2.02	0.76
1:C:173:THR:HG23	1:C:175:VAL:HG23	1.68	0.75
1:C:110:ASN:ND2	1:C:155:THR:HG21	2.01	0.74
1:C:173:THR:CG2	1:C:175:VAL:HG23	2.17	0.74
1:B:36:GLU:OE1	1:B:56:THR:HG21	1.89	0.72
1:A:211:ILE:HG21	1:A:216:ILE:CD1	2.19	0.72
1:C:150:HIS:CD2	1:C:151:VAL:H	2.09	0.71
1:B:150:HIS:HD2	1:B:151:VAL:H	1.38	0.71
1:D:150:HIS:HD2	1:D:151:VAL:H	1.40	0.70
1:B:215:ASP:O	1:B:219:THR:HG22	1.91	0.69
1:A:36:GLU:HG3	1:A:56:THR:OG1	1.93	0.68
1:B:184:LEU:H	1:B:242:GLN:HE22	1.41	0.67
1:A:85:ASN:HD22	1:A:137[B]:LEU:CD2	2.06	0.67
1:A:211:ILE:CG2	1:A:216:ILE:CD1	2.73	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:110:ASN:ND2	1:D:155:THR:HG21	2.08	0.66
1:A:150:HIS:CD2	1:A:151:VAL:H	2.16	0.63
1:C:150:HIS:HD2	1:C:151:VAL:H	1.44	0.63
1:D:13:GLY:HA3	3:D:262:HOH:O	1.96	0.63
1:B:215:ASP:O	1:B:219:THR:CG2	2.47	0.62
1:A:93:ASP:O	1:A:150:HIS:HE1	1.83	0.62
1:D:118:THR:O	1:D:122:LEU:HB2	2.02	0.60
1:A:114:LEU:O	1:A:118:THR:CG2	2.51	0.59
1:A:59:VAL:HA	1:A:65:MSE:HE3	1.85	0.58
1:D:114:LEU:O	1:D:118:THR:HG23	2.03	0.58
1:A:35:ARG:HH21	1:A:38:ARG:HD3	1.68	0.57
1:D:114:LEU:O	1:D:118:THR:CG2	2.52	0.57
1:C:32:THR:CG2	3:C:288:HOH:O	2.54	0.56
1:D:215:ASP:O	1:D:219:THR:CG2	2.53	0.55
1:D:143:LYS:HE3	3:D:263:HOH:O	2.05	0.55
1:A:114:LEU:O	1:A:118:THR:HG23	2.06	0.55
1:A:150:HIS:HD2	1:A:151:VAL:H	1.53	0.55
1:C:110:ASN:HB3	1:C:155:THR:HG23	1.89	0.54
1:C:57:LEU:HD21	1:C:65:MSE:SE	2.58	0.53
1:B:93:ASP:O	1:B:150:HIS:HE1	1.91	0.53
1:D:139:SER:HB3	1:D:156:LYS:HG3	1.91	0.53
1:C:8:THR:HA	1:C:32:THR:HB	1.89	0.53
1:D:184:LEU:H	1:D:242:GLN:HE22	1.55	0.52
1:D:215:ASP:O	1:D:219:THR:HG23	2.08	0.52
1:A:11:THR:HG23	2:A:254:SO4:O3	2.09	0.52
1:D:50:THR:HG22	3:D:320:HOH:O	2.08	0.52
1:D:27:TRP:O	1:D:50:THR:HG21	2.09	0.52
1:C:187:SER:CB	1:C:213:PRO:HG3	2.39	0.51
1:D:103:TRP:CD2	1:D:151:VAL:HG21	2.46	0.51
1:C:135:VAL:HG11	1:C:220:ILE:HG12	1.93	0.51
1:D:2:SER:HB3	1:D:128:HIS:CD2	2.46	0.50
1:B:35:ARG:NH2	1:B:35:ARG:HG3	2.19	0.50
1:C:139:SER:HB3	1:C:156:LYS:HG3	1.93	0.50
1:A:139:SER:HB3	1:A:156:LYS:HG3	1.93	0.49
1:A:14:PHE:HZ	1:A:185[A]:CYS:HG	1.61	0.49
1:C:33:GLY:O	1:C:56:THR:HA	2.13	0.49
1:B:14:PHE:HD2	1:B:137:LEU:HD22	1.78	0.49
1:D:93:ASP:O	1:D:150:HIS:HE1	1.96	0.49
1:C:14:PHE:HZ	1:C:185:CYS:SG	2.36	0.48
1:C:36:GLU:O	1:C:40:GLN:HB2	2.12	0.48
1:D:14:PHE:HZ	1:D:185:CYS:HG	1.56	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:184:LEU:H	1:D:242:GLN:NE2	2.11	0.48
1:D:24:GLU:OE1	1:D:49:LYS:HE2	2.14	0.48
1:B:238:MSE:SE	1:D:233:ASN:HD21	2.47	0.47
1:A:222:TRP:CZ3	1:A:232:ILE:CD1	2.98	0.47
1:B:103:TRP:CD2	1:B:151:VAL:HG21	2.49	0.47
1:D:144:TRP:HA	1:D:145:PRO:HD3	1.83	0.47
1:A:103:TRP:CE3	1:B:115:LEU:HG	2.50	0.47
1:A:85:ASN:HD22	1:A:137[A]:LEU:HD13	1.80	0.47
1:B:184:LEU:H	1:B:242:GLN:NE2	2.10	0.47
1:D:13:GLY:C	1:D:15:GLY:N	2.65	0.47
1:A:11:THR:HA	3:A:356:HOH:O	2.15	0.46
1:B:5:LEU:HD11	1:B:83:ILE:HG13	1.98	0.46
1:A:114:LEU:O	1:A:118:THR:HG22	2.15	0.46
1:B:139:SER:HB3	1:B:156:LYS:HG3	1.98	0.46
1:C:122:LEU:O	1:C:126:ILE:HG12	2.15	0.46
1:D:216:ILE:O	1:D:220:ILE:HG13	2.15	0.45
1:B:44:GLY:O	1:B:47:SER:HB2	2.16	0.45
1:A:178:THR:HG21	1:A:223:ILE:HD13	1.98	0.45
1:B:8:THR:HG21	1:B:117:SER:OG	2.17	0.44
1:B:239:PRO:HD2	1:B:242:GLN:HE21	1.82	0.44
1:C:211:ILE:HG13	1:C:239:PRO:HD3	1.99	0.44
1:D:14:PHE:HZ	1:D:185:CYS:SG	2.40	0.44
1:D:14:PHE:HD2	1:D:137:LEU:HD22	1.81	0.44
1:A:211:ILE:CG2	1:A:216:ILE:HD12	2.46	0.43
1:A:93:ASP:O	1:A:150:HIS:CE1	2.69	0.43
1:D:179:ASN:O	1:D:234:SER:HA	2.18	0.43
1:A:168:CYS:O	1:A:171:GLN:NE2	2.50	0.43
1:D:2:SER:HB3	1:D:128:HIS:HD2	1.83	0.43
1:A:35:ARG:NH2	1:A:38:ARG:HD3	2.32	0.43
1:C:180:LEU:O	1:C:182:PRO:HD3	2.18	0.43
1:A:30:VAL:CG1	1:A:55:LEU:HD22	2.48	0.43
1:C:150:HIS:CD2	3:C:264:HOH:O	2.71	0.43
1:B:35:ARG:HE	1:B:38:ARG:HE	1.67	0.43
1:A:158:PHE:CD2	1:A:158:PHE:C	2.93	0.42
1:B:151:VAL:O	1:B:155:THR:HG23	2.19	0.42
1:D:122:LEU:HA	1:D:125:LEU:HD12	2.01	0.42
1:D:215:ASP:O	1:D:219:THR:HG22	2.18	0.42
1:A:171:GLN:HG2	3:C:306:HOH:O	2.19	0.42
1:B:93:ASP:HB3	3:B:302:HOH:O	2.19	0.42
1:C:173:THR:CG2	1:C:175:VAL:CG2	2.93	0.41
1:D:81:GLY:HA2	1:D:133:SER:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:32:THR:HG23	3:C:288:HOH:O	2.17	0.41
1:B:239:PRO:HD2	1:B:242:GLN:NE2	2.35	0.41
1:C:149:SER:O	1:C:150:HIS:C	2.59	0.41
1:C:32:THR:HG22	3:C:288:HOH:O	2.16	0.41
1:B:144:TRP:HA	1:B:145:PRO:HD3	1.87	0.41
1:A:14:PHE:H	1:A:85:ASN:HD21	1.68	0.41
1:A:57:LEU:HD13	1:A:65:MSE:HE2	1.97	0.41
1:B:35:ARG:NE	1:B:38:ARG:HE	2.19	0.40
1:A:14:PHE:HD2	1:A:137[B]:LEU:CD2	2.34	0.40
1:C:178:THR:HG21	1:C:223:ILE:HD13	2.03	0.40
1:D:114:LEU:O	1:D:118:THR:HG22	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:276:HOH:O	3:D:293:HOH:O[2_746]	2.17	0.03

## 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	227/272 (84%)	224 (99%)	2 (1%)	1 (0%)	34	42
1	B	227/272 (84%)	221 (97%)	5 (2%)	1 (0%)	34	42
1	C	226/272 (83%)	218 (96%)	7 (3%)	1 (0%)	34	42
1	D	226/272 (83%)	220 (97%)	5 (2%)	1 (0%)	34	42
All	All	906/1088 (83%)	883 (98%)	19 (2%)	4 (0%)	34	42

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	150	HIS
1	B	150	HIS
1	C	150	HIS
1	D	150	HIS

### 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	183/212 (86%)	172 (94%)	11 (6%)	19	26
1	B	183/212 (86%)	174 (95%)	9 (5%)	25	35
1	C	181/212 (85%)	174 (96%)	7 (4%)	32	46
1	D	182/212 (86%)	170 (93%)	12 (7%)	16	22
All	All	729/848 (86%)	690 (95%)	39 (5%)	23	31

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	THR
1	A	47	SER
1	A	55	LEU
1	A	75	GLU
1	A	93	ASP
1	A	118	THR
1	A	121	LEU
1	A	122	LEU
1	A	137[A]	LEU
1	A	137[B]	LEU
1	A	231	ASN
1	B	29	LEU
1	B	47	SER
1	B	115	LEU
1	B	117	SER
1	B	121	LEU
1	B	122	LEU
1	B	214	GLU

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Mol	Chain	Res	Type
1	B	219	THR
1	B	231	ASN
1	C	2	SER
1	C	37	GLU
1	C	40	GLN
1	C	56	THR
1	C	155	THR
1	C	171	GLN
1	C	173	THR
1	D	29	LEU
1	D	32	THR
1	D	47	SER
1	D	50	THR
1	D	55	LEU
1	D	92	THR
1	D	118	THR
1	D	137	LEU
1	D	155	THR
1	D	171	GLN
1	D	187	SER
1	D	219	THR

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

Mol	Chain	Res	Type
1	A	40	GLN
1	A	85	ASN
1	A	150	HIS
1	B	150	HIS
1	B	212	GLN
1	B	242	GLN
1	C	85	ASN
1	C	150	HIS
1	C	171	GLN
1	D	85	ASN
1	D	150	HIS
1	D	171	GLN
1	D	209	HIS
1	D	212	GLN
1	D	242	GLN



### 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

4 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	$\# Z  > 2$
2	SO4	C	254	-	4,4,4	0.20	0	6,6,6	0.15	0
2	SO4	A	254	-	4,4,4	0.25	0	6,6,6	0.26	0
2	SO4	D	254	-	4,4,4	0.16	0	6,6,6	0.39	0
2	SO4	B	254	-	4,4,4	0.17	0	6,6,6	0.35	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	254	SO4	1	0

## 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	225/272 (82%)	-0.19	8 (3%) 42 49	21, 24, 30, 34	0
1	B	226/272 (83%)	-0.12	6 (2%) 54 62	21, 24, 30, 44	0
1	C	226/272 (83%)	-0.03	9 (3%) 38 45	21, 24, 31, 38	0
1	D	226/272 (83%)	-0.10	6 (2%) 54 62	19, 24, 31, 42	0
All	All	903/1088 (82%)	-0.11	29 (3%) 47 54	19, 24, 31, 44	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	187	SER	5.3
1	D	2	SER	4.6
1	C	92	THR	4.5
1	B	92	THR	4.4
1	A	2	SER	4.2
1	B	207	GLY	3.9
1	B	251	ARG	3.7
1	C	12	SER	3.5
1	A	12	SER	3.4
1	D	74	GLU	3.3
1	D	187	SER	3.2
1	C	13	GLY	3.2
1	B	93	ASP	3.2
1	D	12	SER	3.1
1	B	91	GLY	3.1
1	A	67	ALA	2.7
1	D	71	ASN	2.5
1	C	2	SER	2.4
1	B	48	ALA	2.4
1	C	38	ARG	2.4
1	A	13	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	71	ASN	2.3
1	C	186	GLU	2.3
1	A	71	ASN	2.3
1	A	172	GLY	2.2
1	A	92	THR	2.2
1	A	207	GLY	2.1
1	C	93	ASP	2.0
1	D	78	THR	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, 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( $\text{\AA}^2$ )	Q<0.9
2	SO4	B	254	5/5	0.90	0.23	27,28,29,29	5
2	SO4	C	254	5/5	0.97	0.15	40,41,42,43	0
2	SO4	D	254	5/5	0.99	0.12	25,25,27,28	0
2	SO4	A	254	5/5	0.99	0.13	25,25,28,29	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.